(19) 世界知的所有権機関
国際事務局

(71) 出願人 (米国を除く全ての指定国について): 萬有製薬株式会社 (BANYU PHARMACEUTICAL CO., LTD.) [JP/JP]; 〒103-8416 東京都 中央区 日本橋本町 2 丁目 2 番 3 号 Tokyo (JP).

(72) 発明者; および
(75) 発明者/出願人 (米国についてのみ): 鎌田 健司 (KAMATA,Kenji) [JP/JP]; 〒300-2611 茨城県 つくば市 大久保 3 番 萬有製薬株式会社 つくば研究所内 Ibaraki (JP). 長田 安史 (NAGATA,Yasufumi) [JP/JP]; 〒300-2611 茨城県 つくば市 大久保 3 番 萬有製薬株式会社 つくば研究所内 Ibaraki (JP). 岩間 年治 (IWAMA,Toshiharu) [JP/JP]; 〒300-2611 茨城県 つくば市 大久保 3 番 萬有製薬株式会社 つくば研究所内 Ibaraki (JP).

(74) 代理人: 小林 浩, 外(KOBAYASHI,Hiroshi et al.); 〒104-0028 東京都 中央区 八重洲 2 丁目 8 番 7 号 福岡ビル 9 階 Tokyo (JP).

(54) Title: CRYSTAL OF GLUCOKINASE PROTEIN, AND METHOD FOR DRUG DESIGN USING THE CRYSTAL

(54) 発明の名称: グルコキナーゼタンパク質の結晶、及びその結晶を用いたドラッグデザイン方法

(57) Abstract: Glucokinase is crystallized, the three-dimensional structure thereof is analyzed, and then a compound to be bonded to glucokinase is designed on the basis of the coordinate for the resulting three-dimensional structure. Specifically, glucokinase is freed of a part of amino acid residues being on the N-terminal side thereof, to thereby crystallize it, and the three-dimensional structure of the resulting crystal is elucidated through the X-ray crystallographic analysis thereof.

(57) 要約: 本発明は、グルコキナーゼを結晶化し、その三次元構造を解析し、得られる三次元構造座標に基づいてグルコキナーゼに結合する化合物を設計する。 具体的には、グルコキナーゼのN末端側のアミノ酸残基の一部を欠失させることによってグルコキナーゼを結晶化し、この結晶についてX線結晶構造解析によってその三次元構造を解明することによって達成される。

- 1 -

明細書

グルコキナーゼタンパク質の結晶、及びその結晶を用いたドラッグデザイン方法

5　技術分野

　本発明は、新規なグルコキナーゼタンパク質（以下、「GKタンパク質」ともいう）の結晶、その結晶を用いて得られる三次元構造座標を用いたドラッグデザイン方法などに関する。

10　背景技術

　グルコキナーゼ（ATP：D-hexose 6-phosphotransferaze，EC2.7.1.1）は、哺乳類の4種のヘキソキナーゼアイソザイムのうちの一つ（ヘキソキナーゼIV）である。これらのアイソザイムは同じ反応を触媒するが、グルコースに対する Km 値に差がある。すなわち、

15　ヘキソキナーゼI、II、IIIのKm値は $10^{-6}$〜$10^{-4}$M であるのに対し、グルコキナーゼともよばれるヘキソキナーゼIVのグルコースに対するKm値はずっと大きく、約 $10^{-2}$M である。ヘキソキナーゼは、解糖系の初期段階に関与する酵素であり、グルコースからグルコース６リン酸への反応を触媒する。

　グルコキナーゼは、主に肝臓と膵臓ベータ細胞に発現が限局しており、それ

20　らの細胞におけるグルコース代謝の律速段階を制御することで、体全体の糖代謝に重要な役割を果たしている。肝臓と膵臓ベータ細胞のグルコキナーゼは、それぞれスプライシングの違いによりN末端の１５アミノ酸の配列が異なっているが、酵素学的性質は同一である。

　１０年ほど前から、グルコキナーゼは膵臓ベータ細胞や肝臓のグルコースセ

25　ンサーとして働くという仮説が提唱されている（Garfinkel D, et al: Am J Physiol 247(3Pt2):R527-536, 1984）。最近のグルコキナーゼ遺伝子操作マウスの結果から、実際にグルコキナーゼは全身のグルコース恒常性に重要な役割を担うことが明らかになっている。

　グルコキナーゼ遺伝子を破壊したマウスは、生後まもなく糖尿病で死亡する

- 2 -

(Grupe A, et al: Cell 83:69-78. 1995)。一方、グルコキナーゼを過剰発現
させたマウスは血糖値が低くなる (Ferre T, et al: Proc Natl Acad Sci U S
A 93:7225-7230. 1996)。グルコース濃度上昇によってグルコキナーゼ活性が
上昇すると、膵臓ベータ細胞と肝細胞の反応は異なるが、いずれも血糖を低下
5    させる方向に作用する。膵臓ベータ細胞は、より多くのインスリンを分泌する
ようになり、肝臓は糖を取り込みグリコーゲンとして貯蔵すると同時に糖放出
を低下させる。

　　このようにグルコキナーゼ酵素活性の変動は、肝臓および膵臓ベータ細胞を
介した哺乳類のグルコースホメオスタシスにおいて重要な役割を果たしている。
10   MODY2 (maturity-onset diabetes of th
e young) と呼ばれる若年に糖尿病を発症する症例においてグルコキナ
ーゼ遺伝子の突然変異が発見され、グルコキナーゼ活性の低下が血糖上昇の原
因となっている (Vionnet N, et al: Nature 356:721-722, 1992)。一方グル
コキナーゼ活性を上昇させる突然変異をもつ家系も見つかっており、このよう
15   な人たちは低血糖症状を示す (Glaser B , et al: N Engl J Med 338: 226-
230, 1998)。

　　以上より、グルコキナーゼはヒトにおいてもグルコースセンサーとして働き、
グルコース恒常性に重要な役割を果たしている。一方、多くのII型糖尿病患
者のグルコキナーゼは変位を受けていないので、グルコキナーゼセンサーシス
20   テムを利用した血糖調節は可能と考えられる。グルコキナーゼ活性化物質には
膵臓ベータ細胞のインスリン分泌促進作用と肝臓の糖取り込み亢進および糖放
出抑制作用が期待できるので、II型糖尿病患者の治療薬として有用と考えら
れる。

　　近年、膵臓ベータ細胞型グルコキナーゼが、ラット脳、なかでも特に摂食中
25   枢である視床下部腹内側核 (Ventromedial hypothala
mus, VMH) に限局して発現していることが明らかにされた。VMHの約
2割の神経細胞は、グルコースレスポンシブニューロンと呼ばれ、従来から体
重コントロールに重要な役割を果たすと考えられてきた。ラットの脳内へグル
コースを投与すると摂食量が低下するのに対して、グルコース類縁体のグルコ

- 3 -

サミンの脳内投与によってグルコース代謝を抑制すると過食となる。電気生理
学的実験からグルコースレスポンシブニューロンは生理的なグルコース濃度変
化（5－20mM）に呼応して活性化されるがグルコサミン等でグルコース代
謝を抑制すると活性抑制が認められる。VMHのグルコース濃度感知システム
には膵臓ベータ細胞のインスリン分泌と同様なグルコキナーゼを介したメカニ
ズムが想定されている。従って肝臓、膵臓ベータ細胞に加えVHMのグルコキ
ナーゼ活性化を行う物質には血糖是正効果のみならず、多くのII型糖尿病患
者で問題となっている肥満をも是正できる可能性がある。

　一方、DIABETES, vol. 48, 1698-1705, September 1999にはヘキソキナー
ゼIからグルコキナーゼの立体構造を予測した旨が記載されているが、実際に
結晶化はされていないし、実用的なものではなかった。

　以上より、グルコキナーゼの三次元立体構造を明らかにし、グルコキナーゼ
と相互作用する化合物を効率的に見いだすことを可能にすることは、例えば、
糖尿病の治療剤、又は予防剤；網膜症、腎症、神経症、虚血性心疾患、動脈硬
化等の糖尿病の慢性合併症の治療剤、又は予防剤；肥満の治療剤、又は予防剤
の開発に大きな進展をもたらすと考えられる。

　現在ではタンパク質の活性中心の解析や反応機作の予測といった作業にコン
ピュータを利用したCARDD(Computer Aided Rational Drug Design)が実
用的なレベルで活用されるようになっている。

　CARDDによる創薬システムにおいては、ターゲットとなるタンパク質の
3次元構造解析データに基づき、タンパク質の活性部位の構造が予測される。
そして、その活性部位の構造と結合し得る化合物の候補に関する情報が化合物
データベースから取得される。その後、ターゲットとなるタンパク質の活性部
位と候補化合物の3次元構造や物理的性質を考慮し、ターゲットとなるタンパ
ク質に結合しうる化合物の候補を選択する。これらの工程が、いわゆるインシ
リコスクリーニング工程である。

　インシリコスクリーニング工程で選択された化合物が、ターゲットとなるタ
ンパク質と結合し、その活性を変化させるかどうかは、実際の試験（ウエット
実験）により調べられる。そして、実際にターゲットとなるタンパク質の活性

- 4 -

を変化させる化合物が医薬の有効成分となる。これにより、実験室で無数の化合物を標的タンパク質に一つ一つ作用させて相互作用を確認するという操作を行うことなく、標的タンパク質と相互作用する化合物を効率よく探し出される。

　インシリコスクリーニングは、ターゲットとなるタンパク質と結合する化合物の候補を大幅に絞ることができるため医薬品開発に有効な手段であるといえる。

　CARDDによる創薬システムにおいては、ターゲットとなるタンパク質のX線構造解析による3次元構造解析データが重要な情報となる。X線構造解析による3次元構造解析には、解析試料としてターゲットとなるタンパク質の結晶が必要である。したがってCARDDによる創薬システムに基づいてGKに関連する創薬の開発を進めるためには、GKの結晶が必要である。しかしながら、前述のとおりGKは結晶化が困難で、CARDDに必要な情報を与えうるものではなかった。

　本発明は、上記従来技術の有する課題に鑑みてなされたものであり、グルコキナーゼの結晶を得ること、及び、当該結晶から得られた情報に基づいてグルコキナーゼに結合する化合物を設計することを目的とする。


発明の開示

　上記目的の少なくともひとつ以上は、以下の発明により解決される。

　［1］結晶化に用いることを特徴とする、グルコキナーゼタンパク質。

　［2］配列番号5に記載のアミノ酸配列からなることを特徴とする、前記［1］に記載のタンパク質。

　［3］配列番号5に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列からなることを特徴とするタンパク質の結晶。

　［4］前記タンパク質がグルコキナーゼタンパク質である、前記［3］に記載の結晶。

　［5］配列番号5に記載のアミノ酸配列を有するタンパク質の結晶である、前記［3］に記載の結晶。

- 5 -

　　　［６］格子定数が、下記式（１）～（４）

　a＝b＝79.9±4オングストローム　…（１）

　c＝322.2±15オングストローム　…（２）

　$\alpha = \beta = 90°$　…（３）

　$\gamma = 120°$　…（４）

を満たす、前記［３］に記載の結晶。

　　　［７］空間群がP6₅22である、前記［６］に記載の結晶。

　　　［８］表１に記載の三次元構造座標データによって特定されるタンパク質の結晶。

　　　［９］表１に記載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座標データにおいて、表１に記載の三次元構造座標データで示されるアミノ酸の主鎖の原子（Ｃα原子）と、該Ｃα原子と対応する前記変更した三次元構造座標データで示されるＣα原子との平均二乗偏差が、０．６オングストローム以下である結晶。

　　　［１０］化合物結合部位が、配列番号５に示すアミノ酸配列における、チロシン６１～セリン６９、グルタミン酸９６～グルタミン９８、イソロイシン１５９、メチオニン２１０～チロシン２１５、ヒスチジン２１８～グルタミン酸２２１、メチオニン２３５、アルギニン２５０、ロイシン４５１～リジン４５９のアミノ酸残基の少なくともひとつによって構成される、［３］～［９］のいずれかに記載の結晶。

　　　［１１］配列番号５に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列からなるタンパク質と該タンパク質に結合可能な化合物との複合体を含む結晶。

　　　［１２］前記化合物が、式（Ｉ）で表される、前記［１１］に記載の結晶。

- 6 -
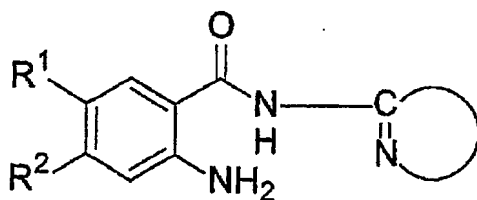


(I)

[式中、R¹は、ハロゲン原子、－S－(O)p－A、－S－(O)q－B又は－O
－Bを示し（ここで、p及びqは同一又は異なって、0～2の整数を示し、A
は置換されていてもよい直鎖の$C_1$－$C_6$アルキル基を示し、Bは置換されてい
5　てもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、
R²は水素原子又はハロゲン原子を示し、



(II)
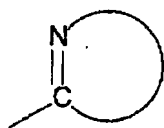
は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていても
10　よい単環の又は双環のヘテロアリール基を示す]

　　[１３] 前記化合物が、式(IIIa)～式(IIIc)で表されるいずれかの化合
物である前記[１２]に記載の結晶。
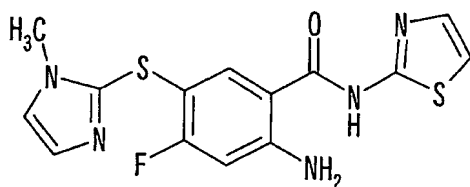


(IIIa)

- 7 -
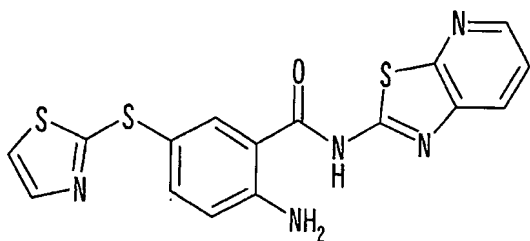


(IIIb)
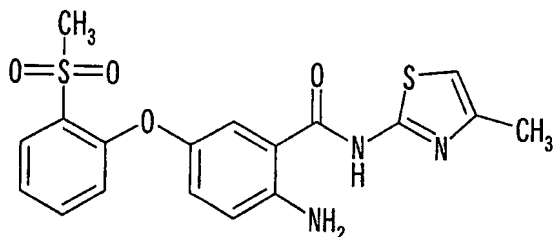


(IIIc)

5

　[１４]　　配列番号８に記載のアミノ酸配列からなることを特徴とする、前記
[１]に記載のタンパク質。

　[１５]　　配列番号８に記載のアミノ酸配列又はそのアミノ酸配列と実質的に
同一のアミノ酸配列からなることを特徴とするタンパク質の結晶。

10　[１６]　　前記タンパク質がグルコキナーゼタンパク質である、前記[１５]
に記載の結晶。

　[１７]　　配列番号８に記載のアミノ酸配列を有するタンパク質の結晶である、
前記[１５]に記載の結晶。

　[１８]　　格子定数が、下記式

15　a=b=103.2±5 オングストローム　…（５）

　c=281.0±7 オングストローム　…（６）

　$\alpha=\beta=90°$　…（７）

　$\gamma=120°$　…（８）

を満たす、前記[１５]に記載の結晶。

20　[１９]　　空間群が $P6_522$ である、前記[１８]に記載の結晶。

- 8 -

［２０］　表２に記載の三次元構造座標データによって特定されるタンパク質の結晶。

［２１］　表２に記載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座標データにおいて、表２に記載の三次元構造座標データで示されるアミノ酸の主鎖の原子（Ｃα原子）と、該Ｃα原子と対応する前記変更した三次元構造座標データで示されるＣα原子との平均二乗偏差が、０．６オングストローム以下である結晶。

［２２］　配列番号２に記載のアミノ酸配列を有するタンパク質のＮ末端、Ｃ末端のいずれかまたは両方から、１～５０個のアミノ酸残基を欠損したアミノ酸配列を有するタンパク質を製造するタンパク質製造工程と、

前記タンパク質製造工程で得られたタンパク質と結合する化合物と、前記タンパク質製造工程で得られたタンパク質とを反応させるタンパク質反応工程とを含む、

タンパク質及びそのタンパク質と結合する化合物の複合体を含む結晶の製造方法。

［２３］　タンパク質の結晶を製造する方法であって、

配列番号５に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含みグルコキナーゼ活性を有するタンパク質、及び該タンパク質に結合可能な化合物を用いることを特徴とする、結晶の製造方法。

［２４］　前記タンパク質に結合可能な化合物が、式（Ｉ）で表される化合物であることを特徴とする、前記［２３］に記載のタンパク質の結晶の製造方法。
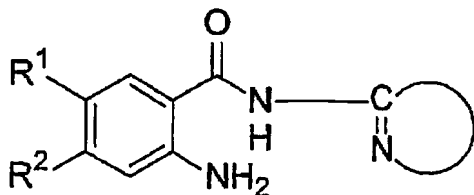


(I)

- 9 -

[式中、R¹は、ハロゲン原子、－S－(O)p－A、－S－(O)q－B又は－O
－Bを示し（ここで、p及びqは同一又は異なって、0～2の整数を示し、A
は置換されていてもよい直鎖のC₁－C₆アルキル基を示し、Bは置換されてい
てもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、

R²は水素原子又はハロゲン原子を示し、

(II)
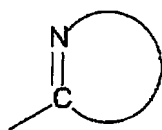
は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていても
よい単環の又は双環のヘテロアリール基を示す）

[25] 共結晶法又はソーキング法による、前記［23］、又は［24］に
記載の結晶の製造方法。

[26] タンパク質の立体構造情報に基づいて該タンパク質に結合する化合
物の構造をデザインするドラッグデザイン方法であって、

該タンパク質の立体構造情報が、前記［3］～［13］、又は［15］～［2
1］のうちのいずれか一項に記載の結晶を解析することによって得られる情報
であることを特徴とする、ドラッグデザイン方法。

[27] 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を
推測する結合部位推測工程と、

前記結合部位推測工程で推測された化合物結合部位に適合する化合物を、化合
物ライブラリより選択する選択工程と、

を含むことを特徴とする、前記［26］に記載のドラッグデザイン方法。

[28] 前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を
推測する結合部位推測工程と、

前記結合部位推測工程で推測された化合物結合部位に適合する化合物の構造を
構築する化合物構造構築工程と、

を含むことを特徴とする、前記［26］に記載のドラッグデザイン方法。

- 10 -

［２９］　前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

前記結合部位推測工程で推測された化合物結合部位と該化合物結合部位に適合する化合物とが相互作用するように化合物の構造を目視によりデザインするデ

5 　ザイン工程と、

を含むことを特徴とする、前記［２６］に記載のドラッグデザイン方法。

［３０］　前記化合物結合部位が、配列番号５に示すアミノ酸配列における、チロシン６１〜セリン６９、グルタミン酸９６〜グルタミン９８、イソロイシン１５９、メチオニン２１０〜チロシン２１５、ヒスチジン２１８〜グルタミ

10 　ン酸２２１、メチオニン２３５、アルギニン２５０、ロイシン４５１〜リジン４５９のアミノ酸残基の少なくともひとつによって構成されている、前記［２６］〜［２９］のうちのいずれか一項に記載のドラッグデザイン方法。

［３１］　さらに、前記化合物結合部位に適合すると推定される候補化合物の生理活性を測定する工程を含む、前記［２６］〜［３０］のいずれか一項に記

15 　載のドラッグデザイン方法。

［３２］　さらに、前記化合物結合部位に適合すると推定される候補化合物と、配列番号５に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質とを接触させ、その候補化合物が該タンパク質に結合するか否か判定する結合判定工程を含む、前記［２６］〜［３０］のいずれ

20 　か一項に記載のドラッグデザイン方法。

［３３］　前記［２６］〜［３０］のいずれか一項に記載のドラッグデザイン方法によって選択された化合物群を化合物アレイとして組み合わせることを含む化合物アレイの製造方法。


25 　　図面の簡単な説明

図１は、グルコキナーゼの三次元構造を示すリボン図である。

（図１ａは、グルコキナーゼ（Δ１−１１）／グルコース／化合物１（式IIIaの化合物）の構造を示すリボン図である。また、右図は、左図を回転した図である。）

- 11 -

（図１ｂは、グルコキナーゼ(Δ１－１５)単体の構造を示すリボン図である。
また、右図は、左図を回転した図である。）

　　　図２は、グルコキナーゼ(Δ１－１１)の結合部位に対する化合物１（式
IIIaの化合物）の結合様式を示す図である。

　　　図３は、グルコキナーゼ(Δ１－１１)の結合部位の構造を示す図である。


発明を実施するための最良の形態

　　本明細書において、アミノ酸、ペプチド、蛋白質は下記に示すＩＵＰＡＣ－
ＩＵＢ生化学命名委員会（ＣＢＮ）で採用された略号を用いて表される。また、
特に明示しない限りペプチド及び蛋白質のアミノ酸残基の配列は、左端から右
端にかけてＮ末端からＣ末端となるように、またＮ末端が１番になるように表
される。

　　以下、本発明の各実施態様について詳細に説明する。


（グルコキナーゼタンパク質）

　　まず、本発明は、結晶化に用いることを特徴とする、グルコキナーゼタンパ
ク質を提供する。グルコキナーゼタンパク質（ＧＫタンパク質）は、上述のよ
うに、生体内で極めて重要な糖の代謝に関与している。したがって、ＧＫタン
パク質の三次元構造を明らかにし、ＧＫタンパク質の活性部位を解明すること
によって、ＧＫタンパク質に結合する化合物（すなわち、活性化剤又は阻害
剤）を探索することができる。よって、ＧＫタンパク質の三次元構造を明らか
にすることは重要である。

　　タンパク質の３次元構造を明らかにする手法として、Ｘ線結晶構造解析が良
く知られている。即ち、タンパク質を結晶化し、その結晶に単色化されたＸ線
をあて、得られたＸ線の回折像をもとに、該タンパク質の３次元構造を解明す
る（Ｂｌｕｎｄｅｌｌ，Ｔ．Ｌ．及びＪｏｈｎｓｏｎ，Ｌ．Ｎ．，ＰＲＯＴ
ＥＩＮ　ＣＲＹＳＴＡＬＬＯＧＲＡＰＨＹ，１－５６５頁，（１９７６）Ａｃ
ａｄｅｍｉｃ　Ｐｒｅｓｓ，Ｎｅｗ　Ｙｏｒｋ）。ＧＫタンパク質のＸ線結晶
構造解析に供するために、まず、ＧＫタンパク質を結晶化する必要がある。

- 12 -

　ここで、本発明の「GKタンパク質」とは、配列番号2に示すアミノ酸配列を有するヒト由来の肝臓型グルコキナーゼと、配列番号2と実質的に同一のアミノ酸配列を含有するタンパク質をいう。ここで当該実質的に同一のアミノ酸配列を含有するタンパク質としては、グルコキナーゼ活性を有するものが好ましい。したがって、本明細書では、GKタンパク質は、ヒト由来の肝臓型グルコキナーゼのみならず、ヒト由来の膵臓型グルコキナーゼ、マウス、ラット、サル等の非ヒト由来GKタンパク質をも含む。本発明では、ヒト肝臓型グルコキナーゼが好ましく用いられる。ヒト由来のグルコキナーゼにおいて、肝臓型と膵臓型ではN末端の15アミノ酸残基が相違する。ここで、「グルコキナーゼ活性」とは、グルコースからグルコース6リン酸への反応を触媒する活性をいう。

　タンパク質の結晶化が一般的に困難なことは良く知られており、GKタンパク質をそのまま結晶化することはできなかった。本発明者らは、種々、試行錯誤による実験の結果、GKタンパク質のN末端側のアミノ酸を11個、又は15個を欠失させることによって、始めてGKタンパク質の結晶化に成功した。欠失させた領域は、結晶化を試みた際に球状のGKタンパク質分子より突出し、その結果、結晶内で隣接するGKタンパク質分子との間で立体的な障害となりGKタンパク質が結晶となるのを妨げていたと考えられる。すなわち、本発明では、アミノ酸配列が既知でありながら結晶化には成功していなかったグルコキナーゼにおいて、N末端側の11個のアミノ酸残基を欠失させたGKタンパク質（配列番号5）、又はN末端側の15個のアミノ酸残基を欠失させたGKタンパク質（配列番号8）を用いることにより、GKタンパク質の結晶を得た。ただし、欠失させるアミノ酸は、隣接する結晶との間で立体的な障害がなくなる範囲であればその数は限定されない。具体的には、例えば、配列番号2で表されるアミノ酸配列において、N末端側の1～50個、好ましくは3～30個、より好ましくは5～25個、さらに好ましくは8～18個、特に好ましくは11～15個のアミノ酸残基を欠失させたアミノ酸配列などが本発明において用いられる。また、C末端側の1～8個、好ましくは1～7個、より好ましくは2～6個のアミノ酸残基を欠失させたアミノ酸配列などが本発明において用い

- 13 -

られる。


（グルコキナーゼタンパク質の結晶及びその製造方法）

　　　次に、本発明においては、配列番号５、及び配列番号８に記載のアミノ酸配
5　　列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質を含
　　む結晶を提供する。

　　　上述したように、結晶化に供するＧＫタンパク質としては、配列番号５、及び
　　／又は配列番号８で表されるアミノ酸配列又はそれと実質的に同一のアミノ酸
　　配列を含むタンパク質などが用いられる。

10　　配列番号５、及び／又は配列番号８で表されるアミノ酸配列又はそれと実質
　　的に同一のアミノ酸配列を含むタンパク質（以下、配列番号２で表されるアミ
　　ノ酸配列又はそれと実質的に同一のアミノ酸配列を有するタンパク質と併せて
　　「ＧＫタンパク質」と略すこともある）は、結晶化が可能であればよく、その
　　アミノ酸配列は特に制限されない。ここで、配列番号５、及び／又は配列番号

15　　８に記載のアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質は、
　　グルコキナーゼ活性を有している必要はなく、ドラッグデザインに必要な情報
　　を得ることができる結晶構造を有するものであれば、不活性な変異体（例えば、
　　ＡＴＰの結合部位に変異を有することにより不活性化した変異体）であっても
　　よい。ここで、配列番号２又は５で表されるアミノ酸配列と実質的に同一のアミ

20　　ノ酸配列を含むタンパク質としては、配列番号２又は５で表わされるアミノ酸
　　配列と約６０％以上、好ましくは約７０％以上、さらに好ましくは約８０％以
　　上、なかでも好ましくは約９０％以上、最も好ましくは約９５％以上の相同性
　　を有するアミノ酸配列などが挙げられる。また、配列番号２又は５で表される
　　アミノ酸配列と実質的に同一のアミノ酸配列を含むタンパク質として、例えば、

25　　配列番号２又は５に記載のアミノ酸配列において１～１０個、好ましくは１～
　　５個、さらに好ましくは１～３個、さらに好ましくは１～２個のアミノ酸残基
　　が置換、欠失、付加および／または挿入されたアミノ酸配列が例示される。

　　　ＧＫタンパク質の３次元構造解析は、例えば、次のようにして行う。まず、
　　タンパク質を精製する。そして、結晶化、Ｘ線回折強度データ収集、各回折斑

- 14 -

点の位相決定、電子密度計算、分子モデル作成、構造の精密化などの一連の工
程を行う。タンパク質構造解析を行うための主要な設備として、結晶化用イン
キュベーター、双眼顕微鏡、X線回折計、3次元コンピュータグラフィックス
装置などが用いられる。具体的にタンパク質の結晶を作製する実験過程は、タ
5  ンパク質を大量に（数mg以上が好ましい。）精製する段階、結晶が得られる条
件を広く検索する段階、X線解析に適した良質の結晶を得る段階に分けられる。
以下、各工程について具体的に説明する。

　　結晶化に際しては、GKタンパク質を、高純度に精製する。精製方法として
は、公知のものが利用でき、例えば、カラムクロマトグラフィー、塩析、遠心
10 分離などが用いられる。

　　精製されたGKタンパク質は、結晶化し、X線結晶構造解析のための試料と
する。結晶化は、蒸気拡散法や透析法等の公知の方法に基づいて行われる。タ
ンパク質の結晶を得る際に、タンパク質の純度・濃度、温度、pH、使用する沈
殿剤濃度等多くの要素を検討する必要がある。結晶化条件の検討は、市販のス
15 クリーニング試薬を使用して広い範囲で行うことができ、1つの条件に1〜
2％濃度のタンパク質溶液を1〜2μLずつ使用して検索することが好ましい。
こうして微結晶などが得られた場合には、さらに条件を精密化することが好ま
しい。

　　なお、GKタンパク質の結晶を得るためには非常に多くの条件を検索しなけれ
20 ばならない。従って、結晶化条件の検討のためにも、タンパク質の大量発現系
を構築することが好ましい。一般にタンパク質のうち、結晶になるものの多く
は、溶液状態で単分散であり、多分散のものは大体において結晶化しない。そ
こで、GKタンパク質のN末端を順次切除し、得られたタンパク質について、光
散乱装置を用いてタンパク質溶液の単分散性を判定し、試料が結晶化に適して
25 いるかどうかを検討しても良い。

　　次に，得られたGKタンパク質の結晶を用いて、X線回折強度測定を行う。
最近では、結晶を細い糸の輪などですくって液体窒素温度に急速冷却してその
まま低温で測定する方法も利用されている。回折X線の強度測定は、通常、イ
メージングプレートなどの2次元検出器によって行う。X線を当てながら結晶

- 15 -

を回転させることで発生する多くの回折線をイメージングプレートに記録し、記録された回折強度をレーザーを当てることにより読み取る。

次に、重原子ソーキング法や共結晶化法により重原子同型置換体を調製することが好ましい。これを使用して多重同型置換法（MIR法）によりタンパク質
5 結晶の位相を決定することができる。重原子を導入する代わりに、複雑な波長のX線による回折強度データに基づいて位相を決定する多波長異常散乱法（MAD法）も利用できる。類似構造を有する分子が既に解析されている場合には、その分子構造を結晶中にあてはめて初期構造を得ることができ、これをもとにフーリエ合成図を描き、残りの部分の構造を解明して全構造を決定する分
10 子置換法（MR法）も知られている。

位相が上記の方法で決定したならば、これより電子密度を求める。この精度は、反射の数（分解能）と使用した反射の精度による。分解能は使用する反射の最小面間隔で表す。この電子密度図から分子モデルを組み立てる。分子モデルを組み立てると原子座標が得られるので、これより構造因子の計算値を求め、
15 この大きさを観測値に近づける最小自乗法により原子パラメータの精密化を行う。このようにしてできるだけ妥当な構造情報を取得する。

本発明においては、配列番号5に示すGKタンパク質の結晶を調製することに成功している（後述の実施例参照）。そしてこのようにして得られたGKタンパク質の結晶は、格子定数が、下記式（1）〜（4）：
20 　　a=b=79.9±4オングストローム　…（1）
　　c=322.2±15オングストローム　…（2）
　　$\alpha=\beta=90°$　…（3）
　　$\gamma=120°$　…（4）
を満たすものであった。また、この結晶は、空間群が$P6_522$であることが解明さ
25 れた。ここで、前記a=bは79.9±3オングストロームであることが好ましく、79.9±2オングストロームであることがより好ましく、79.9±1オングストロームであることがさらに好ましい。また、前記cは322.2±10オングストロームであることが好ましく、322.2±8オングストロームであることがより好ましく、322.2±5オングストロームであることがさらに好ましい。

- 16 -

このようにして得られたGKタンパク質結晶の3次元構造座標を表1に示す。


表1

|  | ATOM | 1 | CB | THR | 14 | 25.972 | -34.025 | 76.567 | 1.00 | 51.12 |
|---|---|---|---|---|---|---|---|---|---|---|
| 5 | ATOM | 2 | OG1 | THR | 14 | 27.398 | -34.012 | 76.715 | 1.00 | 51.49 |
|  | ATOM | 3 | CG2 | THR | 14 | 25.626 | -34.173 | 75.095 | 1.00 | 49.96 |
|  | ATOM | 4 | C | THR | 14 | 24.138 | -32.317 | 76.374 | 1.00 | 50.95 |
|  | ATOM | 5 | O | THR | 14 | 24.246 | -31.685 | 75.330 | 1.00 | 52.42 |
|  | ATOM | 6 | N | THR | 14 | 25.108 | -32.861 | 78.611 | 1.00 | 51.41 |
| 10 | ATOM | 7 | CA | THR | 14 | 25.384 | -32.717 | 77.154 | 1.00 | 50.49 |
|  | ATOM | 8 | N | LEU | 15 | 22.957 | -32.673 | 76.871 | 1.00 | 49.75 |
|  | ATOM | 9 | CA | LEU | 15 | 21.733 | -32.307 | 76.167 | 1.00 | 49.25 |
|  | ATOM | 10 | CB | LEU | 15 | 20.496 | -32.824 | 76.904 | 1.00 | 52.56 |
|  | ATOM | 11 | CG | LEU | 15 | 20.439 | -34.307 | 77.291 | 1.00 | 55.08 |
| 15 | ATOM | 12 | CD1 | LEU | 15 | 21.186 | -34.524 | 78.610 | 1.00 | 53.67 |
|  | ATOM | 13 | CD2 | LEU | 15 | 18.980 | -34.742 | 77.438 | 1.00 | 54.84 |
|  | ATOM | 14 | C | LEU | 15 | 21.676 | -30.781 | 76.078 | 1.00 | 48.68 |
|  | ATOM | 15 | O | LEU | 15 | 21.397 | -30.208 | 75.023 | 1.00 | 47.52 |
|  | ATOM | 16 | N | VAL | 16 | 21.955 | -30.128 | 77.201 | 1.00 | 47.07 |
| 20 | ATOM | 17 | CA | VAL | 16 | 21.950 | -28.677 | 77.265 | 1.00 | 44.96 |
|  | ATOM | 18 | CB | VAL | 16 | 21.988 | -28.188 | 78.733 | 1.00 | 46.09 |
|  | ATOM | 19 | CG1 | VAL | 16 | 22.239 | -26.684 | 78.784 | 1.00 | 44.09 |
|  | ATOM | 20 | CG2 | VAL | 16 | 20.670 | -28.523 | 79.418 | 1.00 | 45.38 |
|  | ATOM | 21 | C | VAL | 16 | 23.142 | -28.097 | 76.512 | 1.00 | 43.58 |
| 25 | ATOM | 22 | O | VAL | 16 | 23.004 | -27.110 | 75.790 | 1.00 | 41.54 |
|  | ATOM | 23 | N | GLU | 17 | 24.310 | -28.712 | 76.672 | 1.00 | 43.48 |
|  | ATOM | 24 | CA | GLU | 17 | 25.507 | -28.223 | 75.998 | 1.00 | 45.62 |
|  | ATOM | 25 | CB | GLU | 17 | 26.759 | -28.931 | 76.532 | 1.00 | 46.30 |
|  | ATOM | 26 | CG | GLU | 17 | 27.140 | -28.571 | 77.984 | 1.00 | 49.19 |

- 17 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 27 | CD | GLU | 17 | 27.467 | -27.087 | 78.191 | 1.00 50.74 |
| | ATOM | 28 | OE1 | GLU | 17 | 28.238 | -26.520 | 77.386 | 1.00 50.39 |
| | ATOM | 29 | OE2 | GLU | 17 | 26.966 | -26.488 | 79.170 | 1.00 50.85 |
| | ATOM | 30 | C | GLU | 17 | 25.417 | -28.378 | 74.479 | 1.00 45.93 |
| 5 | ATOM | 31 | O | GLU | 17 | 26.097 | -27.666 | 73.735 | 1.00 44.10 |
| | ATOM | 32 | N | GLN | 18 | 24.577 | -29.303 | 74.020 | 1.00 45.41 |
| | ATOM | 33 | CA | GLN | 18 | 24.400 | -29.513 | 72.588 | 1.00 46.37 |
| | ATOM | 34 | CB | GLN | 18 | 23.643 | -30.818 | 72.307 | 1.00 49.99 |
| | ATOM | 35 | CG | GLN | 18 | 24.488 | -32.086 | 72.423 | 1.00 55.59 |
| 10 | ATOM | 36 | CD | GLN | 18 | 23.701 | -33.352 | 72.088 | 1.00 58.40 |
| | ATOM | 37 | OE1 | GLN | 18 | 23.158 | -33.489 | 70.988 | 1.00 60.78 |
| | ATOM | 38 | NE2 | GLN | 18 | 23.638 | -34.280 | 73.037 | 1.00 56.40 |
| | ATOM | 39 | C | GLN | 18 | 23.617 | -28.338 | 72.014 | 1.00 44.35 |
| | ATOM | 40 | O | GLN | 18 | 23.849 | -27.912 | 70.885 | 1.00 43.20 |
| 15 | ATOM | 41 | N | ILE | 19 | 22.677 | -27.821 | 72.791 | 1.00 41.97 |
| | ATOM | 42 | CA | ILE | 19 | 21.895 | -26.689 | 72.327 | 1.00 40.37 |
| | ATOM | 43 | CB | ILE | 19 | 20.631 | -26.500 | 73.193 | 1.00 39.71 |
| | ATOM | 44 | CG2 | ILE | 19 | 19.976 | -25.166 | 72.894 | 1.00 39.42 |
| | ATOM | 45 | CG1 | ILE | 19 | 19.653 | -27.653 | 72.915 | 1.00 40.83 |
| 20 | ATOM | 46 | CD1 | ILE | 19 | 18.356 | -27.599 | 73.719 | 1.00 38.38 |
| | ATOM | 47 | C | ILE | 19 | 22.764 | -25.431 | 72.344 | 1.00 39.01 |
| | ATOM | 48 | O | ILE | 19 | 22.746 | -24.644 | 71.394 | 1.00 40.12 |
| | ATOM | 49 | N | LEU | 20 | 23.550 | -25.267 | 73.404 | 1.00 35.38 |
| | ATOM | 50 | CA | LEU | 20 | 24.423 | -24.109 | 73.537 | 1.00 34.35 |
| 25 | ATOM | 51 | CB | LEU | 20 | 25.026 | -24.050 | 74.944 | 1.00 32.09 |
| | ATOM | 52 | CG | LEU | 20 | 24.050 | -23.887 | 76.106 | 1.00 30.92 |
| | ATOM | 53 | CD1 | LEU | 20 | 24.813 | -23.722 | 77.420 | 1.00 27.61 |
| | ATOM | 54 | CD2 | LEU | 20 | 23.171 | -22.689 | 75.843 | 1.00 29.31 |
| | ATOM | 55 | C | LEU | 20 | 25.555 | -24.135 | 72.518 | 1.00 34.62 |

- 18 -

| | ATOM | 56 | O | LEU | 20 | 26.066 | -23.087 | 72.112 | 1.00 | 34.19 |
|---|------|----|----|-----|-----|--------|---------|--------|------|-------|
| | ATOM | 57 | N | ALA | 21 | 25.946 | -25.336 | 72.116 | 1.00 | 33.16 |
| | ATOM | 58 | CA | ALA | 21 | 27.030 | -25.509 | 71.163 | 1.00 | 34.30 |
| | ATOM | 59 | CB | ALA | 21 | 27.344 | -26.992 | 70.993 | 1.00 | 34.49 |
| 5 | ATOM | 60 | C | ALA | 21 | 26.696 | -24.886 | 69.814 | 1.00 | 35.20 |
| | ATOM | 61 | O | ALA | 21 | 27.587 | -24.619 | 69.007 | 1.00 | 35.57 |
| | ATOM | 62 | N | GLU | 22 | 25.412 | -24.652 | 69.578 | 1.00 | 36.75 |
| | ATOM | 63 | CA | GLU | 22 | 24.961 | -24.053 | 68.329 | 1.00 | 37.80 |
| | ATOM | 64 | CB | GLU | 22 | 23.435 | -24.102 | 68.256 | 1.00 | 41.47 |
| 10 | ATOM | 65 | CG | GLU | 22 | 22.878 | -23.851 | 66.867 | 1.00 | 47.91 |
| | ATOM | 66 | CD | GLU | 22 | 21.384 | -24.128 | 66.767 | 1.00 | 49.95 |
| | ATOM | 67 | OE1 | GLU | 22 | 20.857 | -24.163 | 65.630 | 1.00 | 50.84 |
| | ATOM | 68 | OE2 | GLU | 22 | 20.741 | -24.307 | 67.822 | 1.00 | 50.26 |
| | ATOM | 69 | C | GLU | 22 | 25.444 | -22.605 | 68.177 | 1.00 | 37.38 |
| 15 | ATOM | 70 | O | GLU | 22 | 25.380 | -22.039 | 67.088 | 1.00 | 38.34 |
| | ATOM | 71 | N | PHE | 23 | 25.928 | -22.012 | 69.268 | 1.00 | 35.41 |
| | ATOM | 72 | CA | PHE | 23 | 26.426 | -20.636 | 69.249 | 1.00 | 33.38 |
| | ATOM | 73 | CB | PHE | 23 | 26.224 | -19.962 | 70.614 | 1.00 | 31.59 |
| | ATOM | 74 | CG | PHE | 23 | 24.826 | -19.470 | 70.843 | 1.00 | 29.81 |
| 20 | ATOM | 75 | CD1 | PHE | 23 | 23.836 | -20.328 | 71.310 | 1.00 | 26.48 |
| | ATOM | 76 | CD2 | PHE | 23 | 24.489 | -18.151 | 70.555 | 1.00 | 28.79 |
| | ATOM | 77 | CE1 | PHE | 23 | 22.520 | -19.882 | 71.487 | 1.00 | 29.30 |
| | ATOM | 78 | CE2 | PHE | 23 | 23.177 | -17.691 | 70.727 | 1.00 | 31.65 |
| | ATOM | 79 | CZ | PHE | 23 | 22.189 | -18.563 | 71.195 | 1.00 | 28.91 |
| 25 | ATOM | 80 | C | PHE | 23 | 27.899 | -20.542 | 68.877 | 1.00 | 33.33 |
| | ATOM | 81 | O | PHE | 23 | 28.396 | -19.467 | 68.549 | 1.00 | 34.12 |
| | ATOM | 82 | N | GLN | 24 | 28.596 | -21.670 | 68.940 | 1.00 | 32.75 |
| | ATOM | 83 | CA | GLN | 24 | 30.016 | -21.716 | 68.620 | 1.00 | 32.56 |
| | ATOM | 84 | CB | GLN | 24 | 30.543 | -23.147 | 68.778 | 1.00 | 35.53 |

- 19 -

```
    ATOM  85  CG  GLN 24    30.817 -23.603  70.210  1.00 37.84
    ATOM  86  CD  GLN 24    31.214 -25.074  70.266  1.00 42.36
    ATOM  87  OE1 GLN 24    31.802 -25.601  69.320  1.00 43.06
    ATOM  88  NE2 GLN 24    30.902 -25.739  71.375  1.00 40.61
 5  ATOM  89  C   GLN 24    30.335 -21.233  67.208  1.00 31.93
    ATOM  90  O   GLN 24    29.508 -21.320  66.299  1.00 30.32
    ATOM  91  N   LEU 25    31.548 -20.717  67.043  1.00 31.64
    ATOM  92  CA  LEU 25    32.029 -20.257  65.751  1.00 31.85
    ATOM  93  CB  LEU 25    31.876 -18.742  65.615  1.00 31.24
10  ATOM  94  CG  LEU 25    30.441 -18.211  65.563  1.00 29.93
    ATOM  95  CD1 LEU 25    30.436 -16.690  65.710  1.00 28.63
    ATOM  96  CD2 LEU 25    29.801 -18.640  64.262  1.00 27.61
    ATOM  97  C   LEU 25    33.502 -20.635  65.667  1.00 33.30
    ATOM  98  O   LEU 25    34.298 -20.218  66.502  1.00 33.97
15  ATOM  99  N   GLN 26    33.856 -21.450  64.679  1.00 34.57
    ATOM 100  CA  GLN 26    35.244 -21.860  64.496  1.00 36.87
    ATOM 101  CB  GLN 26    35.330 -23.053  63.540  1.00 40.20
    ATOM 102  CG  GLN 26    35.105 -24.414  64.182  1.00 46.34
    ATOM 103  CD  GLN 26    33.863 -24.462  65.041  1.00 48.48
20  ATOM 104  OE1 GLN 26    33.918 -24.229  66.253  1.00 49.27
    ATOM 105  NE2 GLN 26    32.725 -24.757  64.417  1.00 51.72
    ATOM 106  C   GLN 26    36.024 -20.688  63.910  1.00 36.49
    ATOM 107  O   GLN 26    35.430 -19.735  63.403  1.00 35.76
    ATOM 108  N   GLU 27    37.347 -20.761  63.981  1.00 35.17
25  ATOM 109  CA  GLU 27    38.181 -19.705  63.441  1.00 37.77
    ATOM 110  CB  GLU 27    39.658 -20.047  63.627  1.00 40.11
    ATOM 111  CG  GLU 27    40.596 -19.156  62.831  1.00 47.14
    ATOM 112  CD  GLU 27    41.754 -18.639  63.662  1.00 52.56
    ATOM 113  OE1 GLU 27    41.507 -17.808  64.567  1.00 54.72
```

- 20 -

```
    ATOM 114  OE2 GLU 27    42.906 -19.067  63.415  1.00 54.43
    ATOM 115  C   GLU 27    37.878 -19.511  61.961  1.00 37.80
    ATOM 116  O   GLU 27    37.915 -18.392  61.446  1.00 37.09
    ATOM 117  N   GLU 28    37.557 -20.605  61.282  1.00 36.94
 5  ATOM 118  CA  GLU 28    37.261 -20.535  59.862  1.00 36.18
    ATOM 119  CB  GLU 28    37.175 -21.939  59.267  1.00 37.83
    ATOM 120  CG  GLU 28    37.826 -22.039  57.902  1.00 41.72
    ATOM 121  CD  GLU 28    39.154 -21.287  57.843  1.00 44.57
    ATOM 122  OE1 GLU 28    40.033 -21.531  58.706  1.00 46.91
10  ATOM 123  OE2 GLU 28    39.313 -20.446  56.933  1.00 44.10
    ATOM 124  C   GLU 28    35.973 -19.779  59.588  1.00 34.66
    ATOM 125  O   GLU 28    35.860 -19.089  58.575  1.00 33.91
    ATOM 126  N   ASP 29    34.994 -19.926  60.472  1.00 32.44
    ATOM 127  CA  ASP 29    33.738 -19.219  60.301  1.00 32.41
15  ATOM 128  CB  ASP 29    32.713 -19.625  61.370  1.00 34.13
    ATOM 129  CG  ASP 29    32.302 -21.091  61.285  1.00 34.13
    ATOM 130  OD1 ASP 29    32.012 -21.580  60.173  1.00 34.03
    ATOM 131  OD2 ASP 29    32.246 -21.749  62.347  1.00 35.16
    ATOM 132  C   ASP 29    34.054 -17.728  60.456  1.00 31.21
20  ATOM 133  O   ASP 29    33.542 -16.895  59.717  1.00 29.93
    ATOM 134  N   LEU 30    34.912 -17.403  61.419  1.00 29.60
    ATOM 135  CA  LEU 30    35.274 -16.016  61.674  1.00 28.38
    ATOM 136  CB  LEU 30    36.101 -15.901  62.964  1.00 23.67
    ATOM 137  CG  LEU 30    35.435 -16.298  64.289  1.00 23.54
25  ATOM 138  CD1 LEU 30    36.314 -15.823  65.433  1.00 22.55
    ATOM 139  CD2 LEU 30    34.038 -15.674  64.418  1.00 24.55
    ATOM 140  C   LEU 30    36.032 -15.390  60.499  1.00 29.80
    ATOM 141  O   LEU 30    35.775 -14.242  60.139  1.00 29.56
    ATOM 142  N   LYS 31    36.963 -16.131  59.906  1.00 29.13
```

| ATOM 143 | CA  | LYS 31 | 37.704 | -15.609 | 58.770 | 1.00 | 30.46 |
|----------|-----|--------|--------|---------|--------|------|-------|
| ATOM 144 | CB  | LYS 31 | 38.823 | -16.574 | 58.365 | 1.00 | 32.24 |
| ATOM 145 | CG  | LYS 31 | 39.970 | -16.653 | 59.374 | 1.00 | 36.80 |
| ATOM 146 | CD  | LYS 31 | 41.091 | -17.577 | 58.885 | 1.00 | 40.49 |
| ATOM 147 | CE  | LYS 31 | 42.291 | -17.534 | 59.829 | 1.00 | 44.52 |
| ATOM 148 | NZ  | LYS 31 | 43.443 | -18.369 | 59.363 | 1.00 | 47.22 |
| ATOM 149 | C   | LYS 31 | 36.746 | -15.391 | 57.599 | 1.00 | 31.28 |
| ATOM 150 | O   | LYS 31 | 36.918 | -14.464 | 56.816 | 1.00 | 32.79 |
| ATOM 151 | N   | LYS 32 | 35.730 | -16.243 | 57.486 | 1.00 | 30.96 |
| ATOM 152 | CA  | LYS 32 | 34.758 | -16.116 | 56.406 | 1.00 | 32.66 |
| ATOM 153 | CB  | LYS 32 | 33.868 | -17.364 | 56.324 | 1.00 | 32.27 |
| ATOM 154 | CG  | LYS 32 | 32.921 | -17.362 | 55.135 | 1.00 | 34.72 |
| ATOM 155 | CD  | LYS 32 | 32.203 | -18.701 | 54.965 | 1.00 | 39.55 |
| ATOM 156 | CE  | LYS 32 | 31.272 | -18.678 | 53.745 | 1.00 | 42.65 |
| ATOM 157 | NZ  | LYS 32 | 30.699 | -20.026 | 53.417 | 1.00 | 42.72 |
| ATOM 158 | C   | LYS 32 | 33.890 | -14.868 | 56.609 | 1.00 | 32.63 |
| ATOM 159 | O   | LYS 32 | 33.607 | -14.140 | 55.652 | 1.00 | 32.25 |
| ATOM 160 | N   | VAL 33 | 33.463 | -14.629 | 57.847 | 1.00 | 30.17 |
| ATOM 161 | CA  | VAL 33 | 32.654 | -13.451 | 58.149 | 1.00 | 29.03 |
| ATOM 162 | CB  | VAL 33 | 32.154 | -13.460 | 59.626 | 1.00 | 30.49 |
| ATOM 163 | CG1 | VAL 33 | 31.519 | -12.123 | 59.985 | 1.00 | 31.03 |
| ATOM 164 | CG2 | VAL 33 | 31.130 | -14.562 | 59.815 | 1.00 | 32.03 |
| ATOM 165 | C   | VAL 33 | 33.538 | -12.226 | 57.908 | 1.00 | 26.62 |
| ATOM 166 | O   | VAL 33 | 33.091 | -11.237 | 57.338 | 1.00 | 22.25 |
| ATOM 167 | N   | MET 34 | 34.802 | -12.321 | 58.317 | 1.00 | 25.50 |
| ATOM 168 | CA  | MET 34 | 35.750 | -11.226 | 58.142 | 1.00 | 27.22 |
| ATOM 169 | CB  | MET 34 | 37.108 | -11.583 | 58.748 | 1.00 | 24.41 |
| ATOM 170 | CG  | MET 34 | 38.150 | -10.512 | 58.537 | 1.00 | 26.32 |
| ATOM 171 | SD  | MET 34 | 39.793 | -11.040 | 59.074 | 1.00 | 32.95 |

- 22 -

```
   ATOM 172  CE  MET 34   40.162 -12.313  57.821  1.00 30.64
   ATOM 173  C   MET 34   35.927 -10.879  56.665  1.00 29.30
   ATOM 174  O   MET 34   35.850  -9.717  56.286  1.00 29.01
   ATOM 175  N   ARG 35   36.164 -11.883  55.827  1.00 30.96
 5 ATOM 176  CA  ARG 35   36.340 -11.621  54.403  1.00 32.99
   ATOM 177  CB  ARG 35   36.664 -12.913  53.641  1.00 34.85
   ATOM 178  CG  ARG 35   37.948 -13.585  54.081  1.00 38.82
   ATOM 179  CD  ARG 35   38.377 -14.682  53.126  1.00 43.22
   ATOM 180  NE  ARG 35   38.963 -15.791  53.869  1.00 47.35
10 ATOM 181  CZ  ARG 35   38.260 -16.801  54.366  1.00 47.12
   ATOM 182  NH1 ARG 35   36.946 -16.850  54.186  1.00 48.27
   ATOM 183  NH2 ARG 35   38.868 -17.746  55.064  1.00 50.91
   ATOM 184  C   ARG 35   35.090 -10.997  53.797  1.00 33.31
   ATOM 185  O   ARG 35   35.178 -10.089  52.966  1.00 33.49
15 ATOM 186  N   ARG 36   33.926 -11.493  54.206  1.00 32.00
   ATOM 187  CA  ARG 36   32.673 -10.982  53.675  1.00 31.76
   ATOM 188  CB  ARG 36   31.511 -11.857  54.158  1.00 29.95
   ATOM 189  CG  ARG 36   30.191 -11.607  53.441  1.00 31.90
   ATOM 190  CD  ARG 36   30.386 -11.434  51.929  1.00 33.67
20 ATOM 191  NE  ARG 36   29.114 -11.263  51.230  1.00 38.02
   ATOM 192  CZ  ARG 36   28.229 -12.238  51.018  1.00 40.67
   ATOM 193  NH1 ARG 36   28.477 -13.471  51.447  1.00 40.50
   ATOM 194  NH2 ARG 36   27.087 -11.979  50.382  1.00 41.02
   ATOM 195  C   ARG 36   32.459  -9.510  54.060  1.00 31.54
25 ATOM 196  O   ARG 36   31.959  -8.718  53.260  1.00 30.75
   ATOM 197  N   MET 37   32.856  -9.147  55.276  1.00 30.98
   ATOM 198  CA  MET 37   32.720  -7.774  55.742  1.00 30.21
   ATOM 199  CB  MET 37   33.134  -7.663  57.208  1.00 27.60
   ATOM 200  CG  MET 37   33.102  -6.240  57.761  1.00 27.98
```

- 23 -

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ATOM | 201 | SD | MET | 37 | 31.418 | -5.613 | 57.981 | 1.00 30.18 |
| ATOM | 202 | CE | MET | 37 | 31.115 | -6.153 | 59.683 | 1.00 28.30 |
| ATOM | 203 | C | MET | 37 | 33.598 | -6.852 | 54.892 | 1.00 30.32 |
| ATOM | 204 | O | MET | 37 | 33.162 | -5.782 | 54.479 | 1.00 31.66 |
| ATOM | 205 | N | GLN | 38 | 34.835 | -7.272 | 54.642 | 1.00 30.60 |
| ATOM | 206 | CA | GLN | 38 | 35.774 | -6.500 | 53.829 | 1.00 31.68 |
| ATOM | 207 | CB | GLN | 38 | 37.126 | -7.206 | 53.750 | 1.00 32.18 |
| ATOM | 208 | CG | GLN | 38 | 38.051 | -6.918 | 54.898 | 1.00 36.36 |
| ATOM | 209 | CD | GLN | 38 | 39.318 | -7.743 | 54.831 | 1.00 37.65 |
| ATOM | 210 | OE1 | GLN | 38 | 39.352 | -8.890 | 55.275 | 1.00 41.25 |
| ATOM | 211 | NE2 | GLN | 38 | 40.362 | -7.170 | 54.258 | 1.00 39.99 |
| ATOM | 212 | C | GLN | 38 | 35.241 | -6.337 | 52.419 | 1.00 32.20 |
| ATOM | 213 | O | GLN | 38 | 35.471 | -5.318 | 51.769 | 1.00 32.83 |
| ATOM | 214 | N | LYS | 39 | 34.541 | -7.360 | 51.947 | 1.00 31.94 |
| ATOM | 215 | CA | LYS | 39 | 33.965 | -7.343 | 50.611 | 1.00 33.33 |
| ATOM | 216 | CB | LYS | 39 | 33.515 | -8.754 | 50.220 | 1.00 34.32 |
| ATOM | 217 | CG | LYS | 39 | 33.757 | -9.105 | 48.756 | 1.00 41.05 |
| ATOM | 218 | CD | LYS | 39 | 32.994 | -8.183 | 47.799 | 1.00 43.55 |
| ATOM | 219 | CE | LYS | 39 | 33.319 | -8.502 | 46.336 | 1.00 47.30 |
| ATOM | 220 | NZ | LYS | 39 | 32.587 | -7.625 | 45.363 | 1.00 48.42 |
| ATOM | 221 | C | LYS | 39 | 32.774 | -6.378 | 50.555 | 1.00 32.37 |
| ATOM | 222 | O | LYS | 39 | 32.578 | -5.676 | 49.564 | 1.00 33.02 |
| ATOM | 223 | N | GLU | 40 | 31.975 | -6.342 | 51.613 | 1.00 31.82 |
| ATOM | 224 | CA | GLU | 40 | 30.831 | -5.442 | 51.632 | 1.00 33.50 |
| ATOM | 225 | CB | GLU | 40 | 29.845 | -5.831 | 52.737 | 1.00 34.39 |
| ATOM | 226 | CG | GLU | 40 | 29.159 | -7.167 | 52.507 | 1.00 36.32 |
| ATOM | 227 | CD | GLU | 40 | 28.562 | -7.293 | 51.112 | 1.00 38.53 |
| ATOM | 228 | OE1 | GLU | 40 | 27.878 | -6.350 | 50.660 | 1.00 39.61 |
| ATOM | 229 | OE2 | GLU | 40 | 28.770 | -8.342 | 50.469 | 1.00 38.22 |

- 24 -

| ATOM 230 | C | GLU 40 | 31.309 | -4.009 | 51.833 | 1.00 | 33.20 |
|---|---|---|---|---|---|---|---|
| ATOM 231 | O | GLU 40 | 30.691 | -3.072 | 51.345 | 1.00 | 33.12 |
| ATOM 232 | N | MET 41 | 32.409 | -3.844 | 52.556 | 1.00 | 33.18 |
| ATOM 233 | CA | MET 41 | 32.957 | -2.515 | 52.783 | 1.00 | 34.90 |
| ATOM 234 | CB | MET 41 | 34.173 | -2.585 | 53.706 | 1.00 | 32.91 |
| ATOM 235 | CG | MET 41 | 33.838 | -2.927 | 55.154 | 1.00 | 34.83 |
| ATOM 236 | SD | MET 41 | 35.327 | -2.987 | 56.170 | 1.00 | 34.41 |
| ATOM 237 | CE | MET 41 | 35.747 | -1.216 | 56.267 | 1.00 | 36.69 |
| ATOM 238 | C | MET 41 | 33.368 | -1.941 | 51.430 | 1.00 | 36.56 |
| ATOM 239 | O | MET 41 | 33.058 | -0.792 | 51.108 | 1.00 | 34.98 |
| ATOM 240 | N | ASP 42 | 34.054 | -2.758 | 50.639 | 1.00 | 36.46 |
| ATOM 241 | CA | ASP 42 | 34.508 | -2.346 | 49.317 | 1.00 | 38.91 |
| ATOM 242 | CB | ASP 42 | 35.318 | -3.470 | 48.674 | 1.00 | 42.09 |
| ATOM 243 | CG | ASP 42 | 36.130 | -2.999 | 47.490 | 1.00 | 43.40 |
| ATOM 244 | OD1 | ASP 42 | 37.081 | -2.216 | 47.705 | 1.00 | 45.67 |
| ATOM 245 | OD2 | ASP 42 | 35.817 | -3.411 | 46.350 | 1.00 | 42.51 |
| ATOM 246 | C | ASP 42 | 33.311 | -1.990 | 48.433 | 1.00 | 38.61 |
| ATOM 247 | O | ASP 42 | 33.366 | -1.036 | 47.656 | 1.00 | 39.03 |
| ATOM 248 | N | ARG 43 | 32.232 | -2.761 | 48.559 | 1.00 | 36.74 |
| ATOM 249 | CA | ARG 43 | 31.012 | -2.524 | 47.788 | 1.00 | 33.90 |
| ATOM 250 | CB | ARG 43 | 30.037 | -3.688 | 47.967 | 1.00 | 33.80 |
| ATOM 251 | CG | ARG 43 | 30.324 | -4.890 | 47.080 | 1.00 | 34.68 |
| ATOM 252 | CD | ARG 43 | 29.654 | -6.163 | 47.614 | 1.00 | 34.89 |
| ATOM 253 | NE | ARG 43 | 28.232 | -5.997 | 47.906 | 1.00 | 35.11 |
| ATOM 254 | CZ | ARG 43 | 27.296 | -5.729 | 46.998 | 1.00 | 37.42 |
| ATOM 255 | NH1 | ARG 43 | 27.620 | -5.589 | 45.719 | 1.00 | 39.98 |
| ATOM 256 | NH2 | ARG 43 | 26.028 | -5.615 | 47.366 | 1.00 | 36.46 |
| ATOM 257 | C | ARG 43 | 30.313 | -1.229 | 48.193 | 1.00 | 34.64 |
| ATOM 258 | O | ARG 43 | 29.712 | -0.550 | 47.357 | 1.00 | 35.89 |

- 25 -

```
    ATOM 259  N   GLY 44   30. 382  -0. 892  49. 475  1. 00  31. 21
    ATOM 260  CA  GLY 44   29. 744   0. 318  49. 940  1. 00  31. 87
    ATOM 261  C   GLY 44   30. 463   1. 579  49. 490  1. 00  33. 29
    ATOM 262  O   GLY 44   29. 854   2. 645  49. 397  1. 00  31. 49
 5  ATOM 263  N   LEU 45   31. 756   1. 455  49. 200  1. 00  31. 44
    ATOM 264  CA  LEU 45   32. 563   2. 595  48. 778  1. 00  32. 24
    ATOM 265  CB  LEU 45   34. 033   2. 358  49. 129  1. 00  27. 43
    ATOM 266  CG  LEU 45   34. 415   2. 487  50. 601  1. 00  29. 59
    ATOM 267  CD1 LEU 45   35. 832   1. 992  50. 827  1. 00  30. 31
10  ATOM 268  CD2 LEU 45   34. 281   3. 941  51. 022  1. 00  30. 45
    ATOM 269  C   LEU 45   32. 455   2. 933  47. 294  1. 00  33. 00
    ATOM 270  O   LEU 45   32. 537   4. 098  46. 924  1. 00  32. 78
    ATOM 271  N   ARG 46   32. 277   1. 911  46. 460  1. 00  34. 18
    ATOM 272  CA  ARG 46   32. 179   2. 074  45. 009  1. 00  34. 76
15  ATOM 273  CB  ARG 46   32. 320   0. 714  44. 312  1. 00  36. 33
    ATOM 274  CG  ARG 46   33. 519  -0. 119  44. 756  1. 00  39. 02
    ATOM 275  CD  ARG 46   34. 794   0. 267  44. 035  1. 00  43. 71
    ATOM 276  NE  ARG 46   35. 913  -0. 593  44. 431  1. 00  48. 60
    ATOM 277  CZ  ARG 46   37. 142  -0. 527  43. 915  1. 00  49. 59
20  ATOM 278  NH1 ARG 46   37. 429   0. 359  42. 969  1. 00  49. 57
    ATOM 279  NH2 ARG 46   38. 091  -1. 344  44. 354  1. 00  50. 09
    ATOM 280  C   ARG 46   30. 856   2. 710  44. 587  1. 00  34. 95
    ATOM 281  O   ARG 46   29. 785   2. 361  45. 091  1. 00  32. 49
    ATOM 282  N   LEU 47   30. 935   3. 638  43. 644  1. 00  34. 90
25  ATOM 283  CA  LEU 47   29. 741   4. 311  43. 162  1. 00  34. 40
    ATOM 284  CB  LEU 47   30. 100  ·5. 297  42. 049  1. 00  34. 27
    ATOM 285  CG  LEU 47   28. 929   6. 085  41. 447  1. 00  33. 85
    ATOM 286  CD1 LEU 47   28. 445   7. 144  42. 442  1. 00  31. 01
    ATOM 287  CD2 LEU 47   29. 381   6. 741  40. 144  1. 00  31. 08
```

- 26 -

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 288 | C | LEU | 47 | 28.727 | 3.316 | 42.625 | 1.00 34.52 |
|  | ATOM | 289 | O | LEU | 47 | 27.535 | 3.411 | 42.922 | 1.00 32.39 |
|  | ATOM | 290 | N | GLU | 48 | 29.202 | 2.353 | 41.841 | 1.00 34.67 |
|  | ATOM | 291 | CA | GLU | 48 | 28.301 | 1.378 | 41.242 | 1.00 36.59 |
| 5 | ATOM | 292 | CB | GLU | 48 | 29.010 | 0.589 | 40.134 | 1.00 38.07 |
|  | ATOM | 293 | CG | GLU | 48 | 30.205 | -0.248 | 40.562 | 1.00 39.26 |
|  | ATOM | 294 | CD | GLU | 48 | 31.499 | 0.534 | 40.580 | 1.00 40.85 |
|  | ATOM | 295 | OE1 | GLU | 48 | 32.571 | -0.106 | 40.497 | 1.00 44.46 |
|  | ATOM | 296 | OE2 | GLU | 48 | 31.454 | 1.779 | 40.682 | 1.00 38.21 |
| 10 | ATOM | 297 | C | GLU | 48 | 27.600 | 0.406 | 42.188 | 1.00 37.46 |
|  | ATOM | 298 | O | GLU | 48 | 26.654 | -0.268 | 41.778 | 1.00 37.82 |
|  | ATOM | 299 | N | THR | 49 | 28.037 | 0.321 | 43.441 | 1.00 36.85 |
|  | ATOM | 300 | CA | THR | 49 | 27.371 | -0.591 | 44.370 | 1.00 36.40 |
|  | ATOM | 301 | CB | THR | 49 | 28.212 | -1.855 | 44.645 | 1.00 34.37 |
| 15 | ATOM | 302 | OG1 | THR | 49 | 29.554 | -1.480 | 44.969 | 1.00 33.33 |
|  | ATOM | 303 | CG2 | THR | 49 | 28.215 | -2.770 | 43.437 | 1.00 32.44 |
|  | ATOM | 304 | C | THR | 49 | 27.032 | 0.037 | 45.703 | 1.00 38.54 |
|  | ATOM | 305 | O | THR | 49 | 26.536 | -0.647 | 46.599 | 1.00 40.86 |
|  | ATOM | 306 | N | HIS | 50 | 27.272 | 1.335 | 45.842 | 1.00 38.89 |
| 20 | ATOM | 307 | CA | HIS | 50 | 26.994 | 1.990 | 47.115 | 1.00 41.74 |
|  | ATOM | 308 | CB | HIS | 50 | 27.548 | 3.422 | 47.130 | 1.00 44.04 |
|  | ATOM | 309 | CG | HIS | 50 | 26.666 | 4.426 | 46.451 | 1.00 46.35 |
|  | ATOM | 310 | CD2 | HIS | 50 | 25.795 | 5.331 | 46.959 | 1.00 48.65 |
|  | ATOM | 311 | ND1 | HIS | 50 | 26.607 | 4.565 | 45.081 | 1.00 47.18 |
| 25 | ATOM | 312 | CE1 | HIS | 50 | 25.738 | 5.512 | 44.772 | 1.00 48.13 |
|  | ATOM | 313 | NE2 | HIS | 50 | 25.231 | 5.993 | 45.894 | 1.00 49.20 |
|  | ATOM | 314 | C | HIS | 50 | 25.512 | 2.030 | 47.466 | 1.00 42.66 |
|  | ATOM | 315 | O | HIS | 50 | 25.153 | 2.046 | 48.642 | 1.00 42.85 |
|  | ATOM | 316 | N | GLU | 51 | 24.657 | 2.034 | 46.447 | 1.00 43.12 |

- 27 -

|  | ATOM 317 | CA | GLU 51 | 23.213 | 2.120 | 46.645 | 1.00 44.07 |
|---|---|---|---|---|---|---|---|
|  | ATOM 318 | CB | GLU 51 | 22.555 | 2.574 | 45.329 | 1.00 44.83 |
|  | ATOM 319 | CG | GLU 51 | 21.051 | 2.824 | 45.399 | 1.00 46.43 |
|  | ATOM 320 | CD | GLU 51 | 20.531 | 3.691 | 44.243 | 1.00 48.89 |
| 5 | ATOM 321 | OE1 | GLU 51 | 20.822 | 3.385 | 43.064 | 1.00 46.31 |
|  | ATOM 322 | OE2 | GLU 51 | 19.821 | 4.683 | 44.522 | 1.00 50.83 |
|  | ATOM 323 | C | GLU 51 | 22.543 | 0.848 | 47.179 | 1.00 44.27 |
|  | ATOM 324 | O | GLU 51 | 21.630 | 0.925 | 48.000 | 1.00 45.14 |
|  | ATOM 325 | N | GLU 52 | 22.991 | -0.317 | 46.723 | 1.00 44.47 |
| 10 | ATOM 326 | CA | GLU 52 | 22.422 | -1.585 | 47.178 | 1.00 44.81 |
|  | ATOM 327 | CB | GLU 52 | 22.199 | -2.521 | 45.988 | 1.00 47.15 |
|  | ATOM 328 | CG | GLU 52 | 23.485 | -2.920 | 45.264 | 1.00 53.66 |
|  | ATOM 329 | CD | GLU 52 | 23.698 | -2.164 | 43.951 | 1.00 57.63 |
|  | ATOM 330 | OE1 | GLU 52 | 23.646 | -0.909 | 43.953 | 1.00 55.90 |
| 15 | ATOM 331 | OE2 | GLU 52 | 23.925 | -2.835 | 42.917 | 1.00 57.72 |
|  | ATOM 332 | C | GLU 52 | 23.313 | -2.297 | 48.206 | 1.00 42.49 |
|  | ATOM 333 | O | GLU 52 | 23.052 | -3.441 | 48.575 | 1.00 43.45 |
|  | ATOM 334 | N | ALA 53 | 24.362 | -1.626 | 48.666 | 1.00 39.72 |
|  | ATOM 335 | CA | ALA 53 | 25.285 | -2.224 | 49.628 | 1.00 37.01 |
| 20 | ATOM 336 | CB | ALA 53 | 26.589 | -1.438 | 49.645 | 1.00 35.23 |
|  | ATOM 337 | C | ALA 53 | 24.700 | -2.291 | 51.038 | 1.00 35.27 |
|  | ATOM 338 | O | ALA 53 | 24.125 | -1.321 | 51.528 | 1.00 34.63 |
|  | ATOM 339 | N | SER 54 | 24.845 | -3.439 | 51.689 | 1.00 32.88 |
|  | ATOM 340 | CA | SER 54 | 24.339 | -3.594 | 53.052 | 1.00 32.06 |
| 25 | ATOM 341 | CB | SER 54 | 24.397 | -5.062 | 53.476 | 1.00 30.23 |
|  | ATOM 342 | OG | SER 54 | 25.694 | -5.576 | 53.261 | 1.00 35.67 |
|  | ATOM 343 | C | SER 54 | 25.188 | -2.741 | 53.990 | 1.00 28.49 |
|  | ATOM 344 | O | SER 54 | 24.682 | -2.147 | 54.934 | 1.00 29.57 |
|  | ATOM 345 | N | VAL 55 | 26.485 | -2.684 | 53.724 | 1.00 28.44 |

- 28 -

```
        ATOM 346  CA   VAL 55   27.386  -1.876  54.535  1.00 28.63
        ATOM 347  CB   VAL 55   28.737  -2.594  54.726  1.00 27.89
        ATOM 348  CG1  VAL 55   29.660  -1.766  55.599  1.00 26.89
        ATOM 349  CG2  VAL 55   28.497  -3.957  55.365  1.00 27.94
  5     ATOM 350  C    VAL 55   27.559  -0.551  53.788  1.00 29.80
        ATOM 351  O    VAL 55   28.367  -0.430  52.868  1.00 28.14
        ATOM 352  N    LYS 56   26.787   0.446  54.205  1.00 31.68
        ATOM 353  CA   LYS 56   26.788   1.750  53.550  1.00 30.06
        ATOM 354  CB   LYS 56   25.727   2.628  54.203  1.00 29.96
  10    ATOM 355  CG   LYS 56   24.312   2.124  53.933  1.00 29.47
        ATOM 356  CD   LYS 56   23.279   2.935  54.689  1.00 31.68
        ATOM 357  CE   LYS 56   23.417   2.767  56.196  1.00 30.78
        ATOM 358  NZ   LYS 56   22.911   1.428  56.648  1.00 36.66
        ATOM 359  C    LYS 56   28.087   2.535  53.374  1.00 28.33
  15    ATOM 360  O    LYS 56   28.222   3.256  52.388  1.00 30.83
        ATOM 361  N    MET 57   29.044   2.410  54.287  1.00 25.97
        ATOM 362  CA   MET 57   30.299   3.149  54.137  1.00 23.92
        ATOM 363  CB   MET 57   31.098   2.577  52.964  1.00 24.05
        ATOM 364  CG   MET 57   31.383   1.078  53.075  1.00 27.54
  20    ATOM 365  SD   MET 57   32.303   0.659  54.580  1.00 26.48
        ATOM 366  CE   MET 57   33.991   1.127  54.113  1.00 21.76
        ATOM 367  C    MET 57   30.006   4.643  53.887  1.00 26.44
        ATOM 368  O    MET 57   30.460   5.237  52.903  1.00 24.39
        ATOM 369  N    LEU 58   29.250   5.235  54.803  1.00 26.42
  25    ATOM 370  CA   LEU 58   28.843   6.630  54.713  1.00 26.83
        ATOM 371  CB   LEU 58   27.684   6.884  55.677  1.00 24.27
        ATOM 372  CG   LEU 58   26.440   6.043  55.386  1.00 30.26
        ATOM 373  CD1  LEU 58   25.401   6.250  56.473  1.00 28.51
        ATOM 374  CD2  LEU 58   25.874   6.430  54.016  1.00 31.10
```

- 29 -

|       | ATOM 375 | C   | LEU 58 | 29. 932 | 7. 665  | 54. 965 | 1. 00 | 25. 48 |
|-------|----------|-----|--------|---------|---------|---------|-------|--------|
|       | ATOM 376 | O   | LEU 58 | 30. 495 | 7. 742  | 56. 053 | 1. 00 | 25. 30 |
|       | ATOM 377 | N   | PRO 59 | 30. 242 | 8. 476  | 53. 946 | 1. 00 | 24. 56 |
|       | ATOM 378 | CD  | PRO 59 | 29. 764 | 8. 341  | 52. 557 | 1. 00 | 24. 76 |
| 5     | ATOM 379 | CA  | PRO 59 | 31. 262 | 9. 528  | 54. 063 | 1. 00 | 26. 48 |
|       | ATOM 380 | CB  | PRO 59 | 31. 217 | 10. 196 | 52. 686 | 1. 00 | 26. 76 |
|       | ATOM 381 | CG  | PRO 59 | 30. 865 | 9. 036  | 51. 769 | 1. 00 | 26. 41 |
|       | ATOM 382 | C   | PRO 59 | 30. 820 | 10. 478 | 55. 190 | 1. 00 | 26. 49 |
|       | ATOM 383 | O   | PRO 59 | 29. 656 | 10. 863 | 55. 239 | 1. 00 | 28. 20 |
| 10    | ATOM 384 | N   | THR 60 | 31. 728 | 10. 845 | 56. 092 | 1. 00 | 27. 28 |
|       | ATOM 385 | CA  | THR 60 | 31. 372 | 11. 720 | 57. 220 | 1. 00 | 27. 77 |
|       | ATOM 386 | CB  | THR 60 | 31. 994 | 11. 217 | 58. 544 | 1. 00 | 24. 87 |
|       | ATOM 387 | OG1 | THR 60 | 33. 400 | 11. 482 | 58. 536 | 1. 00 | 22. 66 |
|       | ATOM 388 | CG2 | THR 60 | 31. 767 | 9. 713  | 58. 726 | 1. 00 | 28. 80 |
| 15    | ATOM 389 | C   | THR 60 | 31. 800 | 13. 196 | 57. 085 | 1. 00 | 30. 72 |
|       | ATOM 390 | O   | THR 60 | 31. 405 | 14. 041 | 57. 897 | 1. 00 | 29. 67 |
|       | ATOM 391 | N   | TYR 61 | 32. 623 | 13. 485 | 56. 084 | 1. 00 | 30. 13 |
|       | ATOM 392 | CA  | TYR 61 | 33. 144 | 14. 824 | 55. 844 | 1. 00 | 33. 87 |
|       | ATOM 393 | CB  | TYR 61 | 32. 005 | 15. 837 | 55. 684 | 1. 00 | 32. 96 |
| 20    | ATOM 394 | CG  | TYR 61 | 31. 409 | 15. 730 | 54. 298 | 1. 00 | 35. 37 |
|       | ATOM 395 | CD1 | TYR 61 | 32. 084 | 16. 251 | 53. 192 | 1. 00 | 36. 43 |
|       | ATOM 396 | CE1 | TYR 61 | 31. 621 | 16. 036 | 51. 890 | 1. 00 | 34. 05 |
|       | ATOM 397 | CD2 | TYR 61 | 30. 244 | 14. 995 | 54. 068 | 1. 00 | 34. 99 |
|       | ATOM 398 | CE2 | TYR 61 | 29. 778 | 14. 772 | 52. 768 | 1. 00 | 33. 96 |
| 25    | ATOM 399 | CZ  | TYR 61 | 30. 475 | 15. 294 | 51. 689 | 1. 00 | 33. 72 |
|       | ATOM 400 | OH  | TYR 61 | 30. 039 | 15. 064 | 50. 402 | 1. 00 | 37. 69 |
|       | ATOM 401 | C   | TYR 61 | 34. 156 | 15. 264 | 56. 890 | 1. 00 | 34. 78 |
|       | ATOM 402 | O   | TYR 61 | 34. 712 | 16. 357 | 56. 806 | 1. 00 | 34. 09 |
|       | ATOM 403 | N   | VAL 62 | 34. 407 | 14. 407 | 57. 875 | 1. 00 | 36. 47 |

- 30 -

| | ATOM | 404 | CA | VAL | 62 | 35.426 | 14.713 | 58.869 | 1.00 | 37.40 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 405 | CB | VAL | 62 | 35.283 | 13.825 | 60.116 | 1.00 | 37.42 |
| | ATOM | 406 | CG1 | VAL | 62 | 36.410 | 14.107 | 61.089 | 1.00 | 32.97 |
| | ATOM | 407 | CG2 | VAL | 62 | 33.937 | 14.073 | 60.774 | 1.00 | 36.34 |
| 5 | ATOM | 408 | C | VAL | 62 | 36.695 | 14.335 | 58.104 | 1.00 | 41.04 |
| | ATOM | 409 | O | VAL | 62 | 36.944 | 13.153 | 57.865 | 1.00 | 40.85 |
| | ATOM | 410 | N | ARG | 63 | 37.475 | 15.331 | 57.692 | 1.00 | 43.48 |
| | ATOM | 411 | CA | ARG | 63 | 38.682 | 15.070 | 56.909 | 1.00 | 48.27 |
| | ATOM | 412 | CB | ARG | 63 | 38.843 | 16.126 | 55.814 | 1.00 | 47.25 |
| 10 | ATOM | 413 | CG | ARG | 63 | 37.735 | 16.112 | 54.783 | 1.00 | 49.66 |
| | ATOM | 414 | CD | ARG | 63 | 37.648 | 17.447 | 54.061 | 1.00 | 50.62 |
| | ATOM | 415 | NE | ARG | 63 | 36.482 | 17.523 | 53.185 | 1.00 | 51.28 |
| | ATOM | 416 | CZ | ARG | 63 | 36.405 | 16.961 | 51.982 | 1.00 | 50.52 |
| | ATOM | 417 | NH1 | ARG | 63 | 37.430 | 16.274 | 51.492 | 1.00 | 48.44 |
| 15 | ATOM | 418 | NH2 | ARG | 63 | 35.295 | 17.089 | 51.268 | 1.00 | 49.50 |
| | ATOM | 419 | C | ARG | 63 | 39.952 | 15.006 | 57.728 | 1.00 | 50.30 |
| | ATOM | 420 | O | ARG | 63 | 39.998 | 15.478 | 58.860 | 1.00 | 49.69 |
| | ATOM | 421 | N | SER | 64 | 40.987 | 14.431 | 57.128 | 1.00 | 54.64 |
| | ATOM | 422 | CA | SER | 64 | 42.276 | 14.280 | 57.783 | 1.00 | 60.87 |
| 20 | ATOM | 423 | CB | SER | 64 | 43.315 | 13.760 | 56.794 | 1.00 | 60.13 |
| | ATOM | 424 | OG | SER | 64 | 44.492 | 13.381 | 57.481 | 1.00 | 62.83 |
| | ATOM | 425 | C | SER | 64 | 42.760 | 15.583 | 58.398 | 1.00 | 65.69 |
| | ATOM | 426 | O | SER | 64 | 42.952 | 16.584 | 57.703 | 1.00 | 65.99 |
| | ATOM | 427 | N | THR | 65 | 42.961 | 15.530 | 59.714 | 1.00 | 71.92 |
| 25 | ATOM | 428 | CA | THR | 65 | 43.402 | 16.649 | 60.545 | 1.00 | 77.78 |
| | ATOM | 429 | CB | THR | 65 | 44.529 | 16.194 | 61.524 | 1.00 | 78.35 |
| | ATOM | 430 | OG1 | THR | 65 | 44.959 | 17.309 | 62.317 | 1.00 | 79.07 |
| | ATOM | 431 | CG2 | THR | 65 | 45.714 | 15.611 | 60.757 | 1.00 | 79.19 |
| | ATOM | 432 | C | THR | 65 | 43.839 | 17.925 | 59.817 | 1.00 | 80.90 |

- 31 -

|   | ATOM | 433 | O   | THR | 65 | 45.033 | 18.188 | 59.654 | 1.00 | 80.93 |
|---|------|-----|-----|-----|----|--------|--------|--------|------|-------|
|   | ATOM | 434 | N   | PRO | 66 | 42.863 | 18.732 | 59.364 | 1.00 | 83.72 |
|   | ATOM | 435 | CD  | PRO | 66 | 41.410 | 18.469 | 59.372 | 1.00 | 84.56 |
|   | ATOM | 436 | CA  | PRO | 66 | 43.162 | 19.983 | 58.661 | 1.00 | 85.58 |
| 5 | ATOM | 437 | CB  | PRO | 66 | 41.871 | 20.254 | 57.897 | 1.00 | 85.53 |
|   | ATOM | 438 | CG  | PRO | 66 | 40.827 | 19.776 | 58.864 | 1.00 | 85.36 |
|   | ATOM | 439 | C   | PRO | 66 | 43.468 | 21.057 | 59.710 | 1.00 | 87.07 |
|   | ATOM | 440 | O   | PRO | 66 | 42.581 | 21.812 | 60.119 | 1.00 | 87.87 |
|   | ATOM | 441 | N   | GLU | 67 | 44.726 | 21.109 | 60.144 | 1.00 | 87.71 |
| 10| ATOM | 442 | CA  | GLU | 67 | 45.162 | 22.055 | 61.169 | 1.00 | 87.66 |
|   | ATOM | 443 | CB  | GLU | 67 | 46.683 | 22.238 | 61.110 | 1.00 | 88.42 |
|   | ATOM | 444 | CG  | GLU | 67 | 47.283 | 22.824 | 62.384 | 1.00 | 89.15 |
|   | ATOM | 445 | CD  | GLU | 67 | 46.871 | 22.058 | 63.636 | 1.00 | 89.71 |
|   | ATOM | 446 | OE1 | GLU | 67 | 45.689 | 22.150 | 64.037 | 1.00 | 89.95 |
| 15| ATOM | 447 | OE2 | GLU | 67 | 47.728 | 21.359 | 64.217 | 1.00 | 89.51 |
|   | ATOM | 448 | C   | GLU | 67 | 44.463 | 23.413 | 61.095 | 1.00 | 86.97 |
|   | ATOM | 449 | O   | GLU | 67 | 44.203 | 23.944 | 60.013 | 1.00 | 86.95 |
|   | ATOM | 450 | N   | GLY | 68 | 44.160 | 23.962 | 62.266 | 1.00 | 85.72 |
|   | ATOM | 451 | CA  | GLY | 68 | 43.475 | 25.237 | 62.344 | 1.00 | 83.56 |
| 20| ATOM | 452 | C   | GLY | 68 | 42.274 | 25.073 | 63.251 | 1.00 | 82.01 |
|   | ATOM | 453 | O   | GLY | 68 | 41.136 | 24.970 | 62.784 | 1.00 | 82.39 |
|   | ATOM | 454 | N   | SER | 69 | 42.530 | 25.038 | 64.555 | 1.00 | 79.39 |
|   | ATOM | 455 | CA  | SER | 69 | 41.469 | 24.869 | 65.537 | 1.00 | 77.31 |
|   | ATOM | 456 | CB  | SER | 69 | 41.855 | 23.784 | 66.542 | 1.00 | 77.69 |
| 25| ATOM | 457 | OG  | SER | 69 | 40.877 | 23.677 | 67.561 | 1.00 | 78.20 |
|   | ATOM | 458 | C   | SER | 69 | 41.118 | 26.143 | 66.294 | 1.00 | 75.21 |
|   | ATOM | 459 | O   | SER | 69 | 41.993 | 26.857 | 66.784 | 1.00 | 74.23 |
|   | ATOM | 460 | N   | GLU | 70 | 39.822 | 26.413 | 66.386 | 1.00 | 73.26 |
|   | ATOM | 461 | CA  | GLU | 70 | 39.328 | 27.581 | 67.096 | 1.00 | 71.89 |

- 32 -

```
   ATOM 462  CB  GLU 70   38.004  28.042  66.482  1.00 73.40
   ATOM 463  CG  GLU 70   37.897  29.544  66.297  1.00 77.84
   ATOM 464  CD  GLU 70   38.900  30.073  65.285  1.00 80.27
   ATOM 465  OE1 GLU 70   38.763  29.757  64.082  1.00 81.41
 5 ATOM 466  OE2 GLU 70   39.830  30.801  65.692  1.00 81.33
   ATOM 467  C   GLU 70   39.107  27.144  68.543  1.00 69.48
   ATOM 468  O   GLU 70   38.409  26.163  68.789  1.00 69.73
   ATOM 469  N   VAL 71   39.701  27.853  69.499  1.00 65.92
   ATOM 470  CA  VAL 71   39.536  27.490  70.904  1.00 62.64
10 ATOM 471  CB  VAL 71   40.760  27.909  71.746  1.00 61.59
   ATOM 472  CG1 VAL 71   41.993  27.156  71.275  1.00 61.91
   ATOM 473  CG2 VAL 71   40.979  29.406  71.642  1.00 61.78
   ATOM 474  C   VAL 71   38.278  28.105  71.510  1.00 61.05
   ATOM 475  O   VAL 71   37.608  28.919  70.877  1.00 61.02
15 ATOM 476  N   GLY 72   37.952  27.700  72.734  1.00 59.60
   ATOM 477  CA  GLY 72   36.769  28.225  73.390  1.00 58.10
   ATOM 478  C   GLY 72   35.841  27.169  73.967  1.00 57.74
   ATOM 479  O   GLY 72   36.178  25.982  74.006  1.00 58.27
   ATOM 480  N   ASP 73   34.664  27.607  74.410  1.00 55.55
20 ATOM 481  CA  ASP 73   33.663  26.724  75.003  1.00 54.21
   ATOM 482  CB  ASP 73   32.973  27.426  76.181  1.00 57.20
   ATOM 483  CG  ASP 73   33.846  27.496  77.424  1.00 59.78
   ATOM 484  OD1 ASP 73   35.046  27.830  77.299  1.00 61.37
   ATOM 485  OD2 ASP 73   33.324  27.225  78.529  1.00 60.87
25 ATOM 486  C   ASP 73   32.599  26.310  73.994  1.00 52.36
   ATOM 487  O   ASP 73   31.936  27.161  73.406  1.00 52.44
   ATOM 488  N   PHE 74   32.424  25.005  73.800  1.00 49.73
   ATOM 489  CA  PHE 74   31.412  24.519  72.866  1.00 46.98
   ATOM 490  CB  PHE 74   32.019  23.571  71.837  1.00 46.41
```

- 33 -

```
   ATOM 491  CG  PHE 74   33.117  24.179  71.030  1.00 47.09
   ATOM 492  CD1 PHE 74   34.335  24.492  71.618  1.00 47.62
   ATOM 493  CD2 PHE 74   32.930  24.452  69.681  1.00 47.01
   ATOM 494  CE1 PHE 74   35.359  25.071  70.874  1.00 49.47
5  ATOM 495  CE2 PHE 74   33.943  25.031  68.924  1.00 48.12
   ATOM 496  CZ  PHE 74   35.161  25.342  69.520  1.00 48.82
   ATOM 497  C   PHE 74   30.316  23.783  73.601  1.00 45.68
   ATOM 498  O   PHE 74   30.485  23.382  74.745  1.00 46.35
   ATOM 499  N   LEU 75   29.185  23.615  72.932  1.00 45.12
10 ATOM 500  CA  LEU 75   28.064  22.895  73.501  1.00 44.80
   ATOM 501  CB  LEU 75   26.769  23.686  73.333  1.00 43.29
   ATOM 502  CG  LEU 75   25.535  23.023  73.959  1.00 45.05
   ATOM 503  CD1 LEU 75   25.529  23.278  75.466  1.00 41.53
   ATOM 504  CD2 LEU 75   24.259  23.571  73.326  1.00 43.45
15 ATOM 505  C   LEU 75   27.971  21.598  72.708  1.00 46.04
   ATOM 506  O   LEU 75   28.087  21.611  71.479  1.00 46.97
   ATOM 507  N   SER 76   27.770  20.484  73.405  1.00 45.48
   ATOM 508  CA  SER 76   27.664  19.189  72.744  1.00 43.73
   ATOM 509  CB  SER 76   28.837  18.295  73.143  1.00 43.52
20 ATOM 510  OG  SER 76   30.040  18.741  72.551  1.00 44.64
   ATOM 511  C   SER 76   26.361  18.469  73.051  1.00 41.60
   ATOM 512  O   SER 76   26.026  18.242  74.209  1.00 40.88
   ATOM 513  N   LEU 77   25.617  18.130  72.007  1.00 41.06
   ATOM 514  CA  LEU 77   24.369  17.397  72.175  1.00 43.50
25 ATOM 515  CB  LEU 77   23.281  17.918  71.225  1.00 43.84
   ATOM 516  CG  LEU 77   22.750  19.346  71.401  1.00 45.70
   ATOM 517  CD1 LEU 77   21.587  19.577  70.442  1.00 45.96
   ATOM 518  CD2 LEU 77   22.284  19.550  72.835  1.00 46.75
   ATOM 519  C   LEU 77   24.662  15.933  71.851  1.00 43.78
```

- 34 -

|  | ATOM | 520 | O | LEU | 77 | 25. 529 | 15. 635 | 71. 026 | 1. 00 | 43. 07 |
|---|------|-----|---|-----|----|---------|---------|---------|-------|--------|
|  | ATOM | 521 | N | ASP | 78 | 23. 946 | 15. 021 | 72. 496 | 1. 00 | 44. 50 |
|  | ATOM | 522 | CA | ASP | 78 | 24. 151 | 13. 604 | 72. 244 | 1. 00 | 44. 82 |
|  | ATOM | 523 | CB | ASP | 78 | 25. 126 | 13. 026 | 73. 271 | 1. 00 | 44. 71 |
| 5 | ATOM | 524 | CG | ASP | 78 | 25. 597 | 11. 628 | 72. 905 | 1. 00 | 45. 55 |
|  | ATOM | 525 | OD1 | ASP | 78 | 24. 738 | 10. 750 | 72. 672 | 1. 00 | 41. 76 |
|  | ATOM | 526 | OD2 | ASP | 78 | 26. 828 | 11. 410 | 72. 853 | 1. 00 | 45. 32 |
|  | ATOM | 527 | C | ASP | 78 | 22. 838 | 12. 829 | 72. 276 | 1. 00 | 44. 74 |
|  | ATOM | 528 | O | ASP | 78 | 22. 245 | 12. 633 | 73. 333 | 1. 00 | 45. 25 |
| 10 | ATOM | 529 | N | LEU | 79 | 22. 385 | 12. 398 | 71. 107 | 1. 00 | 45. 72 |
|  | ATOM | 530 | CA | LEU | 79 | 21. 154 | 11. 630 | 70. 994 | 1. 00 | 47. 25 |
|  | ATOM | 531 | CB | LEU | 79 | 20. 137 | 12. 351 | 70. 116 | 1. 00 | 45. 37 |
|  | ATOM | 532 | CG | LEU | 79 | 18. 865 | 11. 530 | 69. 915 | 1. 00 | 43. 65 |
|  | ATOM | 533 | CD1 | LEU | 79 | 18. 067 | 11. 553 | 71. 200 | 1. 00 | 46. 42 |
| 15 | ATOM | 534 | CD2 | LEU | 79 | 18. 045 | 12. 086 | 68. 777 | 1. 00 | 43. 81 |
|  | ATOM | 535 | C | LEU | 79 | 21. 491 | 10. 295 | 70. 354 | 1. 00 | 49. 50 |
|  | ATOM | 536 | O | LEU | 79 | 22. 073 | 10. 249 | 69. 274 | 1. 00 | 49. 35 |
|  | ATOM | 537 | N | GLY | 80 | 21. 123 | 9. 207 | 71. 016 | 1. 00 | 52. 24 |
|  | ATOM | 538 | CA | GLY | 80 | 21. 421 | 7. 902 | 70. 466 | 1. 00 | 56. 31 |
| 20 | ATOM | 539 | C | GLY | 80 | 20. 965 | 6. 833 | 71. 420 | 1. 00 | 59. 13 |
|  | ATOM | 540 | O | GLY | 80 | 20. 278 | 5. 896 | 71. 027 | 1. 00 | 60. 86 |
|  | ATOM | 541 | N | GLY | 81 | 21. 360 | 6. 966 | 72. 679 | 1. 00 | 62. 30 |
|  | ATOM | 542 | CA | GLY | 81 | 20. 940 | 6. 002 | 73. 674 | 1. 00 | 65. 60 |
|  | ATOM | 543 | C | GLY | 81 | 19. 551 | 6. 395 | 74. 137 | 1. 00 | 67. 84 |
| 25 | ATOM | 544 | O | GLY | 81 | 18. 936 | 7. 301 | 73. 564 | 1. 00 | 69. 00 |
|  | ATOM | 545 | N | THR | 82 | 19. 047 | 5. 722 | 75. 165 | 1. 00 | 69. 33 |
|  | ATOM | 546 | CA | THR | 82 | 17. 726 | 6. 037 | 75. 695 | 1. 00 | 70. 36 |
|  | ATOM | 547 | CB | THR | 82 | 17. 110 | 4. 824 | 76. 418 | 1. 00 | 71. 43 |
|  | ATOM | 548 | OG1 | THR | 82 | 18. 032 | 4. 332 | 77. 398 | 1. 00 | 71. 60 |

- 35 -

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ATOM | 549 | CG2 | THR | 82 | 16.784 | 3.716 | 75.420 | 1.00 71.87 |
| ATOM | 550 | C | THR | 82 | 17.846 | 7.196 | 76.679 | 1.00 70.10 |
| ATOM | 551 | O | THR | 82 | 16.933 | 7.458 | 77.464 | 1.00 71.18 |
| ATOM | 552 | N | ASN | 83 | 18.981 | 7.887 | 76.625 | 1.00 69.08 |
| ATOM | 553 | CA | ASN | 83 | 19.232 | 9.017 | 77.508 | 1.00 68.14 |
| ATOM | 554 | CB | ASN | 83 | 20.161 | 8.584 | 78.646 | 1.00 69.98 |
| ATOM | 555 | CG | ASN | 83 | 19.862 | 9.300 | 79.948 | 1.00 70.80 |
| ATOM | 556 | OD1 | ASN | 83 | 20.627 | 9.213 | 80.909 | 1.00 71.46 |
| ATOM | 557 | ND2 | ASN | 83 | 18.739 | 10.004 | 79.990 | 1.00 72.56 |
| ATOM | 558 | C | ASN | 83 | 19.866 | 10.177 | 76.738 | 1.00 66.16 |
| ATOM | 559 | O | ASN | 83 | 21.050 | 10.136 | 76.407 | 1.00 66.52 |
| ATOM | 560 | N | PHE | 84 | 19.073 | 11.203 | 76.447 | 1.00 63.41 |
| ATOM | 561 | CA | PHE | 84 | 19.567 | 12.375 | 75.728 | 1.00 60.93 |
| ATOM | 562 | CB | PHE | 84 | 18.398 | 13.227 | 75.241 | 1.00 61.87 |
| ATOM | 563 | CG | PHE | 84 | 18.817 | 14.477 | 74.528 | 1.00 63.55 |
| ATOM | 564 | CD1 | PHE | 84 | 18.419 | 15.724 | 74.993 | 1.00 63.38 |
| ATOM | 565 | CD2 | PHE | 84 | 19.599 | 14.409 | 73.381 | 1.00 64.28 |
| ATOM | 566 | CE1 | PHE | 84 | 18.793 | 16.888 | 74.325 | 1.00 64.07 |
| ATOM | 567 | CE2 | PHE | 84 | 19.979 | 15.568 | 72.705 | 1.00 65.31 |
| ATOM | 568 | CZ | PHE | 84 | 19.574 | 16.810 | 73.179 | 1.00 64.75 |
| ATOM | 569 | C | PHE | 84 | 20.442 | 13.206 | 76.658 | 1.00 59.07 |
| ATOM | 570 | O | PHE | 84 | 20.011 | 13.582 | 77.744 | 1.00 59.19 |
| ATOM | 571 | N | ARG | 85 | 21.665 | 13.500 | 76.232 | 1.00 57.25 |
| ATOM | 572 | CA | ARG | 85 | 22.583 | 14.272 | 77.064 | 1.00 56.05 |
| ATOM | 573 | CB | ARG | 85 | 23.857 | 13.467 | 77.344 | 1.00 56.68 |
| ATOM | 574 | CG | ARG | 85 | 23.605 | 12.044 | 77.828 | 1.00 58.78 |
| ATOM | 575 | CD | ARG | 85 | 24.896 | 11.367 | 78.267 | 1.00 59.39 |
| ATOM | 576 | NE | ARG | 85 | 25.908 | 11.348 | 77.213 | 1.00 59.87 |
| ATOM | 577 | CZ | ARG | 85 | 27.068 | 11.994 | 77.282 | 1.00 60.09 |

- 36 -

| | ATOM | 578 | NH1 | ARG | 85 | 27.366 | 12.713 | 78.357 | 1.00 | 59.50 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 579 | NH2 | ARG | 85 | 27.931 | 11.920 | 76.277 | 1.00 | 60.92 |
| | ATOM | 580 | C | ARG | 85 | 22.966 | 15.602 | 76.433 | 1.00 | 55.07 |
| | ATOM | 581 | O | ARG | 85 | 23.038 | 15.725 | 75.209 | 1.00 | 54.93 |
| 5 | ATOM | 582 | N | VAL | 86 | 23.211 | 16.593 | 77.288 | 1.00 | 53.13 |
| | ATOM | 583 | CA | VAL | 86 | 23.598 | 17.935 | 76.861 | 1.00 | 51.01 |
| | ATOM | 584 | CB | VAL | 86 | 22.425 | 18.939 | 77.003 | 1.00 | 51.19 |
| | ATOM | 585 | CG1 | VAL | 86 | 22.851 | 20.313 | 76.509 | 1.00 | 51.39 |
| | ATOM | 586 | CG2 | VAL | 86 | 21.216 | 18.446 | 76.225 | 1.00 | 50.96 |
| 10 | ATOM | 587 | C | VAL | 86 | 24.734 | 18.381 | 77.767 | 1.00 | 49.34 |
| | ATOM | 588 | O | VAL | 86 | 24.613 | 18.316 | 78.989 | 1.00 | 48.07 |
| | ATOM | 589 | N | MET | 87 | 25.834 | 18.835 | 77.178 | 1.00 | 49.52 |
| | ATOM | 590 | CA | MET | 87 | 26.970 | 19.260 | 77.981 | 1.00 | 50.78 |
| | ATOM | 591 | CB | MET | 87 | 27.864 | 18.054 | 78.284 | 1.00 | 52.70 |
| 15 | ATOM | 592 | CG | MET | 87 | 28.572 | 17.461 | 77.072 | 1.00 | 54.49 |
| | ATOM | 593 | SD | MET | 87 | 29.005 | 15.694 | 77.269 | 1.00 | 53.62 |
| | ATOM | 594 | CE | MET | 87 | 27.839 | 14.951 | 76.090 | 1.00 | 51.63 |
| | ATOM | 595 | C | MET | 87 | 27.800 | 20.363 | 77.348 | 1.00 | 50.56 |
| | ATOM | 596 | O | MET | 87 | 27.715 | 20.616 | 76.149 | 1.00 | 50.18 |
| 20 | ATOM | 597 | N | LEU | 88 | 28.605 | 21.015 | 78.178 | 1.00 | 50.90 |
| | ATOM | 598 | CA | LEU | 88 | 29.477 | 22.093 | 77.739 | 1.00 | 52.10 |
| | ATOM | 599 | CB | LEU | 88 | 29.278 | 23.325 | 78.631 | 1.00 | 53.23 |
| | ATOM | 600 | CG | LEU | 88 | 30.087 | 24.580 | 78.288 | 1.00 | 54.71 |
| | ATOM | 601 | CD1 | LEU | 88 | 29.618 | 25.140 | 76.951 | 1.00 | 54.33 |
| 25 | ATOM | 602 | CD2 | LEU | 88 | 29.920 | 25.623 | 79.390 | 1.00 | 54.33 |
| | ATOM | 603 | C | LEU | 88 | 30.914 | 21.600 | 77.847 | 1.00 | 52.33 |
| | ATOM | 604 | O | LEU | 88 | 31.311 | 21.048 | 78.877 | 1.00 | 53.12 |
| | ATOM | 605 | N | VAL | 89 | 31.693 | 21.795 | 76.789 | 1.00 | 52.10 |
| | ATOM | 606 | CA | VAL | 89 | 33.078 | 21.342 | 76.788 | 1.00 | 52.46 |

- 37 -

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | ATOM | 607 | CB | VAL | 89 | 33. 241 | 20. 072 | 75. 882 | 1. 00 | 50. 52 |
| | ATOM | 608 | CG1 | VAL | 89 | 32. 289 | 20. 147 | 74. 710 | 1. 00 | 52. 35 |
| | ATOM | 609 | CG2 | VAL | 89 | 34. 674 | 19. 939 | 75. 388 | 1. 00 | 46. 86 |
| | ATOM | 610 | C | VAL | 89 | 34. 049 | 22. 433 | 76. 357 | 1. 00 | 53. 35 |
| 5 | ATOM | 611 | O | VAL | 89 | 33. 858 | 23. 081 | 75. 336 | 1. 00 | 54. 69 |
| | ATOM | 612 | N | LYS | 90 | 35. 096 | 22. 625 | 77. 151 | 1. 00 | 55. 22 |
| | ATOM | 613 | CA | LYS | 90 | 36. 100 | 23. 640 | 76. 868 | 1. 00 | 56. 94 |
| | ATOM | 614 | CB | LYS | 90 | 36. 656 | 24. 205 | 78. 181 | 1. 00 | 57. 66 |
| | ATOM | 615 | CG | LYS | 90 | 37. 642 | 25. 360 | 78. 005 | 1. 00 | 58. 70 |
| 10 | ATOM | 616 | CD | LYS | 90 | 38. 140 | 25. 909 | 79. 345 | 1. 00 | 59. 35 |
| | ATOM | 617 | CE | LYS | 90 | 36. 995 | 26. 399 | 80. 226 | 1. 00 | 60. 64 |
| | ATOM | 618 | NZ | LYS | 90 | 36. 185 | 27. 462 | 79. 568 | 1. 00 | 61. 04 |
| | ATOM | 619 | C | LYS | 90 | 37. 237 | 23. 078 | 76. 019 | 1. 00 | 57. 63 |
| | ATOM | 620 | O | LYS | 90 | 37. 921 | 22. 136 | 76. 417 | 1. 00 | 57. 69 |
| 15 | ATOM | 621 | N | VAL | 91 | 37. 428 | 23. 670 | 74. 846 | 1. 00 | 58. 29 |
| | ATOM | 622 | CA | VAL | 91 | 38. 473 | 23. 254 | 73. 919 | 1. 00 | 57. 11 |
| | ATOM | 623 | CB | VAL | 91 | 37. 920 | 23. 136 | 72. 480 | 1. 00 | 56. 48 |
| | ATOM | 624 | CG1 | VAL | 91 | 39. 010 | 22. 661 | 71. 533 | 1. 00 | 55. 29 |
| | ATOM | 625 | CG2 | VAL | 91 | 36. 741 | 22. 183 | 72. 459 | 1. 00 | 55. 52 |
| 20 | ATOM | 626 | C | VAL | 91 | 39. 598 | 24. 279 | 73. 926 | 1. 00 | 57. 81 |
| | ATOM | 627 | O | VAL | 91 | 39. 365 | 25. 466 | 73. 710 | 1. 00 | 59. 53 |
| | ATOM | 628 | N | GLY | 92 | 40. 817 | 23. 819 | 74. 172 | 1. 00 | 58. 12 |
| | ATOM | 629 | CA | GLY | 92 | 41. 947 | 24. 723 | 74. 200 | 1. 00 | 59. 69 |
| | ATOM | 630 | C | GLY | 92 | 43. 047 | 24. 245 | 73. 286 | 1. 00 | 61. 78 |
| 25 | ATOM | 631 | O | GLY | 92 | 42. 821 | 23. 381 | 72. 448 | 1. 00 | 61. 06 |
| | ATOM | 632 | N | GLU | 93 | 44. 240 | 24. 803 | 73. 449 | 1. 00 | 65. 18 |
| | ATOM | 633 | CA | GLU | 93 | 45. 373 | 24. 426 | 72. 619 | 1. 00 | 69. 00 |
| | ATOM | 634 | CB | GLU | 93 | 45. 897 | 25. 646 | 71. 866 | 1. 00 | 71. 56 |
| | ATOM | 635 | CG | GLU | 93 | 47. 082 | 25. 344 | 70. 965 | 1. 00 | 75. 20 |

- 38 -

|   | ATOM | 636 | CD  | GLU 93 | 47.659 | 26.591 | 70.325 | 1.00 | 78.28 |
|---|------|-----|-----|--------|--------|--------|--------|------|-------|
|   | ATOM | 637 | OE1 | GLU 93 | 46.893 | 27.326 | 69.659 | 1.00 | 80.05 |
|   | ATOM | 638 | OE2 | GLU 93 | 48.877 | 26.834 | 70.485 | 1.00 | 79.21 |
|   | ATOM | 639 | C   | GLU 93 | 46.505 | 23.822 | 73.437 | 1.00 | 71.00 |
| 5 | ATOM | 640 | O   | GLU 93 | 47.118 | 24.500 | 74.263 | 1.00 | 70.74 |
|   | ATOM | 641 | N   | GLY 94 | 46.784 | 22.544 | 73.195 | 1.00 | 72.97 |
|   | ATOM | 642 | CA  | GLY 94 | 47.849 | 21.869 | 73.916 | 1.00 | 74.44 |
|   | ATOM | 643 | C   | GLY 94 | 49.078 | 21.673 | 73.052 | 1.00 | 75.82 |
|   | ATOM | 644 | O   | GLY 94 | 49.485 | 22.577 | 72.315 | 1.00 | 76.47 |
| 10 | ATOM | 645 | N   | GLU 95 | 49.682 | 20.496 | 73.145 | 1.00 | 75.73 |
|   | ATOM | 646 | CA  | GLU 95 | 50.859 | 20.195 | 72.349 | 1.00 | 76.61 |
|   | ATOM | 647 | CB  | GLU 95 | 52.023 | 19.792 | 73.249 | 1.00 | 76.93 |
|   | ATOM | 648 | CG  | GLU 95 | 52.439 | 20.891 | 74.203 | 1.00 | 78.31 |
|   | ATOM | 649 | CD  | GLU 95 | 53.614 | 20.497 | 75.065 | 1.00 | 78.40 |
| 15 | ATOM | 650 | OE1 | GLU 95 | 54.715 | 20.274 | 74.514 | 1.00 | 78.51 |
|   | ATOM | 651 | OE2 | GLU 95 | 53.432 | 20.408 | 76.295 | 1.00 | 78.60 |
|   | ATOM | 652 | C   | GLU 95 | 50.516 | 19.071 | 71.392 | 1.00 | 76.91 |
|   | ATOM | 653 | O   | GLU 95 | 49.833 | 18.116 | 71.764 | 1.00 | 76.81 |
|   | ATOM | 654 | N   | GLU 96 | 50.987 | 19.203 | 70.155 | 1.00 | 77.78 |
| 20 | ATOM | 655 | CA  | GLU 96 | 50.733 | 18.220 | 69.105 | 1.00 | 78.07 |
|   | ATOM | 656 | CB  | GLU 96 | 51.408 | 16.881 | 69.440 | 1.00 | 81.32 |
|   | ATOM | 657 | CG  | GLU 96 | 52.943 | 16.930 | 69.454 | 1.00 | 85.11 |
|   | ATOM | 658 | CD  | GLU 96 | 53.541 | 17.309 | 68.101 | 1.00 | 87.05 |
|   | ATOM | 659 | OE1 | GLU 96 | 53.346 | 16.551 | 67.124 | 1.00 | 88.73 |
| 25 | ATOM | 660 | OE2 | GLU 96 | 54.207 | 18.365 | 68.014 | 1.00 | 87.56 |
|   | ATOM | 661 | C   | GLU 96 | 49.230 | 18.025 | 68.919 | 1.00 | 75.88 |
|   | ATOM | 662 | O   | GLU 96 | 48.784 | 17.039 | 68.327 | 1.00 | 75.92 |
|   | ATOM | 663 | N   | GLY 97 | 48.456 | 18.980 | 69.427 | 1.00 | 72.88 |
|   | ATOM | 664 | CA  | GLY 97 | 47.013 | 18.910 | 69.309 | 1.00 | 69.37 |

- 39 -

```
      ATOM 665   C    GLY 97      46. 296   19. 710   70. 380   1. 00  67. 02
      ATOM 666   O    GLY 97      46. 921   20. 230   71. 305   1. 00  67. 10
      ATOM 667   N    GLN 98      44. 978   19. 811   70. 250   1. 00  64. 76
      ATOM 668   CA   GLN 98      44. 166   20. 543   71. 211   1. 00  62. 45
   5  ATOM 669   CB   GLN 98      42. 872   21. 045   70. 562   1. 00  62. 69
      ATOM 670   CG   GLN 98      43. 026   21. 908   69. 315   1. 00  64. 93
      ATOM 671   CD   GLN 98      43. 191   21. 095   68. 046   1. 00  65. 89
      ATOM 672   OE1  GLN 98      44. 299   20. 684   67. 696   1. 00  65. 96
      ATOM 673   NE2  GLN 98      42. 079   20. 847   67. 353   1. 00  65. 22
  10  ATOM 674   C    GLN 98      43. 781   19. 630   72. 369   1. 00  61. 23
      ATOM 675   O    GLN 98      43. 880   18. 403   72. 269   1. 00  62. 18
      ATOM 676   N    TRP 99      43. 356   20. 233   73. 473   1. 00  57. 45
      ATOM 677   CA   TRP 99      42. 893   19. 459   74. 611   1. 00  54. 44
      ATOM 678   CB   TRP 99      43. 639   19. 822   75. 904   1. 00  55. 51
  15  ATOM 679   CG   TRP 99      43. 770   21. 291   76. 211   1. 00  56. 94
      ATOM 680   CD2  TRP 99      42. 763   22. 151   76. 756   1. 00  56. 03
      ATOM 681   CE2  TRP 99      43. 345   23. 426   76. 922   1. 00  57. 25
      ATOM 682   CE3  TRP 99      41. 422   21. 969   77. 121   1. 00  56. 67
      ATOM 683   CD1  TRP 99      44. 892   22. 062   76. 068   1. 00  56. 29
  20  ATOM 684   NE1  TRP 99      44. 647   23. 342   76. 495   1. 00  56. 55
      ATOM 685   CZ2  TRP 99      42. 635   24. 516   77. 440   1. 00  56. 53
      ATOM 686   CZ3  TRP 99      40. 712   23. 053   77. 637   1. 00  56. 67
      ATOM 687   CH2  TRP 99      41. 322   24. 309   77. 790   1. 00  56. 70
      ATOM 688   C    TRP 99      41. 408   19. 756   74. 737   1. 00  52. 04
  25  ATOM 689   O    TRP 99      40. 899   20. 664   74. 089   1. 00  50. 70
      ATOM 690   N    SER  100    40. 704   18. 981   75. 545   1. 00  49. 57
      ATOM 691   CA   SER  100    39. 277   19. 186   75. 715   1. 00  48. 29
      ATOM 692   CB   SER  100    38. 506   18. 475   74. 597   1. 00  49. 26
      ATOM 693   OG   SER  100    39. 055   17. 196   74. 315   1. 00  47. 27
```

- 40 -

|  | ATOM | 694 | C | SER | 100 | 38.860 | 18.655 | 77.067 | 1.00 | 47.91 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 695 | O | SER | 100 | 39.569 | 17.845 | 77.662 | 1.00 | 48.73 |
|  | ATOM | 696 | N | VAL | 101 | 37.718 | 19.120 | 77.558 | 1.00 | 47.53 |
|  | ATOM | 697 | CA | VAL | 101 | 37.225 | 18.684 | 78.852 | 1.00 | 47.86 |
| 5 | ATOM | 698 | CB | VAL | 101 | 38.102 | 19.233 | 79.995 | 1.00 | 47.92 |
|  | ATOM | 699 | CG1 | VAL | 101 | 38.160 | 20.747 | 79.923 | 1.00 | 49.02 |
|  | ATOM | 700 | CG2 | VAL | 101 | 37.545 | 18.783 | 81.342 | 1.00 | 47.98 |
|  | ATOM | 701 | C | VAL | 101 | 35.784 | 19.102 | 79.101 | 1.00 | 48.77 |
|  | ATOM | 702 | O | VAL | 101 | 35.391 | 20.228 | 78.798 | 1.00 | 49.05 |
| 10 | ATOM | 703 | N | LYS | 102 | 35.004 | 18.176 | 79.649 | 1.00 | 49.04 |
|  | ATOM | 704 | CA | LYS | 102 | 33.607 | 18.422 | 79.969 | 1.00 | 50.31 |
|  | ATOM | 705 | CB | LYS | 102 | 32.875 | 17.101 | 80.220 | 1.00 | 51.15 |
|  | ATOM | 706 | CG | LYS | 102 | 31.385 | 17.263 | 80.452 | 1.00 | 52.57 |
|  | ATOM | 707 | CD | LYS | 102 | 30.835 | 16.229 | 81.425 | 1.00 | 56.56 |
| 15 | ATOM | 708 | CE | LYS | 102 | 30.955 | 14.804 | 80.908 | 1.00 | 57.06 |
|  | ATOM | 709 | NZ | LYS | 102 | 30.275 | 13.804 | 81.787 | 1.00 | 58.08 |
|  | ATOM | 710 | C | LYS | 102 | 33.587 | 19.254 | 81.243 | 1.00 | 51.12 |
|  | ATOM | 711 | O | LYS | 102 | 34.220 | 18.888 | 82.234 | 1.00 | 52.47 |
|  | ATOM | 712 | N | THR | 103 | 32.859 | 20.366 | 81.217 | 1.00 | 51.40 |
| 20 | ATOM | 713 | CA | THR | 103 | 32.774 | 21.252 | 82.373 | 1.00 | 50.47 |
|  | ATOM | 714 | CB | THR | 103 | 33.004 | 22.715 | 81.965 | 1.00 | 50.28 |
|  | ATOM | 715 | OG1 | THR | 103 | 31.992 | 23.113 | 81.032 | 1.00 | 51.29 |
|  | ATOM | 716 | CG2 | THR | 103 | 34.368 | 22.879 | 81.324 | 1.00 | 47.52 |
|  | ATOM | 717 | C | THR | 103 | 31.416 | 21.148 | 83.048 | 1.00 | 50.90 |
| 25 | ATOM | 718 | O | THR | 103 | 31.329 | 21.056 | 84.268 | 1.00 | 50.91 |
|  | ATOM | 719 | N | LYS | 104 | 30.358 | 21.162 | 82.247 | 1.00 | 52.41 |
|  | ATOM | 720 | CA | LYS | 104 | 29.000 | 21.063 | 82.770 | 1.00 | 54.04 |
|  | ATOM | 721 | CB | LYS | 104 | 28.310 | 22.436 | 82.714 | 1.00 | 57.21 |
|  | ATOM | 722 | CG | LYS | 104 | 28.823 | 23.450 | 83.739 | 1.00 | 59.16 |

|  | ATOM | 723 | CD | LYS | 104 | 28.138 | 24.809 | 83.576 | 1.00 | 62.54 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 724 | CE | LYS | 104 | 28.398 | 25.734 | 84.766 | 1.00 | 62.99 |
|  | ATOM | 725 | NZ | LYS | 104 | 27.798 | 25.217 | 86.037 | 1.00 | 64.17 |
|  | ATOM | 726 | C | LYS | 104 | 28.215 | 20.047 | 81.948 | 1.00 | 53.79 |
| 5 | ATOM | 727 | O | LYS | 104 | 28.411 | 19.941 | 80.740 | 1.00 | 53.53 |
|  | ATOM | 728 | N | HIS | 105 | 27.330 | 19.299 | 82.600 | 1.00 | 53.65 |
|  | ATOM | 729 | CA | HIS | 105 | 26.539 | 18.295 | 81.903 | 1.00 | 55.05 |
|  | ATOM | 730 | CB | HIS | 105 | 27.316 | 16.972 | 81.837 | 1.00 | 55.94 |
|  | ATOM | 731 | CG | HIS | 105 | 27.668 | 16.397 | 83.176 | 1.00 | 55.84 |
| 10 | ATOM | 732 | CD2 | HIS | 105 | 28.793 | 16.501 | 83.924 | 1.00 | 55.19 |
|  | ATOM | 733 | ND1 | HIS | 105 | 26.803 | 15.602 | 83.897 | 1.00 | 55.83 |
|  | ATOM | 734 | CE1 | HIS | 105 | 27.380 | 15.241 | 85.030 | 1.00 | 56.35 |
|  | ATOM | 735 | NE2 | HIS | 105 | 28.589 | 15.773 | 85.071 | 1.00 | 55.64 |
|  | ATOM | 736 | C | HIS | 105 | 25.169 | 18.074 | 82.534 | 1.00 | 56.32 |
| 15 | ATOM | 737 | O | HIS | 105 | 24.903 | 18.535 | 83.640 | 1.00 | 56.55 |
|  | ATOM | 738 | N | GLN | 106 | 24.302 | 17.365 | 81.817 | 1.00 | 58.21 |
|  | ATOM | 739 | CA | GLN | 106 | 22.950 | 17.090 | 82.289 | 1.00 | 60.74 |
|  | ATOM | 740 | CB | GLN | 106 | 22.108 | 18.367 | 82.224 | 1.00 | 61.97 |
|  | ATOM | 741 | CG | GLN | 106 | 20.775 | 18.285 | 82.945 | 1.00 | 64.86 |
| 20 | ATOM | 742 | CD | GLN | 106 | 20.928 | 18.379 | 84.447 | 1.00 | 67.03 |
|  | ATOM | 743 | OE1 | GLN | 106 | 21.447 | 19.370 | 84.969 | 1.00 | 68.82 |
|  | ATOM | 744 | NE2 | GLN | 106 | 20.479 | 17.348 | 85.155 | 1.00 | 67.41 |
|  | ATOM | 745 | C | GLN | 106 | 22.322 | 16.025 | 81.396 | 1.00 | 61.62 |
|  | ATOM | 746 | O | GLN | 106 | 22.532 | 16.027 | 80.186 | 1.00 | 62.03 |
| 25 | ATOM | 747 | N | MET | 107 | 21.550 | 15.121 | 81.990 | 1.00 | 63.03 |
|  | ATOM | 748 | CA | MET | 107 | 20.900 | 14.058 | 81.232 | 1.00 | 64.74 |
|  | ATOM | 749 | CB | MET | 107 | 21.322 | 12.688 | 81.769 | 1.00 | 66.23 |
|  | ATOM | 750 | CG | MET | 107 | 22.821 | 12.456 | 81.786 | 1.00 | 68.74 |
|  | ATOM | 751 | SD | MET | 107 | 23.248 | 10.812 | 82.388 | 1.00 | 70.84 |

- 42 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 752 | CE | MET | 107 | 23.427 | 9.926 | 80.853 | 1.00 | 71.13 |
| ATOM | 753 | C | MET | 107 | 19.385 | 14.175 | 81.313 | 1.00 | 65.81 |
| ATOM | 754 | O | MET | 107 | 18.837 | 14.489 | 82.369 | 1.00 | 65.52 |
| ATOM | 755 | N | TYR | 108 | 18.712 | 13.915 | 80.196 | 1.00 | 66.87 |
| ATOM | 756 | CA | TYR | 108 | 17.258 | 13.984 | 80.143 | 1.00 | 68.20 |
| ATOM | 757 | CB | TYR | 108 | 16.800 | 15.167 | 79.286 | 1.00 | 67.20 |
| ATOM | 758 | CG | TYR | 108 | 17.436 | 16.484 | 79.660 | 1.00 | 66.35 |
| ATOM | 759 | CD1 | TYR | 108 | 18.781 | 16.731 | 79.386 | 1.00 | 65.95 |
| ATOM | 760 | CE1 | TYR | 108 | 19.380 | 17.929 | 79.746 | 1.00 | 65.76 |
| ATOM | 761 | CD2 | TYR | 108 | 16.702 | 17.477 | 80.307 | 1.00 | 66.24 |
| ATOM | 762 | CE2 | TYR | 108 | 17.292 | 18.683 | 80.674 | 1.00 | 65.93 |
| ATOM | 763 | CZ | TYR | 108 | 18.633 | 18.902 | 80.391 | 1.00 | 66.14 |
| ATOM | 764 | OH | TYR | 108 | 19.235 | 20.083 | 80.763 | 1.00 | 64.27 |
| ATOM | 765 | C | TYR | 108 | 16.706 | 12.700 | 79.549 | 1.00 | 70.20 |
| ATOM | 766 | O | TYR | 108 | 16.995 | 12.363 | 78.404 | 1.00 | 70.55 |
| ATOM | 767 | N | SER | 109 | 15.912 | 11.982 | 80.331 | 1.00 | 73.54 |
| ATOM | 768 | CA | SER | 109 | 15.322 | 10.739 | 79.863 | 1.00 | 76.84 |
| ATOM | 769 | CB | SER | 109 | 14.524 | 10.082 | 80.992 | 1.00 | 77.63 |
| ATOM | 770 | OG | SER | 109 | 15.353 | 9.837 | 82.120 | 1.00 | 78.13 |
| ATOM | 771 | C | SER | 109 | 14.419 | 11.020 | 78.664 | 1.00 | 78.98 |
| ATOM | 772 | O | SER | 109 | 13.936 | 12.138 | 78.486 | 1.00 | 78.51 |
| ATOM | 773 | N | ILE | 110 | 14.198 | 10.002 | 77.841 | 1.00 | 82.34 |
| ATOM | 774 | CA | ILE | 110 | 13.369 | 10.143 | 76.651 | 1.00 | 86.07 |
| ATOM | 775 | CB | ILE | 110 | 13.892 | 9.249 | 75.511 | 1.00 | 86.28 |
| ATOM | 776 | CG2 | ILE | 110 | 13.092 | 9.505 | 74.242 | 1.00 | 86.56 |
| ATOM | 777 | CG1 | ILE | 110 | 15.379 | 9.529 | 75.275 | 1.00 | 86.19 |
| ATOM | 778 | CD1 | ILE | 110 | 16.025 | 8.612 | 74.258 | 1.00 | 86.76 |
| ATOM | 779 | C | ILE | 110 | 11.916 | 9.772 | 76.927 | 1.00 | 88.58 |
| ATOM | 780 | O | ILE | 110 | 11.596 | 8.606 | 77.152 | 1.00 | 88.69 |

- 43 -

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | ATOM | 781 | N | PRO | 111 | 11. 016 | 10. 767 | 76. 910 | 1. 00 91. 13 |
| | ATOM | 782 | CD | PRO | 111 | 11. 319 | 12. 205 | 76. 811 | 1. 00 91. 83 |
| | ATOM | 783 | CA | PRO | 111 | 9. 585 | 10. 562 | 77. 157 | 1. 00 93. 32 |
| | ATOM | 784 | CB | PRO | 111 | 9. 015 | 11. 975 | 77. 062 | 1. 00 93. 16 |
| 5 | ATOM | 785 | CG | PRO | 111 | 10. 147 | 12. 819 | 77. 536 | 1. 00 92. 31 |
| | ATOM | 786 | C | PRO | 111 | 8. 928 | 9. 613 | 76. 159 | 1. 00 95. 40 |
| | ATOM | 787 | O | PRO | 111 | 9. 466 | 9. 355 | 75. 082 | 1. 00 95. 80 |
| | ATOM | 788 | N | GLU | 112 | 7. 758 | 9. 101 | 76. 529 | 1. 00 97. 55 |
| | ATOM | 789 | CA | GLU | 112 | 7. 006 | 8. 185 | 75. 679 | 1. 00 99. 50 |
| 10 | ATOM | 790 | CB | GLU | 112 | 5. 816 | 7. 611 | 76. 458 | 1. 00100. 31 |
| | ATOM | 791 | CG | GLU | 112 | 4. 745 | 6. 971 | 75. 589 | 1. 00101. 76 |
| | ATOM | 792 | CD | GLU | 112 | 5. 316 | 5. 989 | 74. 587 | 1. 00102. 84 |
| | ATOM | 793 | OE1 | GLU | 112 | 5. 967 | 5. 012 | 75. 014 | 1. 00103. 66 |
| | ATOM | 794 | OE2 | GLU | 112 | 5. 113 | 6. 196 | 73. 372 | 1. 00103. 00 |
| 15 | ATOM | 795 | C | GLU | 112 | 6. 508 | 8. 884 | 74. 418 | 1. 00100. 37 |
| | ATOM | 796 | O | GLU | 112 | 6. 914 | 8. 545 | 73. 304 | 1. 00100. 17 |
| | ATOM | 797 | N | ASP | 113 | 5. 625 | 9. 859 | 74. 606 | 1. 00101. 44 |
| | ATOM | 798 | CA | ASP | 113 | 5. 056 | 10. 620 | 73. 499 | 1. 00102. 05 |
| | ATOM | 799 | CB | ASP | 113 | 4. 087 | 11. 680 | 74. 038 | 1. 00102. 23 |
| 20 | ATOM | 800 | CG | ASP | 113 | 4. 682 | 12. 494 | 75. 177 | 1. 00102. 33 |
| | ATOM | 801 | OD1 | ASP | 113 | 4. 961 | 11. 913 | 76. 249 | 1. 00102. 01 |
| | ATOM | 802 | OD2 | ASP | 113 | 4. 870 | 13. 716 | 74. 999 | 1. 00101. 99 |
| | ATOM | 803 | C | ASP | 113 | 6. 131 | 11. 282 | 72. 638 | 1. 00102. 09 |
| | ATOM | 804 | O | ASP | 113 | 5. 843 | 11. 789 | 71. 553 | 1. 00101. 96 |
| 25 | ATOM | 805 | N | ALA | 114 | 7. 368 | 11. 273 | 73. 126 | 1. 00102. 12 |
| | ATOM | 806 | CA | ALA | 114 | 8. 484 | 11. 869 | 72. 401 | 1. 00102. 09 |
| | ATOM | 807 | CB | ALA | 114 | 9. 590 | 12. 256 | 73. 377 | 1. 00101. 76 |
| | ATOM | 808 | C | ALA | 114 | 9. 022 | 10. 895 | 71. 358 | 1. 00102. 06 |
| | ATOM | 809 | O | ALA | 114 | 9. 763 | 11. 282 | 70. 455 | 1. 00101. 89 |

- 44 -

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
|  | ATOM | 810 | N | MET | 115 | 8.640 | 9.630 | 71.491 | 1.00 | 102.04 |
|  | ATOM | 811 | CA | MET | 115 | 9.081 | 8.592 | 70.569 | 1.00 | 102.05 |
|  | ATOM | 812 | CB | MET | 115 | 9.466 | 7.331 | 71.346 | 1.00 | 102.77 |
|  | ATOM | 813 | CG | MET | 115 | 10.637 | 7.509 | 72.307 | 1.00 | 103.47 |
| 5 | ATOM | 814 | SD | MET | 115 | 12.256 | 7.549 | 71.502 | 1.00 | 104.26 |
|  | ATOM | 815 | CE | MET | 115 | 12.740 | 5.824 | 71.638 | 1.00 | 103.48 |
|  | ATOM | 816 | C | MET | 115 | 8.004 | 8.253 | 69.538 | 1.00 | 101.77 |
|  | ATOM | 817 | O | MET | 115 | 8.268 | 8.275 | 68.337 | 1.00 | 102.14 |
|  | ATOM | 818 | N | THR | 116 | 6.796 | 7.942 | 70.006 | 1.00 | 101.14 |
| 10 | ATOM | 819 | CA | THR | 116 | 5.690 | 7.590 | 69.110 | 1.00 | 100.36 |
|  | ATOM | 820 | CB | THR | 116 | 4.517 | 6.927 | 69.880 | 1.00 | 100.42 |
|  | ATOM | 821 | OG1 | THR | 116 | 5.004 | 5.805 | 70.625 | 1.00 | 100.29 |
|  | ATOM | 822 | CG2 | THR | 116 | 3.441 | 6.441 | 68.911 | 1.00 | 100.05 |
|  | ATOM | 823 | C | THR | 116 | 5.150 | 8.816 | 68.379 | 1.00 | 99.62 |
| 15 | ATOM | 824 | O | THR | 116 | 4.423 | 8.694 | 67.391 | 1.00 | 99.72 |
|  | ATOM | 825 | N | GLY | 117 | 5.510 | 9.996 | 68.870 | 1.00 | 98.62 |
|  | ATOM | 826 | CA | GLY | 117 | 5.048 | 11.224 | 68.252 | 1.00 | 97.42 |
|  | ATOM | 827 | C | GLY | 117 | 5.619 | 11.447 | 66.866 | 1.00 | 96.48 |
|  | ATOM | 828 | O | GLY | 117 | 5.746 | 10.511 | 66.074 | 1.00 | 96.38 |
| 20 | ATOM | 829 | N | THR | 118 | 5.962 | 12.696 | 66.570 | 1.00 | 95.25 |
|  | ATOM | 830 | CA | THR | 118 | 6.521 | 13.050 | 65.273 | 1.00 | 93.78 |
|  | ATOM | 831 | CB | THR | 118 | 5.679 | 14.133 | 64.578 | 1.00 | 93.57 |
|  | ATOM | 832 | OG1 | THR | 118 | 5.735 | 15.343 | 65.342 | 1.00 | 93.50 |
|  | ATOM | 833 | CG2 | THR | 118 | 4.234 | 13.685 | 64.457 | 1.00 | 93.65 |
| 25 | ATOM | 834 | C | THR | 118 | 7.936 | 13.583 | 65.440 | 1.00 | 92.67 |
|  | ATOM | 835 | O | THR | 118 | 8.335 | 13.976 | 66.537 | 1.00 | 92.39 |
|  | ATOM | 836 | N | ALA | 119 | 8.687 | 13.593 | 64.343 | 1.00 | 91.30 |
|  | ATOM | 837 | CA | ALA | 119 | 10.058 | 14.084 | 64.356 | 1.00 | 90.00 |
|  | ATOM | 838 | CB | ALA | 119 | 10.643 | 14.031 | 62.956 | 1.00 | 89.81 |

- 45 -

| | ATOM | 839 | C | ALA | 119 | 10.066 | 15.513 | 64.867 | 1.00 | 89.21 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 840 | O | ALA | 119 | 11.045 | 15.972 | 65.455 | 1.00 | 88.98 |
| | ATOM | 841 | N | GLU | 120 | 8.959 | 16.210 | 64.636 | 1.00 | 88.61 |
| | ATOM | 842 | CA | GLU | 120 | 8.819 | 17.593 | 65.063 | 1.00 | 87.61 |
| 5 | ATOM | 843 | CB | GLU | 120 | 7.505 | 18.177 | 64.536 | 1.00 | 87.74 |
| | ATOM | 844 | CG | GLU | 120 | 7.138 | 17.763 | 63.112 | 1.00 | 86.31 |
| | ATOM | 845 | CD | GLU | 120 | 8.269 | 17.956 | 62.120 | 1.00 | 85.84 |
| | ATOM | 846 | OE1 | GLU | 120 | 8.884 | 19.042 | 62.113 | 1.00 | 84.76 |
| | ATOM | 847 | OE2 | GLU | 120 | 8.535 | 17.020 | 61.336 | 1.00 | 85.71 |
| 10 | ATOM | 848 | C | GLU | 120 | 8.837 | 17.658 | 66.588 | 1.00 | 86.71 |
| | ATOM | 849 | O | GLU | 120 | 9.610 | 18.412 | 67.179 | 1.00 | 86.71 |
| | ATOM | 850 | N | MET | 121 | 7.980 | 16.859 | 67.216 | 1.00 | 85.74 |
| | ATOM | 851 | CA | MET | 121 | 7.895 | 16.817 | 68.671 | 1.00 | 84.85 |
| | ATOM | 852 | CB | MET | 121 | 6.798 | 15.842 | 69.111 | 1.00 | 84.04 |
| 15 | ATOM | 853 | CG | MET | 121 | 5.390 | 16.273 | 68.740 | 1.00 | 81.88 |
| | ATOM | 854 | SD | MET | 121 | 4.152 | 15.078 | 69.268 | 1.00 | 80.83 |
| | ATOM | 855 | CE | MET | 121 | 3.772 | 14.283 | 67.730 | 1.00 | 78.55 |
| | ATOM | 856 | C | MET | 121 | 9.226 | 16.397 | 69.286 | 1.00 | 84.73 |
| | ATOM | 857 | O | MET | 121 | 9.687 | 17.003 | 70.255 | 1.00 | 84.87 |
| 20 | ATOM | 858 | N | LEU | 122 | 9.839 | 15.360 | 68.717 | 1.00 | 84.21 |
| | ATOM | 859 | CA | LEU | 122 | 11.115 | 14.851 | 69.211 | 1.00 | 83.20 |
| | ATOM | 860 | CB | LEU | 122 | 11.711 | 13.847 | 68.221 | 1.00 | 83.29 |
| | ATOM | 861 | CG | LEU | 122 | 12.966 | 13.109 | 68.697 | 1.00 | 83.07 |
| | ATOM | 862 | CD1 | LEU | 122 | 12.612 | 12.232 | 69.885 | 1.00 | 82.78 |
| 25 | ATOM | 863 | CD2 | LEU | 122 | 13.533 | 12.261 | 67.572 | 1.00 | 82.52 |
| | ATOM | 864 | C | LEU | 122 | 12.110 | 15.980 | 69.448 | 1.00 | 82.61 |
| | ATOM | 865 | O | LEU | 122 | 12.546 | 16.204 | 70.575 | 1.00 | 82.47 |
| | ATOM | 866 | N | PHE | 123 | 12.467 | 16.694 | 68.385 | 1.00 | 82.28 |
| | ATOM | 867 | CA | PHE | 123 | 13.414 | 17.794 | 68.512 | 1.00 | 82.09 |

- 46 -

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ATOM | 868 | CB | PHE | 123 | 13.898 | 18.251 | 67.136 | 1.00 82.08 |
| ATOM | 869 | CG | PHE | 123 | 14.948 | 17.357 | 66.547 | 1.00 81.61 |
| ATOM | 870 | CD1 | PHE | 123 | 14.616 | 16.098 | 66.060 | 1.00 81.34 |
| ATOM | 871 | CD2 | PHE | 123 | 16.281 | 17.756 | 66.523 | 1.00 81.33 |
| ATOM | 872 | CE1 | PHE | 123 | 15.594 | 15.246 | 65.559 | 1.00 80.67 |
| ATOM | 873 | CE2 | PHE | 123 | 17.268 | 16.912 | 66.026 | 1.00 81.58 |
| ATOM | 874 | CZ | PHE | 123 | 16.923 | 15.653 | 65.543 | 1.00 81.33 |
| ATOM | 875 | C | PHE | 123 | 12.834 | 18.964 | 69.288 | 1.00 81.98 |
| ATOM | 876 | O | PHE | 123 | 13.570 | 19.838 | 69.747 | 1.00 81.74 |
| ATOM | 877 | N | ASP | 124 | 11.512 | 18.980 | 69.429 | 1.00 82.09 |
| ATOM | 878 | CA | ASP | 124 | 10.852 | 20.028 | 70.195 | 1.00 82.29 |
| ATOM | 879 | CB | ASP | 124 | 9.329 | 19.909 | 70.073 | 1.00 81.96 |
| ATOM | 880 | CG | ASP | 124 | 8.731 | 20.961 | 69.157 | 1.00 81.56 |
| ATOM | 881 | OD1 | ASP | 124 | 7.510 | 20.897 | 68.901 | 1.00 81.25 |
| ATOM | 882 | OD2 | ASP | 124 | 9.477 | 21.855 | 68.701 | 1.00 80.94 |
| ATOM | 883 | C | ASP | 124 | 11.279 | 19.808 | 71.641 | 1.00 82.22 |
| ATOM | 884 | O | ASP | 124 | 11.819 | 20.707 | 72.287 | 1.00 81.61 |
| ATOM | 885 | N | TYR | 125 | 11.047 | 18.595 | 72.133 | 1.00 82.59 |
| ATOM | 886 | CA | TYR | 125 | 11.420 | 18.233 | 73.494 | 1.00 83.66 |
| ATOM | 887 | CB | TYR | 125 | 11.048 | 16.771 | 73.767 | 1.00 85.84 |
| ATOM | 888 | CG | TYR | 125 | 11.533 | 16.240 | 75.100 | 1.00 88.74 |
| ATOM | 889 | CD1 | TYR | 125 | 12.763 | 15.590 | 75.209 | 1.00 89.83 |
| ATOM | 890 | CE1 | TYR | 125 | 13.222 | 15.110 | 76.437 | 1.00 91.28 |
| ATOM | 891 | CD2 | TYR | 125 | 10.770 | 16.399 | 76.257 | 1.00 90.41 |
| ATOM | 892 | CE2 | TYR | 125 | 11.221 | 15.926 | 77.493 | 1.00 91.86 |
| ATOM | 893 | CZ | TYR | 125 | 12.448 | 15.281 | 77.574 | 1.00 92.09 |
| ATOM | 894 | OH | TYR | 125 | 12.896 | 14.807 | 78.789 | 1.00 93.08 |
| ATOM | 895 | C | TYR | 125 | 12.917 | 18.451 | 73.704 | 1.00 82.86 |
| ATOM | 896 | O | TYR | 125 | 13.352 | 18.829 | 74.792 | 1.00 82.74 |

- 47 -

|  | ATOM | 897 | N | ILE | 126 | 13.701 | 18.215 | 72.655 | 1.00 | 81.74 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 898 | CA | ILE | 126 | 15.146 | 18.398 | 72.727 | 1.00 | 80.58 |
|  | ATOM | 899 | CB | ILE | 126 | 15.824 | 18.005 | 71.397 | 1.00 | 79.32 |
|  | ATOM | 900 | CG2 | ILE | 126 | 17.277 | 18.443 | 71.398 | 1.00 | 78.57 |
| 5 | ATOM | 901 | CG1 | ILE | 126 | 15.719 | 16.494 | 71.194 | 1.00 | 78.47 |
|  | ATOM | 902 | CD1 | ILE | 126 | 16.408 | 15.993 | 69.946 | 1.00 | 78.42 |
|  | ATOM | 903 | C | ILE | 126 | 15.479 | 19.852 | 73.047 | 1.00 | 80.87 |
|  | ATOM | 904 | O | ILE | 126 | 16.334 | 20.133 | 73.887 | 1.00 | 79.71 |
|  | ATOM | 905 | N | SER | 127 | 14.799 | 20.772 | 72.370 | 1.00 | 81.80 |
| 10 | ATOM | 906 | CA | SER | 127 | 15.018 | 22.196 | 72.594 | 1.00 | 82.44 |
|  | ATOM | 907 | CB | SER | 127 | 14.160 | 23.021 | 71.636 | 1.00 | 82.62 |
|  | ATOM | 908 | OG | SER | 127 | 14.559 | 22.807 | 70.294 | 1.00 | 83.20 |
|  | ATOM | 909 | C | SER | 127 | 14.668 | 22.543 | 74.034 | 1.00 | 82.44 |
|  | ATOM | 910 | O | SER | 127 | 15.318 | 23.382 | 74.660 | 1.00 | 81.86 |
| 15 | ATOM | 911 | N | GLU | 128 | 13.636 | 21.884 | 74.553 | 1.00 | 83.04 |
|  | ATOM | 912 | CA | GLU | 128 | 13.202 | 22.106 | 75.927 | 1.00 | 83.79 |
|  | ATOM | 913 | CB | GLU | 128 | 11.944 | 21.289 | 76.232 | 1.00 | 84.79 |
|  | ATOM | 914 | CG | GLU | 128 | 11.408 | 21.490 | 77.645 | 1.00 | 86.70 |
|  | ATOM | 915 | CD | GLU | 128 | 10.425 | 20.409 | 78.061 | 1.00 | 88.14 |
| 20 | ATOM | 916 | OE1 | GLU | 128 | 9.408 | 20.222 | 77.357 | 1.00 | 88.36 |
|  | ATOM | 917 | OE2 | GLU | 128 | 10.672 | 19.747 | 79.094 | 1.00 | 88.06 |
|  | ATOM | 918 | C | GLU | 128 | 14.318 | 21.686 | 76.877 | 1.00 | 83.42 |
|  | ATOM | 919 | O | GLU | 128 | 14.483 | 22.261 | 77.952 | 1.00 | 84.16 |
|  | ATOM | 920 | N | CYS | 129 | 15.081 | 20.675 | 76.475 | 1.00 | 82.77 |
| 25 | ATOM | 921 | CA | CYS | 129 | 16.177 | 20.179 | 77.295 | 1.00 | 81.21 |
|  | ATOM | 922 | CB | CYS | 129 | 16.554 | 18.760 | 76.873 | 1.00 | 81.07 |
|  | ATOM | 923 | SG | CYS | 129 | 15.206 | 17.569 | 77.006 | 1.00 | 80.63 |
|  | ATOM | 924 | C | CYS | 129 | 17.391 | 21.089 | 77.178 | 1.00 | 80.64 |
|  | ATOM | 925 | O | CYS | 129 | 18.092 | 21.330 | 78.160 | 1.00 | 79.84 |

- 48 -

|  | ATOM | 926 | N | ILE | 130 | 17.644 | 21.591 | 75.975 | 1.00 | 80.16 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 927 | CA | ILE | 130 | 18.782 | 22.475 | 75.775 | 1.00 | 80.33 |
|  | ATOM | 928 | CB | ILE | 130 | 18.944 | 22.860 | 74.298 | 1.00 | 79.59 |
|  | ATOM | 929 | CG2 | ILE | 130 | 20.253 | 23.614 | 74.102 | 1.00 | 79.29 |
| 5 | ATOM | 930 | CG1 | ILE | 130 | 18.933 | 21.599 | 73.436 | 1.00 | 79.00 |
|  | ATOM | 931 | CD1 | ILE | 130 | 19.069 | 21.860 | 71.958 | 1.00 | 79.73 |
|  | ATOM | 932 | C | ILE | 130 | 18.559 | 23.735 | 76.595 | 1.00 | 80.49 |
|  | ATOM | 933 | O | ILE | 130 | 19.475 | 24.241 | 77.239 | 1.00 | 80.22 |
|  | ATOM | 934 | N | SER | 131 | 17.326 | 24.229 | 76.574 | 1.00 | 81.09 |
| 10 | ATOM | 935 | CA | SER | 131 | 16.970 | 25.428 | 77.320 | 1.00 | 82.28 |
|  | ATOM | 936 | CB | SER | 131 | 15.525 | 25.826 | 77.006 | 1.00 | 83.15 |
|  | ATOM | 937 | OG | SER | 131 | 14.641 | 24.736 | 77.195 | 1.00 | 82.88 |
|  | ATOM | 938 | C | SER | 131 | 17.136 | 25.195 | 78.820 | 1.00 | 82.33 |
|  | ATOM | 939 | O | SER | 131 | 17.843 | 25.940 | 79.501 | 1.00 | 82.07 |
| 15 | ATOM | 940 | N | ASP | 132 | 16.478 | 24.155 | 79.322 | 1.00 | 82.42 |
|  | ATOM | 941 | CA | ASP | 132 | 16.540 | 23.792 | 80.735 | 1.00 | 82.24 |
|  | ATOM | 942 | CB | ASP | 132 | 15.893 | 22.411 | 80.934 | 1.00 | 83.24 |
|  | ATOM | 943 | CG | ASP | 132 | 15.836 | 21.981 | 82.393 | 1.00 | 83.66 |
|  | ATOM | 944 | OD1 | ASP | 132 | 15.165 | 20.963 | 82.678 | 1.00 | 83.28 |
| 20 | ATOM | 945 | OD2 | ASP | 132 | 16.458 | 22.645 | 83.250 | 1.00 | 83.85 |
|  | ATOM | 946 | C | ASP | 132 | 17.996 | 23.778 | 81.200 | 1.00 | 81.62 |
|  | ATOM | 947 | O | ASP | 132 | 18.324 | 24.293 | 82.270 | 1.00 | 82.12 |
|  | ATOM | 948 | N | PHE | 133 | 18.866 | 23.193 | 80.383 | 1.00 | 80.65 |
|  | ATOM | 949 | CA | PHE | 133 | 20.286 | 23.118 | 80.698 | 1.00 | 79.47 |
| 25 | ATOM | 950 | CB | PHE | 133 | 21.033 | 22.331 | 79.616 | 1.00 | 77.80 |
|  | ATOM | 951 | CG | PHE | 133 | 22.528 | 22.391 | 79.750 | 1.00 | 75.86 |
|  | ATOM | 952 | CD1 | PHE | 133 | 23.178 | 21.695 | 80.761 | 1.00 | 75.50 |
|  | ATOM | 953 | CD2 | PHE | 133 | 23.284 | 23.179 | 78.889 | 1.00 | 75.39 |
|  | ATOM | 954 | CE1 | PHE | 133 | 24.562 | 21.785 | 80.914 | 1.00 | 74.78 |

- 49 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 955 | CE2 | PHE | 133 | 24.667 | 23.275 | 79.035 | 1.00 74.59 |
| | ATOM | 956 | CZ | PHE | 133 | 25.305 | 22.578 | 80.049 | 1.00 74.18 |
| | ATOM | 957 | C | PHE | 133 | 20.876 | 24.519 | 80.786 | 1.00 79.33 |
| | ATOM | 958 | O | PHE | 133 | 21.690 | 24.810 | 81.659 | 1.00 79.06 |
| 5 | ATOM | 959 | N | LEU | 134 | 20.459 | 25.382 | 79.869 | 1.00 79.23 |
| | ATOM | 960 | CA | LEU | 134 | 20.951 | 26.748 | 79.828 | 1.00 79.59 |
| | ATOM | 961 | CB | LEU | 134 | 20.482 | 27.412 | 78.534 | 1.00 79.43 |
| | ATOM | 962 | CG | LEU | 134 | 21.043 | 26.703 | 77.297 | 1.00 78.61 |
| | ATOM | 963 | CD1 | LEU | 134 | 20.401 | 27.247 | 76.032 | 1.00 78.47 |
| 10 | ATOM | 964 | CD2 | LEU | 134 | 22.554 | 26.878 | 77.264 | 1.00 77.75 |
| | ATOM | 965 | C | LEU | 134 | 20.524 | 27.565 | 81.043 | 1.00 79.41 |
| | ATOM | 966 | O | LEU | 134 | 21.324 | 28.310 | 81.609 | 1.00 78.74 |
| | ATOM | 967 | N | ASP | 135 | 19.268 | 27.423 | 81.448 | 1.00 80.16 |
| | ATOM | 968 | CA | ASP | 135 | 18.780 | 28.152 | 82.609 | 1.00 80.92 |
| 15 | ATOM | 969 | CB | ASP | 135 | 17.271 | 27.966 | 82.777 | 1.00 80.81 |
| | ATOM | 970 | CG | ASP | 135 | 16.474 | 28.778 | 81.783 | 1.00 81.08 |
| | ATOM | 971 | OD1 | ASP | 135 | 16.801 | 29.970 | 81.599 | 1.00 82.67 |
| | ATOM | 972 | OD2 | ASP | 135 | 15.517 | 28.234 | 81.195 | 1.00 81.12 |
| | ATOM | 973 | C | ASP | 135 | 19.486 | 27.686 | 83.872 | 1.00 81.80 |
| 20 | ATOM | 974 | O | ASP | 135 | 20.090 | 28.490 | 84.578 | 1.00 82.12 |
| | ATOM | 975 | N | LYS | 136 | 19.418 | 26.384 | 84.143 | 1.00 82.43 |
| | ATOM | 976 | CA | LYS | 136 | 20.041 | 25.811 | 85.333 | 1.00 83.25 |
| | ATOM | 977 | CB | LYS | 136 | 19.750 | 24.307 | 85.418 | 1.00 82.64 |
| | ATOM | 978 | CG | LYS | 136 | 18.288 | 23.970 | 85.677 | 1.00 82.57 |
| 25 | ATOM | 979 | CD | LYS | 136 | 18.095 | 22.487 | 85.952 | 1.00 82.49 |
| | ATOM | 980 | CE | LYS | 136 | 16.630 | 22.154 | 86.182 | 1.00 82.31 |
| | ATOM | 981 | NZ | LYS | 136 | 16.053 | 22.914 | 87.323 | 1.00 82.43 |
| | ATOM | 982 | C | LYS | 136 | 21.548 | 26.044 | 85.429 | 1.00 84.12 |
| | ATOM | 983 | O | LYS | 136 | 22.185 | 25.610 | 86.390 | 1.00 84.51 |

- 50 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 984 | N | HIS | 137 | 22.119 | 26.727 | 84.442 | 1.00 | 85.08 |
| ATOM | 985 | CA | HIS | 137 | 23.551 | 27.010 | 84.450 | 1.00 | 86.27 |
| ATOM | 986 | CB | HIS | 137 | 24.280 | 26.115 | 83.438 | 1.00 | 86.74 |
| ATOM | 987 | CG | HIS | 137 | 24.169 | 24.649 | 83.730 | 1.00 | 87.04 |
| ATOM | 988 | CD2 | HIS | 137 | 25.112 | 23.729 | 84.047 | 1.00 | 86.44 |
| ATOM | 989 | ND1 | HIS | 137 | 22.968 | 23.971 | 83.708 | 1.00 | 87.51 |
| ATOM | 990 | CE1 | HIS | 137 | 23.176 | 22.699 | 83.999 | 1.00 | 86.59 |
| ATOM | 991 | NE2 | HIS | 137 | 24.468 | 22.526 | 84.209 | 1.00 | 86.35 |
| ATOM | 992 | C | HIS | 137 | 23.820 | 28.476 | 84.123 | 1.00 | 87.11 |
| ATOM | 993 | O | HIS | 137 | 24.943 | 28.842 | 83.776 | 1.00 | 86.73 |
| ATOM | 994 | N | GLN | 138 | 22.784 | 29.307 | 84.249 | 1.00 | 88.41 |
| ATOM | 995 | CA | GLN | 138 | 22.883 | 30.736 | 83.955 | 1.00 | 89.43 |
| ATOM | 996 | CB | GLN | 138 | 23.469 | 31.512 | 85.140 | 1.00 | 90.47 |
| ATOM | 997 | CG | GLN | 138 | 22.654 | 31.451 | 86.419 | 1.00 | 92.10 |
| ATOM | 998 | CD | GLN | 138 | 22.738 | 30.099 | 87.095 | 1.00 | 93.09 |
| ATOM | 999 | OE1 | GLN | 138 | 23.829 | 29.598 | 87.372 | 1.00 | 93.35 |
| ATOM | 1000 | NE2 | GLN | 138 | 21.584 | 29.501 | 87.371 | 1.00 | 93.71 |
| ATOM | 1001 | C | GLN | 138 | 23.779 | 30.931 | 82.747 | 1.00 | 89.90 |
| ATOM | 1002 | O | GLN | 138 | 24.922 | 31.376 | 82.875 | 1.00 | 89.53 |
| ATOM | 1003 | N | MET | 139 | 23.262 | 30.591 | 81.573 | 1.00 | 89.97 |
| ATOM | 1004 | CA | MET | 139 | 24.046 | 30.725 | 80.359 | 1.00 | 90.27 |
| ATOM | 1005 | CB | MET | 139 | 24.995 | 29.529 | 80.235 | 1.00 | 90.82 |
| ATOM | 1006 | CG | MET | 139 | 26.314 | 29.838 | 79.542 | 1.00 | 91.26 |
| ATOM | 1007 | SD | MET | 139 | 27.526 | 28.508 | 79.736 | 1.00 | 90.73 |
| ATOM | 1008 | CE | MET | 139 | 28.303 | 28.974 | 81.303 | 1.00 | 91.08 |
| ATOM | 1009 | C | MET | 139 | 23.137 | 30.820 | 79.140 | 1.00 | 90.17 |
| ATOM | 1010 | O | MET | 139 | 23.610 | 30.894 | 78.006 | 1.00 | 90.11 |
| ATOM | 1011 | N | LYS | 140 | 21.829 | 30.829 | 79.380 | 1.00 | 89.92 |
| ATOM | 1012 | CA | LYS | 140 | 20.851 | 30.921 | 78.300 | 1.00 | 89.78 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1013 | CB | LYS | 140 | 19.434 | 30.922 | 78.874 | 1.00 89.37 |
| | ATOM | 1014 | CG | LYS | 140 | 18.357 | 31.239 | 77.852 | 1.00 89.17 |
| | ATOM | 1015 | CD | LYS | 140 | 16.972 | 31.055 | 78.438 | 1.00 89.06 |
| | ATOM | 1016 | CE | LYS | 140 | 16.688 | 29.588 | 78.675 | 1.00 88.66 |
| 5 | ATOM | 1017 | NZ | LYS | 140 | 16.797 | 28.822 | 77.406 | 1.00 88.73 |
| | ATOM | 1018 | C | LYS | 140 | 21.067 | 32.179 | 77.466 | 1.00 89.78 |
| | ATOM | 1019 | O | LYS | 140 | 20.593 | 32.278 | 76.334 | 1.00 89.28 |
| | ATOM | 1020 | N | HIS | 141 | 21.794 | 33.133 | 78.037 | 1.00 90.38 |
| | ATOM | 1021 | CA | HIS | 141 | 22.082 | 34.401 | 77.376 | 1.00 90.81 |
| 10 | ATOM | 1022 | CB | HIS | 141 | 22.222 | 35.506 | 78.427 | 1.00 90.98 |
| | ATOM | 1023 | CG | HIS | 141 | 23.294 | 35.243 | 79.443 | 1.00 91.18 |
| | ATOM | 1024 | CD2 | HIS | 141 | 24.520 | 35.794 | 79.610 | 1.00 91.04 |
| | ATOM | 1025 | ND1 | HIS | 141 | 23.163 | 34.294 | 80.434 | 1.00 91.11 |
| | ATOM | 1026 | CE1 | HIS | 141 | 24.262 | 34.273 | 81.168 | 1.00 91.45 |
| 15 | ATOM | 1027 | NE2 | HIS | 141 | 25.102 | 35.174 | 80.688 | 1.00 90.96 |
| | ATOM | 1028 | C | HIS | 141 | 23.349 | 34.367 | 76.516 | 1.00 90.72 |
| | ATOM | 1029 | O | HIS | 141 | 24.048 | 35.374 | 76.399 | 1.00 91.00 |
| | ATOM | 1030 | N | LYS | 142 | 23.648 | 33.220 | 75.912 | 1.00 90.17 |
| | ATOM | 1031 | CA | LYS | 142 | 24.845 | 33.109 | 75.082 | 1.00 89.12 |
| 20 | ATOM | 1032 | CB | LYS | 142 | 26.000 | 32.529 | 75.908 | 1.00 89.54 |
| | ATOM | 1033 | CG | LYS | 142 | 26.424 | 33.406 | 77.079 | 1.00 90.51 |
| | ATOM | 1034 | CD | LYS | 142 | 27.490 | 32.730 | 77.926 | 1.00 91.91 |
| | ATOM | 1035 | CE | LYS | 142 | 27.867 | 33.579 | 79.131 | 1.00 92.42 |
| | ATOM | 1036 | NZ | LYS | 142 | 28.820 | 32.863 | 80.026 | 1.00 92.34 |
| 25 | ATOM | 1037 | C | LYS | 142 | 24.643 | 32.276 | 73.815 | 1.00 87.58 |
| | ATOM | 1038 | O | LYS | 142 | 23.763 | 31.418 | 73.749 | 1.00 87.74 |
| | ATOM | 1039 | N | LYS | 143 | 25.465 | 32.554 | 72.808 | 1.00 85.65 |
| | ATOM | 1040 | CA | LYS | 143 | 25.414 | 31.849 | 71.532 | 1.00 83.45 |
| | ATOM | 1041 | CB | LYS | 143 | 25.052 | 32.819 | 70.402 | 1.00 83.10 |

- 52 -

|   | ATOM | 1042 | CG  | LYS | 143 | 25.199 | 32.262 | 68.988 | 1.00 | 82.55 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 1043 | CD  | LYS | 143 | 24.890 | 33.339 | 67.951 | 1.00 | 82.36 |
|   | ATOM | 1044 | CE  | LYS | 143 | 25.289 | 32.922 | 66.540 | 1.00 | 82.46 |
|   | ATOM | 1045 | NZ  | LYS | 143 | 24.519 | 31.749 | 66.045 | 1.00 | 82.29 |
| 5 | ATOM | 1046 | C   | LYS | 143 | 26.790 | 31.252 | 71.283 | 1.00 | 82.32 |
|   | ATOM | 1047 | O   | LYS | 143 | 27.751 | 31.974 | 71.002 | 1.00 | 82.33 |
|   | ATOM | 1048 | N   | LEU | 144 | 26.884 | 29.932 | 71.409 | 1.00 | 79.90 |
|   | ATOM | 1049 | CA  | LEU | 144 | 28.146 | 29.233 | 71.198 | 1.00 | 77.12 |
|   | ATOM | 1050 | CB  | LEU | 144 | 28.653 | 28.634 | 72.517 | 1.00 | 78.89 |
| 10 | ATOM | 1051 | CG  | LEU | 144 | 29.417 | 29.543 | 73.491 | 1.00 | 80.11 |
|   | ATOM | 1052 | CD1 | LEU | 144 | 28.560 | 30.727 | 73.924 | 1.00 | 81.77 |
|   | ATOM | 1053 | CD2 | LEU | 144 | 29.836 | 28.721 | 74.698 | 1.00 | 80.96 |
|   | ATOM | 1054 | C   | LEU | 144 | 27.993 | 28.132 | 70.156 | 1.00 | 73.23 |
|   | ATOM | 1055 | O   | LEU | 144 | 26.876 | 27.742 | 69.810 | 1.00 | 72.89 |
| 15 | ATOM | 1056 | N   | PRO | 145 | 29.119 | 27.628 | 69.628 | 1.00 | 70.01 |
|   | ATOM | 1057 | CD  | PRO | 145 | 30.498 | 28.104 | 69.833 | 1.00 | 68.83 |
|   | ATOM | 1058 | CA  | PRO | 145 | 29.081 | 26.565 | 68.621 | 1.00 | 67.77 |
|   | ATOM | 1059 | CB  | PRO | 145 | 30.555 | 26.356 | 68.285 | 1.00 | 68.79 |
|   | ATOM | 1060 | CG  | PRO | 145 | 31.159 | 27.706 | 68.542 | 1.00 | 69.21 |
| 20 | ATOM | 1061 | C   | PRO | 145 | 28.434 | 25.299 | 69.181 | 1.00 | 65.49 |
|   | ATOM | 1062 | O   | PRO | 145 | 28.615 | 24.963 | 70.351 | 1.00 | 64.23 |
|   | ATOM | 1063 | N   | LEU | 146 | 27.677 | 24.603 | 68.340 | 1.00 | 63.31 |
|   | ATOM | 1064 | CA  | LEU | 146 | 27.007 | 23.383 | 68.757 | 1.00 | 61.72 |
|   | ATOM | 1065 | CB  | LEU | 146 | 25.492 | 23.532 | 68.602 | 1.00 | 62.15 |
| 25 | ATOM | 1066 | CG  | LEU | 146 | 24.678 | 22.285 | 68.945 | 1.00 | 62.90 |
|   | ATOM | 1067 | CD1 | LEU | 146 | 25.011 | 21.842 | 70.353 | 1.00 | 64.57 |
|   | ATOM | 1068 | CD2 | LEU | 146 | 23.194 | 22.577 | 68.817 | 1.00 | 65.06 |
|   | ATOM | 1069 | C   | LEU | 146 | 27.473 | 22.152 | 67.985 | 1.00 | 59.94 |
|   | ATOM | 1070 | O   | LEU | 146 | 27.342 | 22.086 | 66.763 | 1.00 | 59.04 |

- 53 -

| | ATOM | 1071 | N | GLY | 147 | 28.028 | 21.189 | 68.721 | 1.00 | 58.65 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 1072 | CA | GLY | 147 | 28.492 | 19.939 | 68.136 | 1.00 | 54.15 |
| | ATOM | 1073 | C | GLY | 147 | 27.444 | 18.891 | 68.465 | 1.00 | 49.71 |
| | ATOM | 1074 | O | GLY | 147 | 27.175 | 18.628 | 69.635 | 1.00 | 50.70 |
| 5 | ATOM | 1075 | N | PHE | 148 | 26.854 | 18.287 | 67.440 | 1.00 | 46.12 |
| | ATOM | 1076 | CA | PHE | 148 | 25.795 | 17.297 | 67.635 | 1.00 | 42.39 |
| | ATOM | 1077 | CB | PHE | 148 | 24.610 | 17.675 | 66.740 | 1.00 | 39.68 |
| | ATOM | 1078 | CG | PHE | 148 | 23.366 | 16.864 | 66.977 | 1.00 | 38.24 |
| | ATOM | 1079 | CD1 | PHE | 148 | 22.326 | 16.901 | 66.056 | 1.00 | 36.04 |
| 10 | ATOM | 1080 | CD2 | PHE | 148 | 23.212 | 16.102 | 68.132 | 1.00 | 36.13 |
| | ATOM | 1081 | CE1 | PHE | 148 | 21.148 | 16.194 | 66.279 | 1.00 | 38.53 |
| | ATOM | 1082 | CE2 | PHE | 148 | 22.042 | 15.395 | 68.365 | 1.00 | 35.28 |
| | ATOM | 1083 | CZ | PHE | 148 | 21.005 | 15.440 | 67.437 | 1.00 | 37.48 |
| | ATOM | 1084 | C | PHE | 148 | 26.197 | 15.840 | 67.354 | 1.00 | 41.67 |
| 15 | ATOM | 1085 | O | PHE | 148 | 26.463 | 15.475 | 66.205 | 1.00 | 42.24 |
| | ATOM | 1086 | N | THR | 149 | 26.247 | 15.013 | 68.398 | 1.00 | 40.23 |
| | ATOM | 1087 | CA | THR | 149 | 26.562 | 13.593 | 68.222 | 1.00 | 36.30 |
| | ATOM | 1088 | CB | THR | 149 | 27.281 | 13.001 | 69.442 | 1.00 | 36.36 |
| | ATOM | 1089 | OG1 | THR | 149 | 28.580 | 13.597 | 69.560 | 1.00 | 37.54 |
| 20 | ATOM | 1090 | CG2 | THR | 149 | 27.444 | 11.492 | 69.286 | 1.00 | 37.01 |
| | ATOM | 1091 | C | THR | 149 | 25.212 | 12.909 | 68.039 | 1.00 | 34.65 |
| | ATOM | 1092 | O | THR | 149 | 24.412 | 12.836 | 68.967 | 1.00 | 31.13 |
| | ATOM | 1093 | N | PHE | 150 | 24.972 | 12.422 | 66.825 | 1.00 | 33.67 |
| | ATOM | 1094 | CA | PHE | 150 | 23.714 | 11.782 | 66.456 | 1.00 | 34.60 |
| 25 | ATOM | 1095 | CB | PHE | 150 | 23.061 | 12.614 | 65.336 | 1.00 | 32.78 |
| | ATOM | 1096 | CG | PHE | 150 | 21.739 | 12.086 | 64.854 | 1.00 | 30.57 |
| | ATOM | 1097 | CD1 | PHE | 150 | 21.625 | 11.513 | 63.595 | 1.00 | 30.43 |
| | ATOM | 1098 | CD2 | PHE | 150 | 20.598 | 12.213 | 65.637 | 1.00 | 31.90 |
| | ATOM | 1099 | CE1 | PHE | 150 | 20.382 | 11.076 | 63.115 | 1.00 | 34.54 |

- 54 -

| | ATOM | 1100 | CE2 | PHE | 150 | 19. 356 | 11. 783 | 65. 176 | 1. 00 | 30. 63 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1101 | CZ | PHE | 150 | 19. 241 | 11. 213 | 63. 913 | 1. 00 | 32. 01 |
| | ATOM | 1102 | C | PHE | 150 | 24. 011 | 10. 358 | 65. 991 | 1. 00 | 35. 95 |
| | ATOM | 1103 | O | PHE | 150 | 24. 369 | 10. 128 | 64. 836 | 1. 00 | 38. 42 |
| 5 | ATOM | 1104 | N | SER | 151 | 23. 843 | 9. 412 | 66. 908 | 1. 00 | 36. 96 |
| | ATOM | 1105 | CA | SER | 151 | 24. 129 | 7. 995 | 66. 680 | 1. 00 | 34. 37 |
| | ATOM | 1106 | CB | SER | 151 | 24. 186 | 7. 271 | 68. 025 | 1. 00 | 35. 80 |
| | ATOM | 1107 | OG | SER | 151 | 25. 111 | 7. 897 | 68. 892 | 1. 00 | 39. 97 |
| | ATOM | 1108 | C | SER | 151 | 23. 189 | 7. 228 | 65. 770 | 1. 00 | 32. 05 |
| 10 | ATOM | 1109 | O | SER | 151 | 22. 537 | 6. 292 | 66. 215 | 1. 00 | 32. 11 |
| | ATOM | 1110 | N | PHE | 152 | 23. 110 | 7. 611 | 64. 505 | 1. 00 | 31. 41 |
| | ATOM | 1111 | CA | PHE | 152 | 22. 253 | 6. 902 | 63. 563 | 1. 00 | 31. 81 |
| | ATOM | 1112 | CB | PHE | 152 | 20. 824 | 7. 464 | 63. 570 | 1. 00 | 34. 43 |
| | ATOM | 1113 | CG | PHE | 152 | 20. 149 | 7. 372 | 64. 904 | 1. 00 | 34. 95 |
| 15 | ATOM | 1114 | CD1 | PHE | 152 | 20. 278 | 8. 401 | 65. 838 | 1. 00 | 32. 95 |
| | ATOM | 1115 | CD2 | PHE | 152 | 19. 439 | 6. 228 | 65. 256 | 1. 00 | 35. 34 |
| | ATOM | 1116 | CE1 | PHE | 152 | 19. 713 | 8. 291 | 67. 108 | 1. 00 | 35. 00 |
| | ATOM | 1117 | CE2 | PHE | 152 | 18. 868 | 6. 102 | 66. 526 | 1. 00 | 35. 79 |
| | ATOM | 1118 | CZ | PHE | 152 | 19. 005 | 7. 135 | 67. 454 | 1. 00 | 38. 15 |
| 20 | ATOM | 1119 | C | PHE | 152 | 22. 845 | 7. 010 | 62. 171 | 1. 00 | 31. 95 |
| | ATOM | 1120 | O | PHE | 152 | 23. 727 | 7. 831 | 61. 921 | 1. 00 | 31. 72 |
| | ATOM | 1121 | N | PRO | 153 | 22. 386 | 6. 164 | 61. 247 | 1. 00 | 32. 44 |
| | ATOM | 1122 | CD | PRO | 153 | 21. 374 | 5. 098 | 61. 343 | 1. 00 | 30. 73 |
| | ATOM | 1123 | CA | PRO | 153 | 22. 942 | 6. 248 | 59. 896 | 1. 00 | 34. 59 |
| 25 | ATOM | 1124 | CB | PRO | 153 | 22. 397 | 4. 991 | 59. 225 | 1. 00 | 31. 34 |
| | ATOM | 1125 | CG | PRO | 153 | 21. 072 | 4. 812 | 59. 884 | 1. 00 | 31. 98 |
| | ATOM | 1126 | C | PRO | 153 | 22. 507 | 7. 535 | 59. 201 | 1. 00 | 37. 30 |
| | ATOM | 1127 | O | PRO | 153 | 21. 310 | 7. 813 | 59. 067 | 1. 00 | 39. 02 |
| | ATOM | 1128 | N | VAL | 154 | 23. 483 | 8. 325 | 58. 770 | 1. 00 | 39. 02 |

|  | ATOM | 1129 | CA | VAL | 154 | 23. 187 | 9. 581 | 58. 092 | 1. 00 | 40. 43 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1130 | CB | VAL | 154 | 23. 446 | 10. 792 | 59. 007 | 1. 00 | 39. 28 |
|  | ATOM | 1131 | CG1 | VAL | 154 | 23. 191 | 12. 081 | 58. 238 | 1. 00 | 41. 18 |
|  | ATOM | 1132 | CG2 | VAL | 154 | 22. 557 | 10. 727 | 60. 221 | 1. 00 | 38. 37 |
| 5 | ATOM | 1133 | C | VAL | 154 | 24. 023 | 9. 785 | 56. 837 | 1. 00 | 41. 48 |
|  | ATOM | 1134 | 0 | VAL | 154 | 25. 241 | 9. 602 | 56. 861 | 1. 00 | 41. 28 |
|  | ATOM | 1135 | N | ARG | 155 | 23. 365 | 10. 162 | 55. 743 | 1. 00 | 43. 31 |
|  | ATOM | 1136 | CA | ARG | 155 | 24. 072 | 10. 441 | 54. 495 | 1. 00 | 46. 32 |
|  | ATOM | 1137 | CB | ARG | 155 | 23. 233 | 10. 058 | 53. 280 | 1. 00 | 47. 31 |
| 10 | ATOM | 1138 | CG | ARG | 155 | 23. 809 | 10. 586 | 51. 968 | 1. 00 | 52. 20 |
|  | ATOM | 1139 | CD | ARG | 155 | 23. 563 | 9. 614 | 50. 844 | 1. 00 | 55. 56 |
|  | ATOM | 1140 | NE | ARG | 155 | 24. 419 | 8. 437 | 50. 968 | 1. 00 | 59. 93 |
|  | ATOM | 1141 | CZ | ARG | 155 | 24. 068 | 7. 217 | 50. 573 | 1. 00 | 61. 41 |
|  | ATOM | 1142 | NH1 | ARG | 155 | 22. 874 | 7. 011 | 50. 032 | 1. 00 | 63. 00 |
| 15 | ATOM | 1143 | NH2 | ARG | 155 | 24. 910 | 6. 203 | 50. 717 | 1. 00 | 63. 35 |
|  | ATOM | 1144 | C | ARG | 155 | 24. 367 | 11. 934 | 54. 456 | 1. 00 | 46. 23 |
|  | ATOM | 1145 | 0 | ARG | 155 | 23. 486 | 12. 737 | 54. 166 | 1. 00 | 47. 64 |
|  | ATOM | 1146 | N | HIS | 156 | 25. 613 | 12. 291 | 54. 754 | 1. 00 | 47. 03 |
|  | ATOM | 1147 | CA | HIS | 156 | 26. 046 | 13. 682 | 54. 791 | 1. 00 | 48. 05 |
| 20 | ATOM | 1148 | CB | HIS | 156 | 27. 318 | 13. 834 | 55. 632 | 1. 00 | 49. 62 |
|  | ATOM | 1149 | CG | HIS | 156 | 27. 157 | 13. 444 | 57. 066 | 1. 00 | 52. 65 |
|  | ATOM | 1150 | CD2 | HIS | 156 | 26. 274 | 12. 619 | 57. 676 | 1. 00 | 53. 99 |
|  | ATOM | 1151 | ND1 | HIS | 156 | 27. 990 | 13. 916 | 58. 057 | 1. 00 | 53. 35 |
|  | ATOM | 1152 | CE1 | HIS | 156 | 27. 625 | 13. 401 | 59. 218 | 1. 00 | 54. 78 |
| 25 | ATOM | 1153 | NE2 | HIS | 156 | 26. 586 | 12. 610 | 59. 014 | 1. 00 | 54. 28 |
|  | ATOM | 1154 | C | HIS | 156 | 26. 334 | 14. 317 | 53. 440 | 1. 00 | 48. 30 |
|  | ATOM | 1155 | 0 | HIS | 156 | 26. 872 | 13. 677 | 52. 535 | 1. 00 | 47. 38 |
|  | ATOM | 1156 | N | GLU | 157 | 25. 969 | 15. 589 | 53. 319 | 1. 00 | 47. 98 |
|  | ATOM | 1157 | CA | GLU | 157 | 26. 256 | 16. 343 | 52. 114 | 1. 00 | 48. 38 |

- 56 -

|   | ATOM | 1158 | CB  | GLU | 157 | 25.113 | 17.296 | 51.749 | 1.00 | 51.05 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 1159 | CG  | GLU | 157 | 25.462 | 18.198 | 50.558 | 1.00 | 57.22 |
|   | ATOM | 1160 | CD  | GLU | 157 | 24.422 | 19.276 | 50.275 | 1.00 | 58.92 |
|   | ATOM | 1161 | OE1 | GLU | 157 | 23.299 | 18.931 | 49.845 | 1.00 | 60.91 |
| 5 | ATOM | 1162 | OE2 | GLU | 157 | 24.734 | 20.471 | 50.485 | 1.00 | 60.69 |
|   | ATOM | 1163 | C   | GLU | 157 | 27.475 | 17.138 | 52.547 | 1.00 | 45.12 |
|   | ATOM | 1164 | O   | GLU | 157 | 28.349 | 17.457 | 51.749 | 1.00 | 43.91 |
|   | ATOM | 1165 | N   | ASP | 158 | 27.529 | 17.427 | 53.843 | 1.00 | 43.85 |
|   | ATOM | 1166 | CA  | ASP | 158 | 28.633 | 18.174 | 54.416 | 1.00 | 43.81 |
| 10 | ATOM | 1167 | CB | ASP | 158 | 28.479 | 19.654 | 54.085 | 1.00 | 46.74 |
|   | ATOM | 1168 | CG  | ASP | 158 | 29.743 | 20.445 | 54.349 | 1.00 | 49.54 |
|   | ATOM | 1169 | OD1 | ASP | 158 | 29.760 | 21.651 | 54.016 | 1.00 | 53.34 |
|   | ATOM | 1170 | OD2 | ASP | 158 | 30.716 | 19.869 | 54.884 | 1.00 | 49.62 |
|   | ATOM | 1171 | C   | ASP | 158 | 28.671 | 17.972 | 55.928 | 1.00 | 43.93 |
| 15 | ATOM | 1172 | O  | ASP | 158 | 27.724 | 17.447 | 56.518 | 1.00 | 43.97 |
|   | ATOM | 1173 | N   | ILE | 159 | 29.767 | 18.399 | 56.547 | 1.00 | 43.75 |
|   | ATOM | 1174 | CA  | ILE | 159 | 29.963 | 18.250 | 57.983 | 1.00 | 44.27 |
|   | ATOM | 1175 | CB  | ILE | 159 | 31.248 | 18.971 | 58.452 | 1.00 | 45.07 |
|   | ATOM | 1176 | CG2 | ILE | 159 | 31.069 | 20.480 | 58.354 | 1.00 | 47.24 |
| 20 | ATOM | 1177 | CG1 | ILE | 159 | 31.544 | 18.617 | 59.907 | 1.00 | 45.29 |
|   | ATOM | 1178 | CD1 | ILE | 159 | 31.733 | 17.140 | 60.152 | 1.00 | 48.99 |
|   | ATOM | 1179 | C   | ILE | 159 | 28.795 | 18.744 | 58.829 | 1.00 | 44.47 |
|   | ATOM | 1180 | O   | ILE | 159 | 28.583 | 18.254 | 59.941 | 1.00 | 44.15 |
|   | ATOM | 1181 | N   | ASP | 160 | 28.037 | 19.709 | 58.317 | 1.00 | 44.10 |
| 25 | ATOM | 1182 | CA | ASP | 160 | 26.904 | 20.239 | 59.072 | 1.00 | 42.92 |
|   | ATOM | 1183 | CB  | ASP | 160 | 27.103 | 21.734 | 59.360 | 1.00 | 44.13 |
|   | ATOM | 1184 | CG  | ASP | 160 | 27.448 | 22.533 | 58.118 | 1.00 | 45.52 |
|   | ATOM | 1185 | OD1 | ASP | 160 | 28.258 | 23.479 | 58.239 | 1.00 | 47.57 |
|   | ATOM | 1186 | OD2 | ASP | 160 | 26.912 | 22.228 | 57.031 | 1.00 | 45.51 |

– 57 –

|   | ATOM | 1187 | C   | ASP | 160 | 25.559 | 20.005 | 58.410 | 1.00 | 42.92 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 1188 | O   | ASP | 160 | 24.579 | 20.691 | 58.706 | 1.00 | 44.48 |
|   | ATOM | 1189 | N   | LYS | 161 | 25.509 | 19.026 | 57.518 | 1.00 | 41.57 |
|   | ATOM | 1190 | CA  | LYS | 161 | 24.267 | 18.692 | 56.838 | 1.00 | 41.51 |
| 5 | ATOM | 1191 | CB  | LYS | 161 | 24.067 | 19.597 | 55.618 | 1.00 | 41.19 |
|   | ATOM | 1192 | CG  | LYS | 161 | 22.783 | 19.306 | 54.863 | 1.00 | 41.39 |
|   | ATOM | 1193 | CD  | LYS | 161 | 22.687 | 20.094 | 53.557 | 1.00 | 43.25 |
|   | ATOM | 1194 | CE  | LYS | 161 | 21.366 | 19.809 | 52.860 | 1.00 | 40.06 |
|   | ATOM | 1195 | NZ  | LYS | 161 | 21.335 | 20.312 | 51.468 | 1.00 | 41.02 |
| 10 | ATOM | 1196 | C   | LYS | 161 | 24.258 | 17.224 | 56.397 | 1.00 | 41.66 |
|   | ATOM | 1197 | O   | LYS | 161 | 25.239 | 16.725 | 55.838 | 1.00 | 39.36 |
|   | ATOM | 1198 | N   | GLY | 162 | 23.143 | 16.546 | 56.654 | 1.00 | 40.90 |
|   | ATOM | 1199 | CA  | GLY | 162 | 23.005 | 15.152 | 56.276 | 1.00 | 42.70 |
|   | ATOM | 1200 | C   | GLY | 162 | 21.618 | 14.645 | 56.615 | 1.00 | 43.15 |
| 15 | ATOM | 1201 | O   | GLY | 162 | 21.019 | 15.085 | 57.594 | 1.00 | 43.59 |
|   | ATOM | 1202 | N   | ILE | 163 | 21.096 | 13.722 | 55.816 | 1.00 | 43.93 |
|   | ATOM | 1203 | CA  | ILE | 163 | 19.763 | 13.190 | 56.068 | 1.00 | 45.03 |
|   | ATOM | 1204 | CB  | ILE | 163 | 18.958 | 13.031 | 54.755 | 1.00 | 46.16 |
|   | ATOM | 1205 | CG2 | ILE | 163 | 18.943 | 14.352 | 53.985 | 1.00 | 45.82 |
| 20 | ATOM | 1206 | CG1 | ILE | 163 | 19.585 | 11.938 | 53.889 | 1.00 | 46.11 |
|   | ATOM | 1207 | CD1 | ILE | 163 | 18.812 | 11.638 | 52.613 | 1.00 | 48.51 |
|   | ATOM | 1208 | C   | ILE | 163 | 19.812 | 11.833 | 56.764 | 1.00 | 46.49 |
|   | ATOM | 1209 | O   | ILE | 163 | 20.771 | 11.074 | 56.609 | 1.00 | 45.36 |
|   | ATOM | 1210 | N   | LEU | 164 | 18.767 | 11.545 | 57.533 | 1.00 | 47.21 |
| 25 | ATOM | 1211 | CA  | LEU | 164 | 18.649 | 10.286 | 58.253 | 1.00 | 47.53 |
|   | ATOM | 1212 | CB  | LEU | 164 | 17.623 | 10.414 | 59.379 | 1.00 | 47.11 |
|   | ATOM | 1213 | CG  | LEU | 164 | 17.135 | 9.126  | 60.049 | 1.00 | 47.15 |
|   | ATOM | 1214 | CD1 | LEU | 164 | 18.265 | 8.469  | 60.832 | 1.00 | 45.45 |
|   | ATOM | 1215 | CD2 | LEU | 164 | 15.981 | 9.465  | 60.977 | 1.00 | 47.00 |

- 58 -

| | ATOM | 1216 | C | LEU | 164 | 18. 189 | 9. 220 | 57. 277 | 1. 00 | 48. 06 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1217 | O | LEU | 164 | 17. 137 | 9. 352 | 56. 657 | 1. 00 | 48. 49 |
| | ATOM | 1218 | N | LEU | 165 | 18. 977 | 8. 161 | 57. 137 | 1. 00 | 48. 32 |
| | ATOM | 1219 | CA | LEU | 165 | 18. 614 | 7. 093 | 56. 224 | 1. 00 | 47. 47 |
| 5 | ATOM | 1220 | CB | LEU | 165 | 19. 827 | 6. 208 | 55. 954 | 1. 00 | 45. 44 |
| | ATOM | 1221 | CG | LEU | 165 | 20. 867 | 6. 978 | 55. 140 | 1. 00 | 47. 60 |
| | ATOM | 1222 | CD1 | LEU | 165 | 22. 128 | 6. 155 | 54. 956 | 1. 00 | 47. 47 |
| | ATOM | 1223 | CD2 | LEU | 165 | 20. 261 | 7. 342 | 53. 786 | 1. 00 | 48. 48 |
| | ATOM | 1224 | C | LEU | 165 | 17. 460 | 6. 300 | 56. 814 | 1. 00 | 46. 86 |
| 10 | ATOM | 1225 | O | LEU | 165 | 16. 497 | 5. 985 | 56. 120 | 1. 00 | 46. 90 |
| | ATOM | 1226 | N | ASN | 166 | 17. 562 | 5. 992 | 58. 101 | 1. 00 | 46. 60 |
| | ATOM | 1227 | CA | ASN | 166 | 16. 521 | 5. 266 | 58. 817 | 1. 00 | 47. 23 |
| | ATOM | 1228 | CB | ASN | 166 | 16. 282 | 3. 883 | 58. 200 | 1. 00 | 49. 17 |
| | ATOM | 1229 | CG | ASN | 166 | 17. 542 | 3. 053 | 58. 118 | 1. 00 | 50. 36 |
| 15 | ATOM | 1230 | OD1 | ASN | 166 | 18. 205 | 2. 997 | 57. 076 | 1. 00 | 50. 62 |
| | ATOM | 1231 | ND2 | ASN | 166 | 17. 888 | 2. 406 | 59. 223 | 1. 00 | 50. 50 |
| | ATOM | 1232 | C | ASN | 166 | 16. 913 | 5. 123 | 60. 279 | 1. 00 | 47. 60 |
| | ATOM | 1233 | O | ASN | 166 | 18. 096 | 5. 177 | 60. 623 | 1. 00 | 48. 53 |
| | ATOM | 1234 | N | TRP | 167 | 15. 916 | 4. 966 | 61. 142 | 1. 00 | 46. 96 |
| 20 | ATOM | 1235 | CA | TRP | 167 | 16. 166 | 4. 815 | 62. 571 | 1. 00 | 45. 46 |
| | ATOM | 1236 | CB | TRP | 167 | 14. 890 | 5. 085 | 63. 376 | 1. 00 | 47. 63 |
| | ATOM | 1237 | CG | TRP | 167 | 14. 433 | 6. 519 | 63. 454 | 1. 00 | 49. 15 |
| | ATOM | 1238 | CD2 | TRP | 167 | 15. 093 | 7. 602 | 64. 126 | 1. 00 | 49. 07 |
| | ATOM | 1239 | CE2 | TRP | 167 | 14. 237 | 8. 725 | 64. 050 | 1. 00 | 48. 21 |
| 25 | ATOM | 1240 | CE3 | TRP | 167 | 16. 321 | 7. 732 | 64. 787 | 1. 00 | 49. 17 |
| | ATOM | 1241 | CD1 | TRP | 167 | 13. 242 | 7. 022 | 63. 003 | 1. 00 | 49. 03 |
| | ATOM | 1242 | NE1 | TRP | 167 | 13. 117 | 8. 343 | 63. 361 | 1. 00 | 48. 46 |
| | ATOM | 1243 | CZ2 | TRP | 167 | 14. 569 | 9. 962 | 64. 614 | 1. 00 | 47. 68 |
| | ATOM | 1244 | CZ3 | TRP | 167 | 16. 652 | 8. 966 | 65. 348 | 1. 00 | 49. 58 |

- 59 -

|  | ATOM | 1245 | CH2 | TRP | 167 | 15.777 | 10.064 | 65.256 | 1.00 | 48.80 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1246 | C | TRP | 167 | 16.647 | 3.394 | 62.890 | 1.00 | 43.28 |
|  | ATOM | 1247 | O | TRP | 167 | 16.425 | 2.461 | 62.119 | 1.00 | 42.86 |
|  | ATOM | 1248 | N | THR | 168 | 17.297 | 3.245 | 64.038 | 1.00 | 41.63 |
| 5 | ATOM | 1249 | CA | THR | 168 | 17.796 | 1.953 | 64.501 | 1.00 | 40.13 |
|  | ATOM | 1250 | CB | THR | 168 | 19.275 | 1.723 | 64.086 | 1.00 | 37.87 |
|  | ATOM | 1251 | OG1 | THR | 168 | 20.082 | 2.795 | 64.587 | 1.00 | 33.52 |
|  | ATOM | 1252 | CG2 | THR | 168 | 19.417 | 1.647 | 62.566 | 1.00 | 34.11 |
|  | ATOM | 1253 | C | THR | 168 | 17.719 | 1.943 | 66.029 | 1.00 | 41.33 |
| 10 | ATOM | 1254 | O | THR | 168 | 17.382 | 2.953 | 66.649 | 1.00 | 41.41 |
|  | ATOM | 1255 | N | LYS | 169 | 18.025 | 0.799 | 66.631 | 1.00 | 42.06 |
|  | ATOM | 1256 | CA | LYS | 169 | 18.013 | 0.672 | 68.083 | 1.00 | 42.59 |
|  | ATOM | 1257 | CB | LYS | 169 | 19.077 | 1.594 | 68.683 | 1.00 | 39.56 |
|  | ATOM | 1258 | CG | LYS | 169 | 20.497 | 1.209 | 68.287 | 1.00 | 36.24 |
| 15 | ATOM | 1259 | CD | LYS | 169 | 21.528 | 2.170 | 68.840 | 1.00 | 33.26 |
|  | ATOM | 1260 | CE | LYS | 169 | 21.481 | 3.514 | 68.133 | 1.00 | 30.26 |
|  | ATOM | 1261 | NZ | LYS | 169 | 22.589 | 4.373 | 68.610 | 1.00 | 32.75 |
|  | ATOM | 1262 | C | LYS | 169 | 16.661 | 0.933 | 68.751 | 1.00 | 45.26 |
|  | ATOM | 1263 | O | LYS | 169 | 16.598 | 1.191 | 69.955 | 1.00 | 45.85 |
| 20 | ATOM | 1264 | N | GLY | 170 | 15.583 | 0.881 | 67.975 | 1.00 | 47.46 |
|  | ATOM | 1265 | CA | GLY | 170 | 14.267 | 1.083 | 68.555 | 1.00 | 52.44 |
|  | ATOM | 1266 | C | GLY | 170 | 13.552 | 2.394 | 68.295 | 1.00 | 55.24 |
|  | ATOM | 1267 | O | GLY | 170 | 12.324 | 2.422 | 68.275 | 1.00 | 56.11 |
|  | ATOM | 1268 | N | PHE | 171 | 14.293 | 3.482 | 68.118 | 1.00 | 58.10 |
| 25 | ATOM | 1269 | CA | PHE | 171 | 13.668 | 4.777 | 67.861 | 1.00 | 61.86 |
|  | ATOM | 1270 | CB | PHE | 171 | 14.734 | 5.846 | 67.613 | 1.00 | 62.35 |
|  | ATOM | 1271 | CG | PHE | 171 | 15.449 | 6.285 | 68.856 | 1.00 | 64.08 |
|  | ATOM | 1272 | CD1 | PHE | 171 | 16.060 | 5.354 | 69.691 | 1.00 | 66.00 |
|  | ATOM | 1273 | CD2 | PHE | 171 | 15.511 | 7.630 | 69.196 | 1.00 | 64.53 |

- 60 -

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1274 | CE1 | PHE | 171 | 16.721 | 5.760 | 70.851 | 1.00 | 66.96 |
| | ATOM | 1275 | CE2 | PHE | 171 | 16.170 | 8.046 | 70.352 | 1.00 | 65.93 |
| | ATOM | 1276 | CZ | PHE | 171 | 16.776 | 7.109 | 71.180 | 1.00 | 66.07 |
| | ATOM | 1277 | C | PHE | 171 | 12.727 | 4.697 | 66.663 | 1.00 | 63.91 |
| 5 | ATOM | 1278 | O | PHE | 171 | 12.994 | 3.975 | 65.702 | 1.00 | 63.50 |
| | ATOM | 1279 | N | LYS | 172 | 11.620 | 5.430 | 66.727 | 1.00 | 65.77 |
| | ATOM | 1280 | CA | LYS | 172 | 10.657 | 5.424 | 65.633 | 1.00 | 68.37 |
| | ATOM | 1281 | CB | LYS | 172 | 9.738 | 4.197 | 65.727 | 1.00 | 70.16 |
| | ATOM | 1282 | CG | LYS | 172 | 8.814 | 4.035 | 64.517 | 1.00 | 72.04 |
| 10 | ATOM | 1283 | CD | LYS | 172 | 7.867 | 2.842 | 64.647 | 1.00 | 73.43 |
| | ATOM | 1284 | CE | LYS | 172 | 6.977 | 2.718 | 63.406 | 1.00 | 74.42 |
| | ATOM | 1285 | NZ | LYS | 172 | 5.933 | 1.655 | 63.525 | 1.00 | 73.62 |
| | ATOM | 1286 | C | LYS | 172 | 9.808 | 6.688 | 65.606 | 1.00 | 69.18 |
| | ATOM | 1287 | O | LYS | 172 | 8.599 | 6.642 | 65.838 | 1.00 | 70.01 |
| 15 | ATOM | 1288 | N | ALA | 173 | 10.445 | 7.820 | 65.332 | 1.00 | 68.98 |
| | ATOM | 1289 | CA | ALA | 173 | 9.734 | 9.086 | 65.251 | 1.00 | 69.07 |
| | ATOM | 1290 | CB | ALA | 173 | 10.598 | 10.210 | 65.818 | 1.00 | 68.41 |
| | ATOM | 1291 | C | ALA | 173 | 9.424 | 9.339 | 63.776 | 1.00 | 69.07 |
| | ATOM | 1292 | O | ALA | 173 | 10.336 | 9.471 | 62.962 | 1.00 | 69.61 |
| 20 | ATOM | 1293 | N | SER | 174 | 8.139 | 9.394 | 63.432 | 1.00 | 69.06 |
| | ATOM | 1294 | CA | SER | 174 | 7.735 | 9.620 | 62.047 | 1.00 | 68.32 |
| | ATOM | 1295 | CB | SER | 174 | 6.217 | 9.491 | 61.901 | 1.00 | 69.02 |
| | ATOM | 1296 | OG | SER | 174 | 5.546 | 10.503 | 62.632 | 1.00 | 68.18 |
| | ATOM | 1297 | C | SER | 174 | 8.173 | 10.996 | 61.568 | 1.00 | 67.71 |
| 25 | ATOM | 1298 | O | SER | 174 | 8.410 | 11.897 | 62.370 | 1.00 | 68.23 |
| | ATOM | 1299 | N | GLY | 175 | 8.288 | 11.148 | 60.254 | 1.00 | 67.37 |
| | ATOM | 1300 | CA | GLY | 175 | 8.688 | 12.424 | 59.690 | 1.00 | 67.08 |
| | ATOM | 1301 | C | GLY | 175 | 10.143 | 12.787 | 59.915 | 1.00 | 66.86 |
| | ATOM | 1302 | O | GLY | 175 | 10.507 | 13.962 | 59.855 | 1.00 | 67.38 |

- 61 -

|      | ATOM | 1303 | N   | ALA | 176 | 10.979 | 11.786 | 60.172 | 1.00 | 66.42 |
|------|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|      | ATOM | 1304 | CA  | ALA | 176 | 12.400 | 12.018 | 60.401 | 1.00 | 64.67 |
|      | ATOM | 1305 | CB  | ALA | 176 | 12.828 | 11.360 | 61.699 | 1.00 | 64.11 |
|      | ATOM | 1306 | C   | ALA | 176 | 13.229 | 11.475 | 59.242 | 1.00 | 64.02 |
| 5    | ATOM | 1307 | O   | ALA | 176 | 14.053 | 12.183 | 58.667 | 1.00 | 65.00 |
|      | ATOM | 1308 | N   | GLU | 177 | 12.993 | 10.214 | 58.903 | 1.00 | 63.24 |
|      | ATOM | 1309 | CA  | GLU | 177 | 13.710 | 9.544  | 57.825 | 1.00 | 63.08 |
|      | ATOM | 1310 | CB  | GLU | 177 | 13.147 | 8.127  | 57.639 | 1.00 | 62.97 |
|      | ATOM | 1311 | CG  | GLU | 177 | 13.315 | 7.224  | 58.865 | 1.00 | 64.81 |
| 10   | ATOM | 1312 | CD  | GLU | 177 | 12.712 | 5.837  | 58.682 | 1.00 | 64.99 |
|      | ATOM | 1313 | OE1 | GLU | 177 | 12.948 | 4.972  | 59.552 | 1.00 | 65.80 |
|      | ATOM | 1314 | OE2 | GLU | 177 | 12.003 | 5.612  | 57.677 | 1.00 | 64.52 |
|      | ATOM | 1315 | C   | GLU | 177 | 13.669 | 10.293 | 56.491 | 1.00 | 62.92 |
|      | ATOM | 1316 | O   | GLU | 177 | 12.602 | 10.489 | 55.908 | 1.00 | 63.26 |
| 15   | ATOM | 1317 | N   | GLY | 178 | 14.838 | 10.708 | 56.013 | 1.00 | 62.46 |
|      | ATOM | 1318 | CA  | GLY | 178 | 14.911 | 11.406 | 54.741 | 1.00 | 61.36 |
|      | ATOM | 1319 | C   | GLY | 178 | 15.095 | 12.911 | 54.805 | 1.00 | 60.52 |
|      | ATOM | 1320 | O   | GLY | 178 | 15.337 | 13.539 | 53.777 | 1.00 | 61.73 |
|      | ATOM | 1321 | N   | ASN | 179 | 14.990 | 13.498 | 55.993 | 1.00 | 59.84 |
| 20   | ATOM | 1322 | CA  | ASN | 179 | 15.139 | 14.942 | 56.134 | 1.00 | 59.11 |
|      | ATOM | 1323 | CB  | ASN | 179 | 13.985 | 15.512 | 56.959 | 1.00 | 59.72 |
|      | ATOM | 1324 | CG  | ASN | 179 | 12.630 | 15.217 | 56.342 | 1.00 | 61.46 |
|      | ATOM | 1325 | OD1 | ASN | 179 | 12.423 | 15.416 | 55.143 | 1.00 | 61.86 |
|      | ATOM | 1326 | ND2 | ASN | 179 | 11.696 | 14.743 | 57.161 | 1.00 | 61.02 |
| 25   | ATOM | 1327 | C   | ASN | 179 | 16.463 | 15.349 | 56.765 | 1.00 | 58.81 |
|      | ATOM | 1328 | O   | ASN | 179 | 17.108 | 14.553 | 57.441 | 1.00 | 59.10 |
|      | ATOM | 1329 | N   | ASN | 180 | 16.860 | 16.599 | 56.537 | 1.00 | 58.30 |
|      | ATOM | 1330 | CA  | ASN | 180 | 18.107 | 17.130 | 57.079 | 1.00 | 57.96 |
|      | ATOM | 1331 | CB  | ASN | 180 | 18.362 | 18.539 | 56.539 | 1.00 | 58.57 |

- 62 -

|  | ATOM | 1332 | CG | ASN | 180 | 19.693 | 19.112 | 57.001 | 1.00 | 60.99 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|  | ATOM | 1333 | OD1 | ASN | 180 | 20.278 | 18.647 | 57.983 | 1.00 | 60.88 |
|  | ATOM | 1334 | ND2 | ASN | 180 | 20.171 | 20.139 | 56.302 | 1.00 | 60.74 |
|  | ATOM | 1335 | C | ASN | 180 | 18.036 | 17.183 | 58.600 | 1.00 | 57.30 |
| 5 | ATOM | 1336 | O | ASN | 180 | 17.388 | 18.064 | 59.162 | 1.00 | 57.94 |
|  | ATOM | 1337 | N | VAL | 181 | 18.709 | 16.245 | 59.261 | 1.00 | 55.49 |
|  | ATOM | 1338 | CA | VAL | 181 | 18.716 | 16.189 | 60.720 | 1.00 | 54.19 |
|  | ATOM | 1339 | CB | VAL | 181 | 19.698 | 15.109 | 61.229 | 1.00 | 53.15 |
|  | ATOM | 1340 | CG1 | VAL | 181 | 19.756 | 15.121 | 62.748 | 1.00 | 50.90 |
| 10 | ATOM | 1341 | CG2 | VAL | 181 | 19.258 | 13.742 | 60.731 | 1.00 | 51.33 |
|  | ATOM | 1342 | C | VAL | 181 | 19.089 | 17.534 | 61.333 | 1.00 | 54.31 |
|  | ATOM | 1343 | O | VAL | 181 | 18.473 | 17.979 | 62.299 | 1.00 | 53.21 |
|  | ATOM | 1344 | N | VAL | 182 | 20.110 | 18.174 | 60.777 | 1.00 | 56.27 |
|  | ATOM | 1345 | CA | VAL | 182 | 20.533 | 19.472 | 61.271 | 1.00 | 58.32 |
| 15 | ATOM | 1346 | CB | VAL | 182 | 21.706 | 20.033 | 60.447 | 1.00 | 58.42 |
|  | ATOM | 1347 | CG1 | VAL | 182 | 22.135 | 21.373 | 61.007 | 1.00 | 58.05 |
|  | ATOM | 1348 | CG2 | VAL | 182 | 22.867 | 19.054 | 60.460 | 1.00 | 59.02 |
|  | ATOM | 1349 | C | VAL | 182 | 19.339 | 20.410 | 61.125 | 1.00 | 60.16 |
|  | ATOM | 1350 | O | VAL | 182 | 19.052 | 21.220 | 62.008 | 1.00 | 59.87 |
| 20 | ATOM | 1351 | N | GLY | 183 | 18.640 | 20.275 | 60.003 | 1.00 | 61.05 |
|  | ATOM | 1352 | CA | GLY | 183 | 17.480 | 21.103 | 59.741 | 1.00 | 63.47 |
|  | ATOM | 1353 | C | GLY | 183 | 16.412 | 20.967 | 60.805 | 1.00 | 64.68 |
|  | ATOM | 1354 | O | GLY | 183 | 15.873 | 21.966 | 61.280 | 1.00 | 64.59 |
|  | ATOM | 1355 | N | LEU | 184 | 16.103 | 19.733 | 61.187 | 1.00 | 65.39 |
| 25 | ATOM | 1356 | CA | LEU | 184 | 15.091 | 19.502 | 62.203 | 1.00 | 66.47 |
|  | ATOM | 1357 | CB | LEU | 184 | 14.855 | 18.005 | 62.387 | 1.00 | 66.17 |
|  | ATOM | 1358 | CG | LEU | 184 | 14.407 | 17.254 | 61.132 | 1.00 | 67.51 |
|  | ATOM | 1359 | CD1 | LEU | 184 | 14.116 | 15.805 | 61.486 | 1.00 | 66.63 |
|  | ATOM | 1360 | CD2 | LEU | 184 | 13.168 | 17.913 | 60.546 | 1.00 | 68.22 |

- 63 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1361 | C | LEU | 184 | 15.502 | 20.130 | 63.528 | 1.00 | 67.67 |
| ATOM | 1362 | O | LEU | 184 | 14.651 | 20.570 | 64.301 | 1.00 | 68.91 |
| ATOM | 1363 | N | LEU | 185 | 16.804 | 20.176 | 63.790 | 1.00 | 68.11 |
| ATOM | 1364 | CA | LEU | 185 | 17.297 | 20.759 | 65.031 | 1.00 | 68.91 |
| ATOM | 1365 | CB | LEU | 185 | 18.797 | 20.501 | 65.194 | 1.00 | 67.32 |
| ATOM | 1366 | CG | LEU | 185 | 19.409 | 21.060 | 66.482 | 1.00 | 66.21 |
| ATOM | 1367 | CD1 | LEU | 185 | 18.776 | 20.375 | 67.676 | 1.00 | 65.16 |
| ATOM | 1368 | CD2 | LEU | 185 | 20.913 | 20.851 | 66.486 | 1.00 | 66.43 |
| ATOM | 1369 | C | LEU | 185 | 17.034 | 22.262 | 65.058 | 1.00 | 70.10 |
| ATOM | 1370 | O | LEU | 185 | 16.422 | 22.776 | 65.991 | 1.00 | 70.26 |
| ATOM | 1371 | N | ARG | 186 | 17.505 | 22.962 | 64.033 | 1.00 | 71.83 |
| ATOM | 1372 | CA | ARG | 186 | 17.314 | 24.403 | 63.948 | 1.00 | 73.78 |
| ATOM | 1373 | CB | ARG | 186 | 18.015 | 24.941 | 62.700 | 1.00 | 73.97 |
| ATOM | 1374 | CG | ARG | 186 | 19.533 | 24.881 | 62.804 | 1.00 | 74.09 |
| ATOM | 1375 | CD | ARG | 186 | 20.206 | 24.984 | 61.448 | 1.00 | 74.37 |
| ATOM | 1376 | NE | ARG | 186 | 21.662 | 24.945 | 61.571 | 1.00 | 75.77 |
| ATOM | 1377 | CZ | ARG | 186 | 22.503 | 24.860 | 60.543 | 1.00 | 75.94 |
| ATOM | 1378 | NH1 | ARG | 186 | 22.036 | 24.800 | 59.303 | 1.00 | 75.97 |
| ATOM | 1379 | NH2 | ARG | 186 | 23.815 | 24.841 | 60.755 | 1.00 | 75.99 |
| ATOM | 1380 | C | ARG | 186 | 15.825 | 24.737 | 63.927 | 1.00 | 74.93 |
| ATOM | 1381 | O | ARG | 186 | 15.365 | 25.609 | 64.665 | 1.00 | 74.59 |
| ATOM | 1382 | N | ASP | 187 | 15.074 | 24.023 | 63.095 | 1.00 | 76.23 |
| ATOM | 1383 | CA | ASP | 187 | 13.632 | 24.225 | 62.981 | 1.00 | 77.59 |
| ATOM | 1384 | CB | ASP | 187 | 13.018 | 23.128 | 62.102 | 1.00 | 75.83 |
| ATOM | 1385 | CG | ASP | 187 | 13.203 | 23.391 | 60.614 | 1.00 | 74.87 |
| ATOM | 1386 | OD1 | ASP | 187 | 14.193 | 24.051 | 60.234 | 1.00 | 73.64 |
| ATOM | 1387 | OD2 | ASP | 187 | 12.359 | 22.924 | 59.820 | 1.00 | 74.33 |
| ATOM | 1388 | C | ASP | 187 | 12.945 | 24.236 | 64.349 | 1.00 | 79.78 |
| ATOM | 1389 | O | ASP | 187 | 11.963 | 24.952 | 64.551 | 1.00 | 80.50 |

- 64 -

| | ATOM | 1390 | N | ALA | 188 | 13.461 | 23.445 | 65.286 | 1.00 | 81.21 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1391 | CA | ALA | 188 | 12.883 | 23.379 | 66.625 | 1.00 | 82.86 |
| | ATOM | 1392 | CB | ALA | 188 | 13.118 | 22.000 | 67.230 | 1.00 | 83.00 |
| | ATOM | 1393 | C | ALA | 188 | 13.477 | 24.456 | 67.525 | 1.00 | 84.14 |
| 5 | ATOM | 1394 | O | ALA | 188 | 12.783 | 25.019 | 68.376 | 1.00 | 84.10 |
| | ATOM | 1395 | N | ILE | 189 | 14.763 | 24.736 | 67.338 | 1.00 | 85.33 |
| | ATOM | 1396 | CA | ILE | 189 | 15.445 | 25.753 | 68.127 | 1.00 | 86.87 |
| | ATOM | 1397 | CB | ILE | 189 | 16.947 | 25.819 | 67.776 | 1.00 | 86.40 |
| | ATOM | 1398 | CG2 | ILE | 189 | 17.585 | 27.049 | 68.409 | 1.00 | 85.37 |
| 10 | ATOM | 1399 | CG1 | ILE | 189 | 17.641 | 24.541 | 68.253 | 1.00 | 86.52 |
| | ATOM | 1400 | CD1 | ILE | 189 | 19.136 | 24.516 | 68.004 | 1.00 | 86.36 |
| | ATOM | 1401 | C | ILE | 189 | 14.812 | 27.114 | 67.871 | 1.00 | 88.85 |
| | ATOM | 1402 | O | ILE | 189 | 14.802 | 27.978 | 68.748 | 1.00 | 89.64 |
| | ATOM | 1403 | N | LYS | 190 | 14.278 | 27.295 | 66.666 | 1.00 | 90.36 |
| 15 | ATOM | 1404 | CA | LYS | 190 | 13.638 | 28.551 | 66.291 | 1.00 | 91.75 |
| | ATOM | 1405 | CB | LYS | 190 | 13.678 | 28.729 | 64.770 | 1.00 | 92.26 |
| | ATOM | 1406 | CG | LYS | 190 | 15.032 | 29.205 | 64.234 | 1.00 | 93.56 |
| | ATOM | 1407 | CD | LYS | 190 | 16.174 | 28.282 | 64.652 | 1.00 | 94.17 |
| | ATOM | 1408 | CE | LYS | 190 | 17.507 | 28.722 | 64.064 | 1.00 | 94.42 |
| 20 | ATOM | 1409 | NZ | LYS | 190 | 18.605 | 27.773 | 64.409 | 1.00 | 93.91 |
| | ATOM | 1410 | C | LYS | 190 | 12.202 | 28.645 | 66.803 | 1.00 | 92.34 |
| | ATOM | 1411 | O | LYS | 190 | 11.612 | 29.723 | 66.817 | 1.00 | 92.82 |
| | ATOM | 1412 | N | ARG | 191 | 11.639 | 27.516 | 67.221 | 1.00 | 92.78 |
| | ATOM | 1413 | CA | ARG | 191 | 10.286 | 27.502 | 67.763 | 1.00 | 93.41 |
| 25 | ATOM | 1414 | CB | ARG | 191 | 9.674 | 26.108 | 67.658 | 1.00 | 93.77 |
| | ATOM | 1415 | CG | ARG | 191 | 9.711 | 25.497 | 66.275 | 1.00 | 93.66 |
| | ATOM | 1416 | CD | ARG | 191 | 9.530 | 23.993 | 66.378 | 1.00 | 93.81 |
| | ATOM | 1417 | NE | ARG | 191 | 9.816 | 23.310 | 65.123 | 1.00 | 93.99 |
| | ATOM | 1418 | CZ | ARG | 191 | 10.012 | 22.000 | 65.017 | 1.00 | 94.26 |

- 65 -

| | ATOM | 1419 | NH1 | ARG | 191 | 9.954 | 21.231 | 66.095 | 1.00 | 94.65 |
|---|------|------|-----|-----|-----|-------|--------|--------|------|-------|
| | ATOM | 1420 | NH2 | ARG | 191 | 10.269 | 21.459 | 63.835 | 1.00 | 94.96 |
| | ATOM | 1421 | C | ARG | 191 | 10.432 | 27.866 | 69.233 | 1.00 | 94.00 |
| | ATOM | 1422 | O | ARG | 191 | 9.526 | 27.654 | 70.036 | 1.00 | 94.16 |
| 5 | ATOM | 1423 | N | ARG | 192 | 11.596 | 28.408 | 69.574 | 1.00 | 94.91 |
| | ATOM | 1424 | CA | ARG | 192 | 11.897 | 28.795 | 70.943 | 1.00 | 96.15 |
| | ATOM | 1425 | CB | ARG | 192 | 13.049 | 27.944 | 71.482 | 1.00 | 96.57 |
| | ATOM | 1426 | CG | ARG | 192 | 12.733 | 26.469 | 71.581 | 1.00 | 97.44 |
| | ATOM | 1427 | CD | ARG | 192 | 11.737 | 26.209 | 72.689 | 1.00 | 98.38 |
| 10 | ATOM | 1428 | NE | ARG | 192 | 11.339 | 24.808 | 72.745 | 1.00 | 98.97 |
| | ATOM | 1429 | CZ | ARG | 192 | 10.624 | 24.278 | 73.730 | 1.00 | 99.63 |
| | ATOM | 1430 | NH1 | ARG | 192 | 10.230 | 25.035 | 74.746 | 1.00 | 99.17 |
| | ATOM | 1431 | NH2 | ARG | 192 | 10.300 | 22.992 | 73.700 | 1.00 | 99.97 |
| | ATOM | 1432 | C | ARG | 192 | 12.273 | 30.265 | 71.062 | 1.00 | 96.50 |
| 15 | ATOM | 1433 | O | ARG | 192 | 11.603 | 31.035 | 71.752 | 1.00 | 96.60 |
| | ATOM | 1434 | N | GLY | 193 | 13.352 | 30.652 | 70.386 | 1.00 | 96.89 |
| | ATOM | 1435 | CA | GLY | 193 | 13.812 | 32.026 | 70.465 | 1.00 | 97.08 |
| | ATOM | 1436 | C | GLY | 193 | 14.385 | 32.217 | 71.855 | 1.00 | 97.08 |
| | ATOM | 1437 | O | GLY | 193 | 15.060 | 33.204 | 72.147 | 1.00 | 96.46 |
| 20 | ATOM | 1438 | N | ASP | 194 | 14.104 | 31.235 | 72.707 | 1.00 | 97.36 |
| | ATOM | 1439 | CA | ASP | 194 | 14.552 | 31.205 | 74.092 | 1.00 | 97.35 |
| | ATOM | 1440 | CB | ASP | 194 | 13.938 | 29.984 | 74.789 | 1.00 | 98.43 |
| | ATOM | 1441 | CG | ASP | 194 | 13.764 | 30.181 | 76.284 | 1.00 | 99.62 |
| | ATOM | 1442 | OD1 | ASP | 194 | 13.117 | 31.173 | 76.683 | 1.00 | 100.29 |
| 25 | ATOM | 1443 | OD2 | ASP | 194 | 14.262 | 29.338 | 77.059 | 1.00 | 99.87 |
| | ATOM | 1444 | C | ASP | 194 | 16.078 | 31.122 | 74.122 | 1.00 | 96.90 |
| | ATOM | 1445 | O | ASP | 194 | 16.715 | 31.471 | 75.118 | 1.00 | 97.50 |
| | ATOM | 1446 | N | PHE | 195 | 16.657 | 30.655 | 73.018 | 1.00 | 95.62 |
| | ATOM | 1447 | CA | PHE | 195 | 18.105 | 30.524 | 72.896 | 1.00 | 94.15 |

| | ATOM | 1448 | CB | PHE | 195 | 18.598 | 29.309 | 73.697 | 1.00 | 94.86 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 1449 | CG | PHE | 195 | 18.043 | 27.988 | 73.224 | 1.00 | 95.10 |
| | ATOM | 1450 | CD1 | PHE | 195 | 18.560 | 27.360 | 72.095 | 1.00 | 95.09 |
| | ATOM | 1451 | CD2 | PHE | 195 | 17.005 | 27.369 | 73.916 | 1.00 | 95.17 |
| 5 | ATOM | 1452 | CE1 | PHE | 195 | 18.053 | 26.136 | 71.663 | 1.00 | 95.14 |
| | ATOM | 1453 | CE2 | PHE | 195 | 16.491 | 26.145 | 73.492 | 1.00 | 95.12 |
| | ATOM | 1454 | CZ | PHE | 195 | 17.016 | 25.528 | 72.364 | 1.00 | 94.97 |
| | ATOM | 1455 | C | PHE | 195 | 18.508 | 30.393 | 71.430 | 1.00 | 92.64 |
| | ATOM | 1456 | O | PHE | 195 | 17.667 | 30.131 | 70.569 | 1.00 | 92.22 |
| 10 | ATOM | 1457 | N | GLU | 196 | 19.793 | 30.583 | 71.148 | 1.00 | 90.93 |
| | ATOM | 1458 | CA | GLU | 196 | 20.292 | 30.486 | 69.779 | 1.00 | 89.04 |
| | ATOM | 1459 | CB | GLU | 196 | 20.249 | 31.861 | 69.102 | 1.00 | 89.55 |
| | ATOM | 1460 | CG | GLU | 196 | 18.846 | 32.395 | 68.832 | 1.00 | 90.25 |
| | ATOM | 1461 | CD | GLU | 196 | 18.859 | 33.771 | 68.187 | 1.00 | 90.61 |
| 15 | ATOM | 1462 | OE1 | GLU | 196 | 19.342 | 34.728 | 68.830 | 1.00 | 90.30 |
| | ATOM | 1463 | OE2 | GLU | 196 | 18.390 | 33.895 | 67.035 | 1.00 | 90.79 |
| | ATOM | 1464 | C | GLU | 196 | 21.711 | 29.923 | 69.694 | 1.00 | 87.11 |
| | ATOM | 1465 | O | GLU | 196 | 22.681 | 30.589 | 70.066 | 1.00 | 86.83 |
| | ATOM | 1466 | N | MET | 197 | 21.824 | 28.692 | 69.201 | 1.00 | 84.23 |
| 20 | ATOM | 1467 | CA | MET | 197 | 23.121 | 28.043 | 69.045 | 1.00 | 80.79 |
| | ATOM | 1468 | CB | MET | 197 | 23.067 | 26.586 | 69.524 | 1.00 | 81.16 |
| | ATOM | 1469 | CG | MET | 197 | 22.633 | 26.389 | 70.967 | 1.00 | 80.14 |
| | ATOM | 1470 | SD | MET | 197 | 23.597 | 27.356 | 72.135 | 1.00 | 81.93 |
| | ATOM | 1471 | CE | MET | 197 | 25.195 | 26.640 | 71.968 | 1.00 | 81.72 |
| 25 | ATOM | 1472 | C | MET | 197 | 23.502 | 28.070 | 67.568 | 1.00 | 77.74 |
| | ATOM | 1473 | O | MET | 197 | 22.695 | 28.436 | 66.716 | 1.00 | 76.30 |
| | ATOM | 1474 | N | ASP | 198 | 24.733 | 27.672 | 67.269 | 1.00 | 75.73 |
| | ATOM | 1475 | CA | ASP | 198 | 25.214 | 27.652 | 65.894 | 1.00 | 72.50 |
| | ATOM | 1476 | CB | ASP | 198 | 26.297 | 28.723 | 65.720 | 1.00 | 73.47 |

- 67 -

| | ATOM | 1477 | CG | ASP | 198 | 26.573 | 29.046 | 64.265 | 1.00 | 75.34 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 1478 | OD1 | ASP | 198 | 27.407 | 29.941 | 64.005 | 1.00 | 75.72 |
| | ATOM | 1479 | OD2 | ASP | 198 | 25.954 | 28.407 | 63.384 | 1.00 | 76.53 |
| | ATOM | 1480 | C | ASP | 198 | 25.769 | 26.265 | 65.544 | 1.00 | 69.75 |
| 5 | ATOM | 1481 | O | ASP | 198 | 26.962 | 26.005 | 65.703 | 1.00 | 69.48 |
| | ATOM | 1482 | N | VAL | 199 | 24.892 | 25.383 | 65.068 | 1.00 | 66.43 |
| | ATOM | 1483 | CA | VAL | 199 | 25.266 | 24.018 | 64.697 | 1.00 | 62.47 |
| | ATOM | 1484 | CB | VAL | 199 | 24.055 | 23.266 | 64.113 | 1.00 | 62.19 |
| | ATOM | 1485 | CG1 | VAL | 199 | 24.426 | 21.823 | 63.827 | 1.00 | 61.88 |
| 10 | ATOM | 1486 | CG2 | VAL | 199 | 22.886 | 23.340 | 65.083 | 1.00 | 61.21 |
| | ATOM | 1487 | C | VAL | 199 | 26.409 | 23.986 | 63.682 | 1.00 | 60.44 |
| | ATOM | 1488 | O | VAL | 199 | 26.192 | 24.135 | 62.479 | 1.00 | 59.37 |
| | ATOM | 1489 | N | VAL | 200 | 27.624 | 23.774 | 64.180 | 1.00 | 58.00 |
| | ATOM | 1490 | CA | VAL | 200 | 28.820 | 23.741 | 63.341 | 1.00 | 56.24 |
| 15 | ATOM | 1491 | CB | VAL | 200 | 30.048 | 24.278 | 64.128 | 1.00 | 57.42 |
| | ATOM | 1492 | CG1 | VAL | 200 | 31.326 | 24.071 | 63.331 | 1.00 | 57.94 |
| | ATOM | 1493 | CG2 | VAL | 200 | 29.859 | 25.761 | 64.433 | 1.00 | 59.29 |
| | ATOM | 1494 | C | VAL | 200 | 29.159 | 22.357 | 62.785 | 1.00 | 54.53 |
| | ATOM | 1495 | O | VAL | 200 | 29.759 | 22.242 | 61.715 | 1.00 | 54.29 |
| 20 | ATOM | 1496 | N | ALA | 201 | 28.779 | 21.306 | 63.503 | 1.00 | 52.88 |
| | ATOM | 1497 | CA | ALA | 201 | 29.085 | 19.953 | 63.048 | 1.00 | 49.83 |
| | ATOM | 1498 | CB | ALA | 201 | 30.541 | 19.627 | 63.349 | 1.00 | 47.49 |
| | ATOM | 1499 | C | ALA | 201 | 28.196 | 18.887 | 63.654 | 1.00 | 46.62 |
| | ATOM | 1500 | O | ALA | 201 | 27.803 | 18.973 | 64.810 | 1.00 | 47.96 |
| 25 | ATOM | 1501 | N | MET | 202 | 27.873 | 17.883 | 62.851 | 1.00 | 44.82 |
| | ATOM | 1502 | CA | MET | 202 | 27.065 | 16.762 | 63.309 | 1.00 | 42.12 |
| | ATOM | 1503 | CB | MET | 202 | 25.731 | 16.695 | 62.567 | 1.00 | 39.23 |
| | ATOM | 1504 | CG | MET | 202 | 24.886 | 15.520 | 63.014 | 1.00 | 38.13 |
| | ATOM | 1505 | SD | MET | 202 | 23.425 | 15.193 | 62.026 | 1.00 | 40.98 |

|      | ATOM | 1506 | CE  | MET | 202 | 24.134 | 15.162 | 60.401 | 1.00 | 37.63 |
|------|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|      | ATOM | 1507 | C   | MET | 202 | 27.865 | 15.489 | 63.027 | 1.00 | 40.68 |
|      | ATOM | 1508 | O   | MET | 202 | 28.274 | 15.251 | 61.888 | 1.00 | 38.74 |
|      | ATOM | 1509 | N   | VAL | 203 | 28.092 | 14.679 | 64.060 | 1.00 | 39.90 |
| 5    | ATOM | 1510 | CA  | VAL | 203 | 28.851 | 13.438 | 63.901 | 1.00 | 37.47 |
|      | ATOM | 1511 | CB  | VAL | 203 | 30.264 | 13.549 | 64.517 | 1.00 | 36.73 |
|      | ATOM | 1512 | CG1 | VAL | 203 | 31.078 | 14.615 | 63.796 | 1.00 | 34.96 |
|      | ATOM | 1513 | CG2 | VAL | 203 | 30.155 | 13.852 | 65.996 | 1.00 | 37.90 |
|      | ATOM | 1514 | C   | VAL | 203 | 28.190 | 12.199 | 64.505 | 1.00 | 37.09 |
| 10   | ATOM | 1515 | O   | VAL | 203 | 27.250 | 12.284 | 65.309 | 1.00 | 36.61 |
|      | ATOM | 1516 | N   | ASN | 204 | 28.707 | 11.039 | 64.101 | 1.00 | 36.09 |
|      | ATOM | 1517 | CA  | ASN | 204 | 28.228 | 9.749  | 64.584 | 1.00 | 31.60 |
|      | ATOM | 1518 | CB  | ASN | 204 | 28.461 | 8.695  | 63.497 | 1.00 | 32.07 |
|      | ATOM | 1519 | CG  | ASN | 204 | 27.949 | 7.322  | 63.888 | 1.00 | 31.63 |
| 15   | ATOM | 1520 | OD1 | ASN | 204 | 28.729 | 6.443  | 64.250 | 1.00 | 30.91 |
|      | ATOM | 1521 | ND2 | ASN | 204 | 26.634 | 7.135  | 63.824 | 1.00 | 28.99 |
|      | ATOM | 1522 | C   | ASN | 204 | 29.027 | 9.454  | 65.853 | 1.00 | 28.81 |
|      | ATOM | 1523 | O   | ASN | 204 | 30.122 | 9.990  | 66.019 | 1.00 | 30.24 |
|      | ATOM | 1524 | N   | ASP | 205 | 28.498 | 8.639  | 66.765 | 1.00 | 27.90 |
| 20   | ATOM | 1525 | CA  | ASP | 205 | 29.240 | 8.361  | 67.995 | 1.00 | 26.70 |
|      | ATOM | 1526 | CB  | ASP | 205 | 28.369 | 7.627  | 69.028 | 1.00 | 27.65 |
|      | ATOM | 1527 | CG  | ASP | 205 | 27.642 | 6.438  | 68.455 | 1.00 | 30.26 |
|      | ATOM | 1528 | OD1 | ASP | 205 | 27.079 | 5.655  | 69.256 | 1.00 | 28.60 |
|      | ATOM | 1529 | OD2 | ASP | 205 | 27.623 | 6.289  | 67.213 | 1.00 | 31.99 |
| 25   | ATOM | 1530 | C   | ASP | 205 | 30.573 | 7.630  | 67.791 | 1.00 | 26.87 |
|      | ATOM | 1531 | O   | ASP | 205 | 31.498 | 7.810  | 68.581 | 1.00 | 27.79 |
|      | ATOM | 1532 | N   | THR | 206 | 30.686 | 6.816  | 66.740 | 1.00 | 24.79 |
|      | ATOM | 1533 | CA  | THR | 206 | 31.951 | 6.146  | 66.476 | 1.00 | 24.03 |
|      | ATOM | 1534 | CB  | THR | 206 | 31.886 | 5.236  | 65.206 | 1.00 | 25.43 |

- 69 -

| | ATOM | 1535 | OG1 | THR | 206 | 31. 401 | 5. 999 | 64. 089 | 1. 00 | 26. 30 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1536 | CG2 | THR | 206 | 30. 976 | 4. 032 | 65. 444 | 1. 00 | 16. 83 |
| | ATOM | 1537 | C | THR | 206 | 32. 970 | 7. 258 | 66. 220 | 1. 00 | 24. 75 |
| | ATOM | 1538 | O | THR | 206 | 34. 025 | 7. 326 | 66. 858 | 1. 00 | 25. 65 |
| 5 | ATOM | 1539 | N | VAL | 207 | 32. 632 | 8. 136 | 65. 285 | 1. 00 | 22. 49 |
| | ATOM | 1540 | CA | VAL | 207 | 33. 487 | 9. 257 | 64. 917 | 1. 00 | 23. 51 |
| | ATOM | 1541 | CB | VAL | 207 | 32. 775 | 10. 133 | 63. 855 | 1. 00 | 25. 35 |
| | ATOM | 1542 | CG1 | VAL | 207 | 33. 617 | 11. 362 | 63. 521 | 1. 00 | 24. 61 |
| | ATOM | 1543 | CG2 | VAL | 207 | 32. 509 | 9. 299 | 62. 609 | 1. 00 | 21. 66 |
| 10 | ATOM | 1544 | C | VAL | 207 | 33. 897 | 10. 119 | 66. 126 | 1. 00 | 23. 48 |
| | ATOM | 1545 | O | VAL | 207 | 35. 061 | 10. 470 | 66. 279 | 1. 00 | 26. 51 |
| | ATOM | 1546 | N | ALA | 208 | 32. 948 | 10. 452 | 66. 989 | 1. 00 | 24. 53 |
| | ATOM | 1547 | CA | ALA | 208 | 33. 262 | 11. 251 | 68. 169 | 1. 00 | 26. 32 |
| | ATOM | 1548 | CB | ALA | 208 | 31. 980 | 11..533 | 68. 958 | 1. 00 | 27. 56 |
| 15 | ATOM | 1549 | C | ALA | 208 | 34. 287 | 10. 530 | 69. 055 | 1. 00 | 28. 84 |
| | ATOM | 1550 | O | ALA | 208 | 35. 247 | 11. 138 | 69. 549 | 1. 00 | 27. 69 |
| | ATOM | 1551 | N | THR | 209 | 34. 084 | 9. 228 | 69. 258 | 1. 00 | 28. 76 |
| | ATOM | 1552 | CA | THR | 209 | 35. 006 | 8. 447 | 70. 075 | 1. 00 | 28. 08 |
| | ATOM | 1553 | CB | THR | 209 | 34. 474 | 7. 001 | 70. 271 | 1. 00 | 31. 76 |
| 20 | ATOM | 1554 | OG1 | THR | 209 | 33. 373 | 7. 027 | 71. 181 | 1. 00 | 33. 12 |
| | ATOM | 1555 | CG2 | THR | 209 | 35. 550 | 6. 080 | 70. 818 | 1. 00 | 30. 03 |
| | ATOM | 1556 | C | THR | 209 | 36. 382 | 8. 414 | 69. 418 | 1. 00 | 26. 73 |
| | ATOM | 1557 | O | THR | 209 | 37. 399 | 8. 611 | 70. 078 | 1. 00 | 28. 00 |
| | ATOM | 1558 | N | MET | 210 | 36. 421 | 8. 191 | 68. 110 | 1. 00 | 28. 44 |
| 25 | ATOM | 1559 | CA | MET | 210 | 37. 703 | 8. 143 | 67. 419 | 1. 00 | 28. 08 |
| | ATOM | 1560 | CB | MET | 210 | 37. 516 | 7. 851 | 65. 932 | 1. 00 | 26. 94 |
| | ATOM | 1561 | CG | MET | 210 | 38. 842 | 7. 766 | 65. 168 | 1. 00 | 28. 59 |
| | ATOM | 1562 | SD | MET | 210 | 38. 643 | 7. 734 | 63. 374 | 1. 00 | 32. 14 |
| | ATOM | 1563 | CE | MET | 210 | 38. 216 | 9. 518 | 63. 083 | 1. 00 | 33. 30 |

- 70 -

| | ATOM | 1564 | C | MET | 210 | 38.467 | 9.452 | 67.578 | 1.00 | 29.43 |
|---|------|------|------|-----|-----|--------|-------|--------|------|-------|
| | ATOM | 1565 | O | MET | 210 | 39.636 | 9.459 | 67.972 | 1.00 | 30.57 |
| | ATOM | 1566 | N | ILE | 211 | 37.799 | 10.561 | 67.281 | 1.00 | 31.16 |
| | ATOM | 1567 | CA | ILE | 211 | 38.433 | 11.873 | 67.376 | 1.00 | 30.57 |
| 5 | ATOM | 1568 | CB | ILE | 211 | 37.418 | 13.012 | 67.019 | 1.00 | 29.75 |
| | ATOM | 1569 | CG2 | ILE | 211 | 38.086 | 14.390 | 67.177 | 1.00 | 28.08 |
| | ATOM | 1570 | CG1 | ILE | 211 | 36.928 | 12.837 | 65.578 | 1.00 | 22.83 |
| | ATOM | 1571 | CD1 | ILE | 211 | 38.021 | 12.979 | 64.553 | 1.00 | 26.28 |
| | ATOM | 1572 | C | ILE | 211 | 39.014 | 12.128 | 68.762 | 1.00 | 30.30 |
| 10 | ATOM | 1573 | O | ILE | 211 | 40.185 | 12.489 | 68.897 | 1.00 | 31.89 |
| | ATOM | 1574 | N | SER | 212 | 38.203 | 11.914 | 69.792 | 1.00 | 32.78 |
| | ATOM | 1575 | CA | SER | 212 | 38.639 | 12.146 | 71.164 | 1.00 | 35.84 |
| | ATOM | 1576 | CB | SER | 212 | 37.499 | 11.852 | 72.140 | 1.00 | 35.91 |
| | ATOM | 1577 | OG | SER | 212 | 37.317 | 10.455 | 72.307 | 1.00 | 41.55 |
| 15 | ATOM | 1578 | C | SER | 212 | 39.864 | 11.334 | 71.566 | 1.00 | 37.74 |
| | ATOM | 1579 | O | SER | 212 | 40.684 | 11.803 | 72.354 | 1.00 | 41.44 |
| | ATOM | 1580 | N | CYS | 213 | 39.990 | 10.121 | 71.040 | 1.00 | 38.07 |
| | ATOM | 1581 | CA | CYS | 213 | 41.132 | 9.273 | 71.374 | 1.00 | 39.83 |
| | ATOM | 1582 | CB | CYS | 213 | 40.802 | 7.799 | 71.108 | 1.00 | 38.31 |
| 20 | ATOM | 1583 | SG | CYS | 213 | 39.513 | 7.129 | 72.185 | 1.00 | 38.48 |
| | ATOM | 1584 | C | CYS | 213 | 42.372 | 9.666 | 70.582 | 1.00 | 41.86 |
| | ATOM | 1585 | O | CYS | 213 | 43.503 | 9.426 | 71.012 | 1.00 | 38.47 |
| | ATOM | 1586 | N | TYR | 214 | 42.149 | 10.261 | 69.413 | 1.00 | 45.32 |
| | ATOM | 1587 | CA | TYR | 214 | 43.243 | 10.701 | 68.554 | 1.00 | 45.02 |
| 25 | ATOM | 1588 | CB | TYR | 214 | 42.705 | 11.506 | 67.370 | 1.00 | 45.88 |
| | ATOM | 1589 | CG | TYR | 214 | 43.798 | 12.171 | 66.573 | 1.00 | 45.72 |
| | ATOM | 1590 | CD1 | TYR | 214 | 44.509 | 11.465 | 65.608 | 1.00 | 46.39 |
| | ATOM | 1591 | CE1 | TYR | 214 | 45.556 | 12.061 | 64.913 | 1.00 | 47.16 |
| | ATOM | 1592 | CD2 | TYR | 214 | 44.160 | 13.498 | 66.823 | 1.00 | 44.53 |

- 71 -

| | ATOM | 1593 | CE2 | TYR | 214 | 45.203 | 14.099 | 66.134 | 1.00 | 45.20 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 1594 | CZ | TYR | 214 | 45.896 | 13.375 | 65.183 | 1.00 | 46.22 |
| | ATOM | 1595 | OH | TYR | 214 | 46.942 | 13.955 | 64.510 | 1.00 | 50.31 |
| | ATOM | 1596 | C | TYR | 214 | 44.226 | 11.573 | 69.322 | 1.00 | 44.69 |
| 5 | ATOM | 1597 | O | TYR | 214 | 45.420 | 11.296 | 69.363 | 1.00 | 44.40 |
| | ATOM | 1598 | N | TYR | 215 | 43.713 | 12.635 | 69.924 | 1.00 | 45.92 |
| | ATOM | 1599 | CA | TYR | 215 | 44.556 | 13.552 | 70.667 | 1.00 | 48.38 |
| | ATOM | 1600 | CB | TYR | 215 | 43.713 | 14.716 | 71.175 | 1.00 | 51.93 |
| | ATOM | 1601 | CG | TYR | 215 | 43.192 | 15.545 | 70.021 | 1.00 | 57.70 |
| 10 | ATOM | 1602 | CD1 | TYR | 215 | 41.918 | 15.330 | 69.484 | 1.00 | 58.41 |
| | ATOM | 1603 | CE1 | TYR | 215 | 41.478 | 16.047 | 68.363 | 1.00 | 61.27 |
| | ATOM | 1604 | CD2 | TYR | 215 | 44.011 | 16.498 | 69.413 | 1.00 | 59.13 |
| | ATOM | 1605 | CE2 | TYR | 215 | 43.586 | 17.214 | 68.300 | 1.00 | 61.22 |
| | ATOM | 1606 | CZ | TYR | 215 | 42.325 | 16.991 | 67.780 | 1.00 | 62.20 |
| 15 | ATOM | 1607 | OH | TYR | 215 | 41.928 | 17.728 | 66.688 | 1.00 | 61.67 |
| | ATOM | 1608 | C | TYR | 215 | 45.304 | 12.871 | 71.792 | 1.00 | 48.87 |
| | ATOM | 1609 | O | TYR | 215 | 46.282 | 13.407 | 72.318 | 1.00 | 49.38 |
| | ATOM | 1610 | N | GLU | 216 | 44.852 | 11.672 | 72.142 | 1.00 | 47.69 |
| | ATOM | 1611 | CA | GLU | 216 | 45.496 | 10.889 | 73.181 | 1.00 | 47.03 |
| 20 | ATOM | 1612 | CB | GLU | 216 | 44.474 | 9.979 | 73.863 | 1.00 | 49.83 |
| | ATOM | 1613 | CG | GLU | 216 | 44.837 | 9.550 | 75.270 | 1.00 | 55.37 |
| | ATOM | 1614 | CD | GLU | 216 | 44.998 | 10.735 | 76.208 | 1.00 | 59.31 |
| | ATOM | 1615 | OE1 | GLU | 216 | 44.285 | 11.747 | 76.012 | 1.00 | 59.95 |
| | ATOM | 1616 | OE2 | GLU | 216 | 45.824 | 10.649 | 77.146 | 1.00 | 60.13 |
| 25 | ATOM | 1617 | C | GLU | 216 | 46.552 | 10.044 | 72.477 | 1.00 | 45.45 |
| | ATOM | 1618 | O | GLU | 216 | 47.673 | 9.905 | 72.958 | 1.00 | 45.05 |
| | ATOM | 1619 | N | ASP | 217 | 46.183 | 9.495 | 71.321 | 1.00 | 43.73 |
| | ATOM | 1620 | CA | ASP | 217 | 47.074 | 8.643 | 70.530 | 1.00 | 41.33 |
| | ATOM | 1621 | CB | ASP | 217 | 46.776 | 7.171 | 70.845 | 1.00 | 40.13 |

- 72 -

| | ATOM | 1622 | CG | ASP | 217 | 47.780 | 6.208 | 70.226 | 1.00 | 39.76 |
|---|------|------|-----|-----|-----|--------|-------|--------|------|-------|
| | ATOM | 1623 | OD1 | ASP | 217 | 48.461 | 6.571 | 69.249 | 1.00 | 40.95 |
| | ATOM | 1624 | OD2 | ASP | 217 | 47.876 | 5.062 | 70.712 | 1.00 | 42.61 |
| | ATOM | 1625 | C | ASP | 217 | 46.852 | 8.921 | 69.033 | 1.00 | 40.53 |
| 5 | ATOM | 1626 | O | ASP | 217 | 45.862 | 8.474 | 68.443 | 1.00 | 37.20 |
| | ATOM | 1627 | N | HIS | 218 | 47.779 | 9.657 | 68.427 | 1.00 | 41.94 |
| | ATOM | 1628 | CA | HIS | 218 | 47.689 | 10.008 | 67.007 | 1.00 | 44.23 |
| | ATOM | 1629 | CB | HIS | 218 | 48.912 | 10.828 | 66.603 | 1.00 | 47.00 |
| | ATOM | 1630 | CG | HIS | 218 | 48.860 | 12.244 | 67.079 | 1.00 | 51.95 |
| 10 | ATOM | 1631 | CD2 | HIS | 218 | 49.230 | 13.402 | 66.483 | 1.00 | 54.47 |
| | ATOM | 1632 | ND1 | HIS | 218 | 48.371 | 12.592 | 68.320 | 1.00 | 54.33 |
| | ATOM | 1633 | CE1 | HIS | 218 | 48.439 | 13.903 | 68.467 | 1.00 | 55.83 |
| | ATOM | 1634 | NE2 | HIS | 218 | 48.957 | 14.419 | 67.367 | 1.00 | 55.95 |
| | ATOM | 1635 | C | HIS | 218 | 47.528 | 8.810 | 66.074 | 1.00 | 42.66 |
| 15 | ATOM | 1636 | O | HIS | 218 | 47.157 | 8.963 | 64.909 | 1.00 | 42.00 |
| | ATOM | 1637 | N | GLN | 219 | 47.793 | 7.620 | 66.597 | 1.00 | 41.40 |
| | ATOM | 1638 | CA | GLN | 219 | 47.667 | 6.394 | 65.820 | 1.00 | 41.15 |
| | ATOM | 1639 | CB | GLN | 219 | 48.592 | 5.321 | 66.397 | 1.00 | 45.16 |
| | ATOM | 1640 | CG | GLN | 219 | 50.070 | 5.611 | 66.214 | 1.00 | 49.72 |
| 20 | ATOM | 1641 | CD | GLN | 219 | 50.566 | 5.230 | 64.832 | 1.00 | 55.92 |
| | ATOM | 1642 | OE1 | GLN | 219 | 49.997 | 5.646 | 63.813 | 1.00 | 57.28 |
| | ATOM | 1643 | NE2 | GLN | 219 | 51.636 | 4.429 | 64.787 | 1.00 | 57.32 |
| | ATOM | 1644 | C | GLN | 219 | 46.228 | 5.869 | 65.792 | 1.00 | 37.41 |
| | ATOM | 1645 | O | GLN | 219 | 45.927 | 4.904 | 65.091 | 1.00 | 37.06 |
| 25 | ATOM | 1646 | N | CYS | 220 | 45.342 | 6.488 | 66.562 | 1.00 | 34.18 |
| | ATOM | 1647 | CA | CYS | 220 | 43.955 | 6.038 | 66.578 | 1.00 | 32.52 |
| | ATOM | 1648 | CB | CYS | 220 | 43.199 | 6.597 | 67.783 | 1.00 | 28.93 |
| | ATOM | 1649 | SG | CYS | 220 | 41.420 | 6.288 | 67.739 | 1.00 | 31.90 |
| | ATOM | 1650 | C | CYS | 220 | 43.272 | 6.474 | 65.303 | 1.00 | 32.01 |

- 73 -

|      | ATOM | 1651 | O   | CYS | 220 | 43.010 | 7.664  | 65.096 | 1.00 | 32.91 |
|------|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|      | ATOM | 1652 | N   | GLU | 221 | 42.993 | 5.505  | 64.442 | 1.00 | 29.12 |
|      | ATOM | 1653 | CA  | GLU | 221 | 42.343 | 5.785  | 63.176 | 1.00 | 28.98 |
|      | ATOM | 1654 | CB  | GLU | 221 | 43.273 | 5.437  | 62.009 | 1.00 | 30.00 |
| 5    | ATOM | 1655 | CG  | GLU | 221 | 44.481 | 6.366  | 61.853 | 1.00 | 35.29 |
|      | ATOM | 1656 | CD  | GLU | 221 | 45.190 | 6.166  | 60.515 | 1.00 | 36.83 |
|      | ATOM | 1657 | OE1 | GLU | 221 | 44.490 | 6.007  | 59.498 | 1.00 | 38.09 |
|      | ATOM | 1658 | OE2 | GLU | 221 | 46.436 | 6.176  | 60.465 | 1.00 | 40.80 |
|      | ATOM | 1659 | C   | GLU | 221 | 41.057 | 4.991  | 63.059 | 1.00 | 25.46 |
| 10   | ATOM | 1660 | O   | GLU | 221 | 40.513 | 4.835  | 61.970 | 1.00 | 22.65 |
|      | ATOM | 1661 | N   | VAL | 222 | 40.569 | 4.491  | 64.185 | 1.00 | 25.43 |
|      | ATOM | 1662 | CA  | VAL | 222 | 39.337 | 3.703  | 64.179 | 1.00 | 25.45 |
|      | ATOM | 1663 | CB  | VAL | 222 | 39.625 | 2.172  | 64.189 | 1.00 | 24.36 |
|      | ATOM | 1664 | CG1 | VAL | 222 | 38.318 | 1.391  | 64.122 | 1.00 | 21.56 |
| 15   | ATOM | 1665 | CG2 | VAL | 222 | 40.533 | 1.795  | 63.029 | 1.00 | 21.70 |
|      | ATOM | 1666 | C   | VAL | 222 | 38.527 | 4.016  | 65.414 | 1.00 | 25.44 |
|      | ATOM | 1667 | O   | VAL | 222 | 39.076 | 4.192  | 66.492 | 1.00 | 25.99 |
|      | ATOM | 1668 | N   | GLY | 223 | 37.217 | 4.090  | 65.240 | 1.00 | 25.97 |
|      | ATOM | 1669 | CA  | GLY | 223 | 36.328 | 4.347  | 66.349 | 1.00 | 25.83 |
| 20   | ATOM | 1670 | C   | GLY | 223 | 35.337 | 3.201  | 66.340 | 1.00 | 25.37 |
|      | ATOM | 1671 | O   | GLY | 223 | 34.852 | 2.812  | 65.273 | 1.00 | 25.38 |
|      | ATOM | 1672 | N   | MET | 224 | 35.044 | 2.647  | 67.511 | 1.00 | 24.88 |
|      | ATOM | 1673 | CA  | MET | 224 | 34.114 | 1.527  | 67.587 | 1.00 | 25.47 |
|      | ATOM | 1674 | CB  | MET | 224 | 34.881 | 0.187  | 67.638 | 1.00 | 22.66 |
| 25   | ATOM | 1675 | CG  | MET | 224 | 33.956 | -1.041 | 67.634 | 1.00 | 25.14 |
|      | ATOM | 1676 | SD  | MET | 224 | 34.806 | -2.680 | 67.748 | 1.00 | 22.18 |
|      | ATOM | 1677 | CE  | MET | 224 | 35.380 | -2.594 | 69.396 | 1.00 | 16.01 |
|      | ATOM | 1678 | C   | MET | 224 | 33.177 | 1.618  | 68.780 | 1.00 | 22.20 |
|      | ATOM | 1679 | O   | MET | 224 | 33.577 | 1.978  | 69.881 | 1.00 | 22.65 |

|  | ATOM | 1680 | N | ILE | 225 | 31.915 | 1.295 | 68.543 | 1.00 | 21.12 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1681 | CA | ILE | 225 | 30.936 | 1.314 | 69.604 | 1.00 | 21.34 |
|  | ATOM | 1682 | CB | ILE | 225 | 29.757 | 2.295 | 69.293 | 1.00 | 25.85 |
|  | ATOM | 1683 | CG2 | ILE | 225 | 28.739 | 2.268 | 70.446 | 1.00 | 25.47 |
| 5 | ATOM | 1684 | CG1 | ILE | 225 | 30.273 | 3.734 | 69.107 | 1.00 | 25.08 |
|  | ATOM | 1685 | CD1 | ILE | 225 | 30.838 | 4.355 | 70.382 | 1.00 | 22.09 |
|  | ATOM | 1686 | C | ILE | 225 | 30.321 | -0.080 | 69.789 | 1.00 | 22.30 |
|  | ATOM | 1687 | O | ILE | 225 | 29.885 | -0.712 | 68.826 | 1.00 | 24.03 |
|  | ATOM | 1688 | N | VAL | 226 | 30.313 | -0.563 | 71.025 | 1.00 | 22.67 |
| 10 | ATOM | 1689 | CA | VAL | 226 | 29.645 | -1.817 | 71.341 | 1.00 | 21.60 |
|  | ATOM | 1690 | CB | VAL | 226 | 30.618 | -2.993 | 71.634 | 1.00 | 21.77 |
|  | ATOM | 1691 | CG1 | VAL | 226 | 29.821 | -4.291 | 71.718 | 1.00 | 21.54 |
|  | ATOM | 1692 | CG2 | VAL | 226 | 31.663 | -3.113 | 70.541 | 1.00 | 17.23 |
|  | ATOM | 1693 | C | VAL | 226 | 28.838 | -1.493 | 72.604 | 1.00 | 21.49 |
| 15 | ATOM | 1694 | O | VAL | 226 | 29.316 | -1.633 | 73.723 | 1.00 | 18.90 |
|  | ATOM | 1695 | N | GLY | 227 | 27.615 | -1.016 | 72.402 | 1.00 | 25.39 |
|  | ATOM | 1696 | CA | GLY | 227 | 26.744 | -0.675 | 73.518 | 1.00 | 26.76 |
|  | ATOM | 1697 | C | GLY | 227 | 25.353 | -1.140 | 73.150 | 1.00 | 28.03 |
|  | ATOM | 1698 | O | GLY | 227 | 25.155 | -2.315 | 72.846 | 1.00 | 29.80 |
| 20 | ATOM | 1699 | N | THR | 228 | 24.384 | -0.235 | 73.161 | 1.00 | 27.62 |
|  | ATOM | 1700 | CA | THR | 228 | 23.031 | -0.607 | 72.788 | 1.00 | 27.59 |
|  | ATOM | 1701 | CB | THR | 228 | 22.083 | 0.601 | 72.911 | 1.00 | 29.15 |
|  | ATOM | 1702 | OG1 | THR | 228 | 21.937 | 0.932 | 74.294 | 1.00 | 32.52 |
|  | ATOM | 1703 | CG2 | THR | 228 | 20.719 | 0.291 | 72.339 | 1.00 | 28.08 |
| 25 | ATOM | 1704 | C | THR | 228 | 23.094 | -1.080 | 71.345 | 1.00 | 26.98 |
|  | ATOM | 1705 | O | THR | 228 | 22.460 | -2.065 | 70.960 | 1.00 | 27.95 |
|  | ATOM | 1706 | N | GLY | 229 | 23.890 | -0.374 | 70.554 | 1.00 | 26.02 |
|  | ATOM | 1707 | CA | GLY | 229 | 24.050 | -0.718 | 69.154 | 1.00 | 25.33 |
|  | ATOM | 1708 | C | GLY | 229 | 25.503 | -1.055 | 68.911 | 1.00 | 24.09 |

- 75 -

| | ATOM | 1709 | O | GLY | 229 | 26.312 | -1.004 | 69.838 | 1.00 | 23.25 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 1710 | N | CYS | 230 | 25.850 | -1.395 | 67.677 | 1.00 | 24.12 |
| | ATOM | 1711 | CA | CYS | 230 | 27.235 | -1.750 | 67.376 | 1.00 | 23.83 |
| | ATOM | 1712 | CB | CYS | 230 | 27.395 | -3.280 | 67.425 | 1.00 | 20.39 |
| 5 | ATOM | 1713 | SG | CYS | 230 | 29.076 | -3.879 | 67.182 | 1.00 | 25.34 |
| | ATOM | 1714 | C | CYS | 230 | 27.627 | -1.204 | 66.010 | 1.00 | 20.45 |
| | ATOM | 1715 | O | CYS | 230 | 26.919 | -1.406 | 65.035 | 1.00 | 20.28 |
| | ATOM | 1716 | N | ASN | 231 | 28.763 | -0.526 | 65.935 | 1.00 | 23.86 |
| | ATOM | 1717 | CA | ASN | 231 | 29.196 | 0.076 | 64.669 | 1.00 | 24.35 |
| 10 | ATOM | 1718 | CB | ASN | 231 | 28.267 | 1.261 | 64.355 | 1.00 | 25.51 |
| | ATOM | 1719 | CG | ASN | 231 | 28.598 | 1.962 | 63.042 | 1.00 | 27.76 |
| | ATOM | 1720 | OD1 | ASN | 231 | 28.930 | 1.331 | 62.039 | 1.00 | 24.60 |
| | ATOM | 1721 | ND2 | ASN | 231 | 28.472 | 3.288 | 63.043 | 1.00 | 30.91 |
| | ATOM | 1722 | C | ASN | 231 | 30.640 | 0.553 | 64.784 | 1.00 | 23.81 |
| 15 | ATOM | 1723 | O | ASN | 231 | 31.184 | 0.624 | 65.885 | 1.00 | 23.94 |
| | ATOM | 1724 | N | ALA | 232 | 31.249 | 0.885 | 63.651 | 1.00 | 22.70 |
| | ATOM | 1725 | CA | ALA | 232 | 32.626 | 1.359 | 63.636 | 1.00 | 25.15 |
| | ATOM | 1726 | CB | ALA | 232 | 33.580 | 0.169 | 63.463 | 1.00 | 24.36 |
| | ATOM | 1727 | C | ALA | 232 | 32.867 | 2.372 | 62.511 | 1.00 | 26.31 |
| 20 | ATOM | 1728 | O | ALA | 232 | 32.127 | 2.416 | 61.530 | 1.00 | 28.47 |
| | ATOM | 1729 | N | CYS | 233 | 33.911 | 3.176 | 62.664 | 1.00 | 24.88 |
| | ATOM | 1730 | CA | CYS | 233 | 34.291 | 4.160 | 61.653 | 1.00 | 26.51 |
| | ATOM | 1731 | CB | CYS | 233 | 33.899 | 5.583 | 62.076 | 1.00 | 24.89 |
| | ATOM | 1732 | SG | CYS | 233 | 34.875 | 6.224 | 63.436 | 1.00 | 25.76 |
| 25 | ATOM | 1733 | C | CYS | 233 | 35.805 | 4.055 | 61.555 | 1.00 | 25.08 |
| | ATOM | 1734 | O | CYS | 233 | 36.450 | 3.564 | 62.480 | 1.00 | 25.19 |
| | ATOM | 1735 | N | TYR | 234 | 36.373 | 4.505 | 60.442 | 1.00 | 25.32 |
| | ATOM | 1736 | CA | TYR | 234 | 37.820 | 4.427 | 60.245 | 1.00 | 23.93 |
| | ATOM | 1737 | CB | TYR | 234 | 38.200 | 3.020 | 59.760 | 1.00 | 20.70 |

- 76 -

| ATOM | 1738 | CG | TYR | 234 | 37.782 | 2.771 | 58.328 | 1.00 | 16.78 |
|------|------|------|------|------|--------|--------|--------|------|-------|
| ATOM | 1739 | CD1 | TYR | 234 | 38.712 | 2.786 | 57.302 | 1.00 | 18.75 |
| ATOM | 1740 | CE1 | TYR | 234 | 38.326 | 2.668 | 55.975 | 1.00 | 18.89 |
| ATOM | 1741 | CD2 | TYR | 234 | 36.443 | 2.622 | 57.990 | 1.00 | 19.60 |
| ATOM | 1742 | CE2 | TYR | 234 | 36.043 | 2.506 | 56.666 | 1.00 | 18.40 |
| ATOM | 1743 | CZ | TYR | 234 | 36.990 | 2.535 | 55.665 | 1.00 | 21.55 |
| ATOM | 1744 | OH | TYR | 234 | 36.603 | 2.479 | 54.346 | 1.00 | 23.25 |
| ATOM | 1745 | C | TYR | 234 | 38.254 | 5.452 | 59.194 | 1.00 | 26.41 |
| ATOM | 1746 | O | TYR | 234 | 37.436 | 5.929 | 58.404 | 1.00 | 27.14 |
| ATOM | 1747 | N | MET | 235 | 39.543 | 5.769 | 59.179 | 1.00 | 27.10 |
| ATOM | 1748 | CA | MET | 235 | 40.094 | 6.722 | 58.224 | 1.00 | 28.74 |
| ATOM | 1749 | CB | MET | 235 | 41.383 | 7.331 | 58.789 | 1.00 | 29.38 |
| ATOM | 1750 | CG | MET | 235 | 41.169 | 8.180 | 60.035 | 1.00 | 31.43 |
| ATOM | 1751 | SD | MET | 235 | 39.947 | 9.503 | 59.750 | 1.00 | 32.30 |
| ATOM | 1752 | CE | MET | 235 | 40.866 | 10.535 | 58.591 | 1.00 | 34.11 |
| ATOM | 1753 | C | MET | 235 | 40.374 | 6.066 | 56.869 | 1.00 | 29.42 |
| ATOM | 1754 | O | MET | 235 | 41.170 | 5.134 | 56.767 | 1.00 | 30.49 |
| ATOM | 1755 | N | GLU | 236 | 39.714 | 6.565 | 55.829 | 1.00 | 31.08 |
| ATOM | 1756 | CA | GLU | 236 | 39.867 | 6.040 | 54.476 | 1.00 | 31.04 |
| ATOM | 1757 | CB | GLU | 236 | 38.491 | 5.743 | 53.879 | 1.00 | 31.57 |
| ATOM | 1758 | CG | GLU | 236 | 38.536 | 5.161 | 52.474 | 1.00 | 32.18 |
| ATOM | 1759 | CD | GLU | 236 | 39.330 | 3.875 | 52.427 | 1.00 | 32.52 |
| ATOM | 1760 | OE1 | GLU | 236 | 40.565 | 3.952 | 52.273 | 1.00 | 34.34 |
| ATOM | 1761 | OE2 | GLU | 236 | 38.723 | 2.789 | 52.571 | 1.00 | 30.79 |
| ATOM | 1762 | C | GLU | 236 | 40.598 | 7.030 | 53.574 | 1.00 | 33.43 |
| ATOM | 1763 | O | GLU | 236 | 40.583 | 8.238 | 53.818 | 1.00 | 29.93 |
| ATOM | 1764 | N | GLU | 237 | 41.240 | 6.506 | 52.532 | 1.00 | 35.85 |
| ATOM | 1765 | CA | GLU | 237 | 41.969 | 7.333 | 51.575 | 1.00 | 37.83 |
| ATOM | 1766 | CB | GLU | 237 | 42.934 | 6.462 | 50.764 | 1.00 | 40.16 |

- 77 -

| | ATOM | 1767 | CG | GLU | 237 | 43.684 | 5.426 | 51.602 | 1.00 43.86 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| | ATOM | 1768 | CD | GLU | 237 | 44.466 | 6.049 | 52.743 | 1.00 47.85 |
| | ATOM | 1769 | OE1 | GLU | 237 | 44.806 | 5.322 | 53.704 | 1.00 51.02 |
| | ATOM | 1770 | OE2 | GLU | 237 | 44.747 | 7.264 | 52.681 | 1.00 48.78 |
| 5 | ATOM | 1771 | C | GLU | 237 | 40.920 | 7.969 | 50.657 | 1.00 37.87 |
| | ATOM | 1772 | O | GLU | 237 | 40.058 | 7.268 | 50.122 | 1.00 38.29 |
| | ATOM | 1773 | N | MET | 238 | 40.987 | 9.287 | 50.477 | 1.00 37.42 |
| | ATOM | 1774 | CA | MET | 238 | 40.009 | 9.987 | 49.644 | 1.00 37.50 |
| | ATOM | 1775 | CB | MET | 238 | 40.375 | 11.467 | 49.501 | 1.00 38.62 |
| 10 | ATOM | 1776 | CG | MET | 238 | 39.772 | 12.355 | 50.587 | 1.00 40.32 |
| | ATOM | 1777 | SD | MET | 238 | 37.956 | 12.144 | 50.764 | 1.00 42.83 |
| | ATOM | 1778 | CE | MET | 238 | 37.308 | 13.116 | 49.410 | 1.00 44.06 |
| | ATOM | 1779 | C | MET | 238 | 39.796 | 9.374 | 48.270 | 1.00 36.21 |
| | ATOM | 1780 | O | MET | 238 | 38.685 | 9.413 | 47.740 | 1.00 33.93 |
| 15 | ATOM | 1781 | N | GLN | 239 | 40.848 | 8.803 | 47.690 | 1.00 35.50 |
| | ATOM | 1782 | CA | GLN | 239 | 40.714 | 8.184 | 46.378 | 1.00 36.82 |
| | ATOM | 1783 | CB | GLN | 239 | 42.078 | 7.732 | 45.846 | 1.00 39.35 |
| | ATOM | 1784 | CG | GLN | 239 | 42.839 | 6.804 | 46.774 | 1.00 44.12 |
| | ATOM | 1785 | CD | GLN | 239 | 43.900 | 7.534 | 47.584 | 1.00 49.18 |
| 20 | ATOM | 1786 | OE1 | GLN | 239 | 43.635 | 8.580 | 48.192 | 1.00 49.88 |
| | ATOM | 1787 | NE2 | GLN | 239 | 45.111 | 6.981 | 47.600 | 1.00 49.95 |
| | ATOM | 1788 | C | GLN | 239 | 39.762 | 6.986 | 46.395 | 1.00 35.72 |
| | ATOM | 1789 | O | GLN | 239 | 39.276 | 6.568 | 45.348 | 1.00 37.20 |
| | ATOM | 1790 | N | ASN | 240 | 39.503 | 6.419 | 47.570 | 1.00 34.56 |
| 25 | ATOM | 1791 | CA | ASN | 240 | 38.604 | 5.272 | 47.648 | 1.00 33.20 |
| | ATOM | 1792 | CB | ASN | 240 | 39.118 | 4.239 | 48.658 | 1.00 33.68 |
| | ATOM | 1793 | CG | ASN | 240 | 40.548 | 3.802 | 48.369 | 1.00 34.24 |
| | ATOM | 1794 | OD1 | ASN | 240 | 40.963 | 3.710 | 47.210 | 1.00 33.87 |
| | ATOM | 1795 | ND2 | ASN | 240 | 41.306 | 3.523 | 49.424 | 1.00 34.32 |

- 78 -

|   | ATOM | 1796 | C   | ASN | 240 | 37. 190 | 5. 690  | 48. 011 | 1. 00 | 33. 25 |
|---|------|------|-----|-----|-----|---------|---------|---------|-------|--------|
|   | ATOM | 1797 | O   | ASN | 240 | 36. 259 | 4. 886  | 47. 936 | 1. 00 | 33. 86 |
|   | ATOM | 1798 | N   | VAL | 241 | 37. 024 | 6. 946  | 48. 414 | 1. 00 | 32. 52 |
|   | ATOM | 1799 | CA  | VAL | 241 | 35. 702 | 7. 441  | 48. 753 | 1. 00 | 31. 62 |
| 5 | ATOM | 1800 | CB  | VAL | 241 | 35. 755 | 8. 559  | 49. 811 | 1. 00 | 29. 14 |
|   | ATOM | 1801 | CG1 | VAL | 241 | 34. 339 | 8. 948  | 50. 204 | 1. 00 | 31. 00 |
|   | ATOM | 1802 | CG2 | VAL | 241 | 36. 530 | 8. 107  | 51. 021 | 1. 00 | 26. 87 |
|   | ATOM | 1803 | C   | VAL | 241 | 35. 102 | 8. 010  | 47. 474 | 1. 00 | 33. 73 |
|   | ATOM | 1804 | O   | VAL | 241 | 35. 048 | 9. 224  | 47. 286 | 1. 00 | 35. 18 |
| 10 | ATOM | 1805 | N   | GLU | 242 | 34. 643 | 7. 132  | 46. 595 | 1. 00 | 33. 33 |
|   | ATOM | 1806 | CA  | GLU | 242 | 34. 075 | 7. 572  | 45. 324 | 1. 00 | 33. 69 |
|   | ATOM | 1807 | CB  | GLU | 242 | 33. 788 | 6. 364  | 44. 431 | 1. 00 | 31. 05 |
|   | ATOM | 1808 | CG  | GLU | 242 | 34. 983 | 5. 457  | 44. 222 | 1. 00 | 33. 00 |
|   | ATOM | 1809 | CD  | GLU | 242 | 34. 767 | 4. 451  | 43. 115 | 1. 00 | 33. 45 |
| 15 | ATOM | 1810 | OE1 | GLU | 242 | 33. 595 | 4. 162  | 42. 776 | 1. 00 | 33. 74 |
|   | ATOM | 1811 | OE2 | GLU | 242 | 35. 778 | 3. 940  | 42. 592 | 1. 00 | 35. 96 |
|   | ATOM | 1812 | C   | GLU | 242 | 32. 812 | 8. 437  | 45. 427 | 1. 00 | 34. 45 |
|   | ATOM | 1813 | O   | GLU | 242 | 32. 406 | 9. 061  | 44. 442 | 1. 00 | 32. 92 |
|   | ATOM | 1814 | N   | LEU | 243 | 32. 192 | 8. 471  | 46. 602 | 1. 00 | 33. 82 |
| 20 | ATOM | 1815 | CA  | LEU | 243 | 30. 982 | 9. 262  | 46. 799 | 1. 00 | 36. 13 |
|   | ATOM | 1816 | CB  | LEU | 243 | 30. 080 | 8. 598  | 47. 844 | 1. 00 | 33. 99 |
|   | ATOM | 1817 | CG  | LEU | 243 | 29. 168 | 7. 490  | 47. 297 | 1. 00 | 37. 04 |
|   | ATOM | 1818 | CD1 | LEU | 243 | 27. 999 | 8. 096  | 46. 545 | 1. 00 | 36. 01 |
|   | ATOM | 1819 | CD2 | LEU | 243 | 29. 969 | 6. 560  | 46. 384 | 1. 00 | 36. 49 |
| 25 | ATOM | 1820 | C   | LEU | 243 | 31. 290 | 10. 700 | 47. 199 | 1. 00 | 35. 69 |
|   | ATOM | 1821 | O   | LEU | 243 | 30. 406 | 11. 458 | 47. 585 | 1. 00 | 37. 51 |
|   | ATOM | 1822 | N   | VAL | 244 | 32. 560 | 11. 062 | 47. 117 | 1. 00 | 37. 53 |
|   | ATOM | 1823 | CA  | VAL | 244 | 32. 992 | 12. 411 | 47. 426 | 1. 00 | 37. 50 |
|   | ATOM | 1824 | CB  | VAL | 244 | 33. 537 | 12. 547 | 48. 861 | 1. 00 | 36. 75 |

| | ATOM | 1825 | CG1 | VAL | 244 | 33.967 | 13.990 | 49.109 | 1.00 | 36.55 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1826 | CG2 | VAL | 244 | 32.465 | 12.160 | 49.870 | 1.00 | 37.02 |
| | ATOM | 1827 | C | VAL | 244 | 34.099 | 12.727 | 46.446 | 1.00 | 39.75 |
| | ATOM | 1828 | O | VAL | 244 | 35.090 | 12.003 | 46.361 | 1.00 | 39.55 |
| 5 | ATOM | 1829 | N | GLU | 245 | 33.909 | 13.802 | 45.688 | 1.00 | 42.16 |
| | ATOM | 1830 | CA | GLU | 245 | 34.880 | 14.232 | 44.695 | 1.00 | 42.30 |
| | ATOM | 1831 | CB | GLU | 245 | 34.372 | 15.487 | 43.989 | 1.00 | 45.34 |
| | ATOM | 1832 | CG | GLU | 245 | 34.886 | 15.636 | 42.576 | 1.00 | 48.54 |
| | ATOM | 1833 | CD | GLU | 245 | 34.377 | 16.893 | 41.901 | 1.00 | 50.12 |
| 10 | ATOM | 1834 | OE1 | GLU | 245 | 33.192 | 17.249 | 42.107 | 1.00 | 49.37 |
| | ATOM | 1835 | OE2 | GLU | 245 | 35.164 | 17.511 | 41.152 | 1.00 | 52.40 |
| | ATOM | 1836 | C | GLU | 245 | 36.203 | 14.532 | 45.378 | 1.00 | 41.00 |
| | ATOM | 1837 | O | GLU | 245 | 36.230 | 15.132 | 46.446 | 1.00 | 42.20 |
| | ATOM | 1838 | N | GLY | 246 | 37.297 | 14.107 | 44.761 | 1.00 | 41.28 |
| 15 | ATOM | 1839 | CA | GLY | 246 | 38.606 | 14.349 | 45.336 | 1.00 | 42.88 |
| | ATOM | 1840 | C | GLY | 246 | 39.362 | 13.066 | 45.618 | 1.00 | 45.38 |
| | ATOM | 1841 | O | GLY | 246 | 38.774 | 12.056 | 45.997 | 1.00 | 45.50 |
| | ATOM | 1842 | N | ASP | 247 | 40.675 | 13.105 | 45.443 | 1.00 | 47.31 |
| | ATOM | 1843 | CA | ASP | 247 | 41.509 | 11.940 | 45.687 | 1.00 | 49.13 |
| 20 | ATOM | 1844 | CB | ASP | 247 | 42.139 | 11.454 | 44.384 | 1.00 | 51.65 |
| | ATOM | 1845 | CG | ASP | 247 | 41.131 | 10.836 | 43.449 | 1.00 | 56.09 |
| | ATOM | 1846 | OD1 | ASP | 247 | 41.534 | 10.410 | 42.345 | 1.00 | 58.83 |
| | ATOM | 1847 | OD2 | ASP | 247 | 39.936 | 10.770 | 43.819 | 1.00 | 59.44 |
| | ATOM | 1848 | C | ASP | 247 | 42.611 | 12.274 | 46.667 | 1.00 | 49.51 |
| 25 | ATOM | 1849 | O | ASP | 247 | 43.406 | 11.415 | 47.039 | 1.00 | 49.57 |
| | ATOM | 1850 | N | GLU | 248 | 42.661 | 13.531 | 47.086 | 1.00 | 50.49 |
| | ATOM | 1851 | CA | GLU | 248 | 43.696 | 13.957 | 48.011 | 1.00 | 50.97 |
| | ATOM | 1852 | CB | GLU | 248 | 44.198 | 15.351 | 47.634 | 1.00 | 54.71 |
| | ATOM | 1853 | CG | GLU | 248 | 45.670 | 15.391 | 47.259 | 1.00 | 62.15 |

- 80 -

| | ATOM | 1854 | CD | GLU | 248 | 46. 067 | 14. 259 | 46. 317 | 1. 00 | 66. 63 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1855 | OE1 | GLU | 248 | 46. 196 | 13. 105 | 46. 788 | 1. 00 | 68. 58 |
| | ATOM | 1856 | OE2 | GLU | 248 | 46. 241 | 14. 520 | 45. 105 | 1. 00 | 68. 21 |
| | ATOM | 1857 | C | GLU | 248 | 43. 222 | 13. 955 | 49. 446 | 1. 00 | 47. 90 |
| 5 | ATOM | 1858 | O | GLU | 248 | 42. 063 | 14. 250 | 49. 726 | 1. 00 | 46. 55 |
| | ATOM | 1859 | N | GLY | 249 | 44. 133 | 13. 614 | 50. 351 | 1. 00 | 45. 49 |
| | ATOM | 1860 | CA | GLY | 249 | 43. 799 | 13. 590 | 51. 759 | 1. 00 | 44. 30 |
| | ATOM | 1861 | C | GLY | 249 | 43. 138 | 12. 301 | 52. 205 | 1. 00 | 42. 85 |
| | ATOM | 1862 | O | GLY | 249 | 43. 257 | 11. 259 | 51. 552 | 1. 00 | 42. 97 |
| 10 | ATOM | 1863 | N | ARG | 250 | 42. 444 | 12. 380 | 53. 335 | 1. 00 | 41. 43 |
| | ATOM | 1864 | CA | ARG | 250 | 41. 747 | 11. 232 | 53. 897 | 1. 00 | 39. 63 |
| | ATOM | 1865 | CB | ARG | 250 | 42. 625 | 10. 532 | 54. 931 | 1. 00 | 40. 69 |
| | ATOM | 1866 | CG | ARG | 250 | 44. 092 | 10. 454 | 54. 559 | 1. 00 | 43. 91 |
| | ATOM | 1867 | CD | ARG | 250 | 44. 903 | 9. 902 | 55. 714 | 1. 00 | 45. 22 |
| 15 | ATOM | 1868 | NE | ARG | 250 | 44. 630 | 8. 487 | 55. 940 | 1. 00 | 45. 43 |
| | ATOM | 1869 | CZ | ARG | 250 | 45. 040 | 7. 813 | 57. 007 | 1. 00 | 44. 67 |
| | ATOM | 1870 | NH1 | ARG | 250 | 45. 738 | 8. 426 | 57. 954 | 1. 00 | 46. 95 |
| | ATOM | 1871 | NH2 | ARG | 250 | 44. 761 | 6. 524 | 57. 121 | 1. 00 | 46. 99 |
| | ATOM | 1872 | C | ARG | 250 | 40. 486 | 11. 726 | 54. 580 | 1. 00 | 37. 70 |
| 20 | ATOM | 1873 | O | ARG | 250 | 40. 430 | 12. 865 | 55. 042 | 1. 00 | 37. 51 |
| | ATOM | 1874 | N | MET | 251 | 39. 473 | 10. 867 | 54. 630 | 1. 00 | 35. 10 |
| | ATOM | 1875 | CA | MET | 251 | 38. 216 | 11. 197 | 55. 277 | 1. 00 | 32. 34 |
| | ATOM | 1876 | CB | MET | 251 | 37. 137 | 11. 517 | 54. 242 | 1. 00 | 33. 00 |
| | ATOM | 1877 | CG | MET | 251 | 35. 803 | 11. 907 | 54. 868 | 1. 00 | 31. 56 |
| 25 | ATOM | 1878 | SD | MET | 251 | 34. 474 | 12. 160 | 53. 677 | 1. 00 | 37. 84 |
| | ATOM | 1879 | CE | MET | 251 | 35. 067 | 13. 715 | 52. 885 | 1. 00 | 32. 92 |
| | ATOM | 1880 | C | MET | 251 | 37. 764 | 10. 007 | 56. 121 | 1. 00 | 32. 47 |
| | ATOM | 1881 | O | MET | 251 | 38. 024 | 8. 852 | 55. 777 | 1. 00 | 31. 05 |
| | ATOM | 1882 | N | CYS | 252 | 37. 088 | 10. 292 | 57. 229 | 1. 00 | 30. 16 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1883 | CA | CYS | 252 | 36.595 | 9.236 | 58.092 | 1.00 30.32 |
| | ATOM | 1884 | CB | CYS | 252 | 36.364 | 9.762 | 59.517 | 1.00 30.54 |
| | ATOM | 1885 | SG | CYS | 252 | 35.601 | 8.557 | 60.676 | 1.00 28.61 |
| | ATOM | 1886 | C | CYS | 252 | 35.292 | 8.717 | 57.511 | 1.00 29.86 |
| 5 | ATOM | 1887 | O | CYS | 252 | 34.422 | 9.495 | 57.114 | 1.00 29.84 |
| | ATOM | 1888 | N | VAL | 253 | 35.170 | 7.397 | 57.438 | 1.00 28.79 |
| | ATOM | 1889 | CA | VAL | 253 | 33.960 | 6.776 | 56.921 | 1.00 27.69 |
| | ATOM | 1890 | CB | VAL | 253 | 34.291 | 5.761 | 55.816 | 1.00 28.07 |
| | ATOM | 1891 | CG1 | VAL | 253 | 33.033 | 5.005 | 55.405 | 1.00 26.98 |
| 10 | ATOM | 1892 | CG2 | VAL | 253 | 34.898 | 6.484 | 54.624 | 1.00 24.14 |
| | ATOM | 1893 | C | VAL | 253 | 33.200 | 6.069 | 58.038 | 1.00 28.79 |
| | ATOM | 1894 | O | VAL | 253 | 33.801 | 5.448 | 58.922 | 1.00 31.23 |
| | ATOM | 1895 | N | ASN | 254 | 31.879 | 6.188 | 58.000 | 1.00 28.38 |
| | ATOM | 1896 | CA | ASN | 254 | 31.003 | 5.557 | 58.976 | 1.00 27.73 |
| 15 | ATOM | 1897 | CB | ASN | 254 | 29.834 | 6.473 | 59.328 | 1.00 27.41 |
| | ATOM | 1898 | CG | ASN | 254 | 28.803 | 5.779 | 60.181 | 1.00 31.67 |
| | ATOM | 1899 | OD1 | ASN | 254 | 29.048 | 4.675 | 60.677 | 1.00 32.14 |
| | ATOM | 1900 | ND2 | ASN | 254 | 27.643 | 6.415 | 60.367 | 1.00 29.17 |
| | ATOM | 1901 | C | ASN | 254 | 30.480 | 4.295 | 58.299 | 1.00 27.41 |
| 20 | ATOM | 1902 | O | ASN | 254 | 29.575 | 4.372 | 57.467 | 1.00 25.53 |
| | ATOM | 1903 | N | THR | 255 | 31.049 | 3.142 | 58.654 | 1.00 24.66 |
| | ATOM | 1904 | CA | THR | 255 | 30.662 | 1.883 | 58.016 | 1.00 24.86 |
| | ATOM | 1905 | CB | THR | 255 | 31.501 | 0.665 | 58.527 | 1.00 23.42 |
| | ATOM | 1906 | OG1 | THR | 255 | 31.071 | 0.310 | 59.849 | 1.00 23.50 |
| 25 | ATOM | 1907 | CG2 | THR | 255 | 32.973 | 0.982 | 58.558 | 1.00 23.88 |
| | ATOM | 1908 | C | THR | 255 | 29.207 | 1.488 | 58.195 | 1.00 23.00 |
| | ATOM | 1909 | O | THR | 255 | 28.589 | 0.984 | 57.259 | 1.00 24.38 |
| | ATOM | 1910 | N | GLU | 256 | 28.673 | 1.710 | 59.394 | 1.00 23.70 |
| | ATOM | 1911 | CA | GLU | 256 | 27.306 | 1.305 | 59.721 | 1.00 26.37 |

- 82 -

|    | ATOM | 1912 | CB  | GLU | 256 | 26.271 | 2.017  | 58.838 | 1.00 | 26.22 |
|----|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|    | ATOM | 1913 | CG  | GLU | 256 | 25.974 | 3.471  | 59.204 | 1.00 | 29.32 |
|    | ATOM | 1914 | CD  | GLU | 256 | 25.284 | 3.644  | 60.558 | 1.00 | 31.10 |
|    | ATOM | 1915 | OE1 | GLU | 256 | 24.489 | 2.764  | 60.953 | 1.00 | 31.47 |
| 5  | ATOM | 1916 | OE2 | GLU | 256 | 25.523 | 4.682  | 61.218 | 1.00 | 30.04 |
|    | ATOM | 1917 | C   | GLU | 256 | 27.269 | -0.203 | 59.458 | 1.00 | 27.40 |
|    | ATOM | 1918 | O   | GLU | 256 | 26.369 | -0.713 | 58.782 | 1.00 | 26.71 |
|    | ATOM | 1919 | N   | TRP | 257 | 28.269 | -0.912 | 59.982 | 1.00 | 25.98 |
|    | ATOM | 1920 | CA  | TRP | 257 | 28.335 | -2.356 | 59.774 | 1.00 | 24.56 |
| 10 | ATOM | 1921 | CB  | TRP | 257 | 29.714 | -2.928 | 60.180 | 1.00 | 21.05 |
|    | ATOM | 1922 | CG  | TRP | 257 | 30.100 | -2.891 | 61.653 | 1.00 | 17.51 |
|    | ATOM | 1923 | CD2 | TRP | 257 | 31.429 | -3.026 | 62.182 | 1.00 | 16.19 |
|    | ATOM | 1924 | CE2 | TRP | 257 | 31.320 | -3.077 | 63.588 | 1.00 | 14.42 |
|    | ATOM | 1925 | CE3 | TRP | 257 | 32.705 | -3.112 | 61.597 | 1.00 | 16.23 |
| 15 | ATOM | 1926 | CD1 | TRP | 257 | 29.264 | -2.862 | 62.733 | 1.00 | 18.14 |
|    | ATOM | 1927 | NE1 | TRP | 257 | 29.990 | -2.977 | 63.902 | 1.00 | 19.95 |
|    | ATOM | 1928 | CZ2 | TRP | 257 | 32.435 | -3.214 | 64.421 | 1.00 | 17.46 |
|    | ATOM | 1929 | CZ3 | TRP | 257 | 33.815 | -3.246 | 62.424 | 1.00 | 13.91 |
|    | ATOM | 1930 | CH2 | TRP | 257 | 33.672 | -3.294 | 63.822 | 1.00 | 14.28 |
| 20 | ATOM | 1931 | C   | TRP | 257 | 27.218 | -3.091 | 60.500 | 1.00 | 24.58 |
|    | ATOM | 1932 | O   | TRP | 257 | 27.067 | -4.305 | 60.352 | 1.00 | 24.81 |
|    | ATOM | 1933 | N   | GLY | 258 | 26.427 | -2.354 | 61.273 | 1.00 | 23.21 |
|    | ATOM | 1934 | CA  | GLY | 258 | 25.328 | -2.981 | 61.982 | 1.00 | 23.11 |
|    | ATOM | 1935 | C   | GLY | 258 | 24.385 | -3.640 | 60.991 | 1.00 | 25.72 |
| 25 | ATOM | 1936 | O   | GLY | 258 | 23.758 | -4.660 | 61.285 | 1.00 | 28.37 |
|    | ATOM | 1937 | N   | ALA | 259 | 24.288 | -3.067 | 59.796 | 1.00 | 24.64 |
|    | ATOM | 1938 | CA  | ALA | 259 | 23.406 | -3.630 | 58.789 | 1.00 | 25.53 |
|    | ATOM | 1939 | CB  | ALA | 259 | 22.866 | -2.519 | 57.874 | 1.00 | 25.11 |
|    | ATOM | 1940 | C   | ALA | 259 | 24.084 | -4.724 | 57.961 | 1.00 | 25.44 |

- 83 -

| | ATOM | 1941 | O | ALA | 259 | 23.515 | -5.205 | 56.985 | 1.00 | 24.68 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1942 | N | PHE | 260 | 25.306 | -5.101 | 58.329 | 1.00 | 26.96 |
| | ATOM | 1943 | CA | PHE | 260 | 25.995 | -6.175 | 57.614 | 1.00 | 28.11 |
| | ATOM | 1944 | CB | PHE | 260 | 27.359 | -6.440 | 58.254 | 1.00 | 30.88 |
| 5 | ATOM | 1945 | CG | PHE | 260 | 28.127 | -7.569 | 57.625 | 1.00 | 33.87 |
| | ATOM | 1946 | CD1 | PHE | 260 | 28.496 | -7.525 | 56.286 | 1.00 | 33.60 |
| | ATOM | 1947 | CD2 | PHE | 260 | 28.499 | -8.675 | 58.380 | 1.00 | 37.30 |
| | ATOM | 1948 | CE1 | PHE | 260 | 29.220 | -8.564 | 55.716 | 1.00 | 33.58 |
| | ATOM | 1949 | CE2 | PHE | 260 | 29.229 | -9.720 | 57.808 | 1.00 | 35.65 |
| 10 | ATOM | 1950 | CZ | PHE | 260 | 29.586 | -9.660 | 56.478 | 1.00 | 34.41 |
| | ATOM | 1951 | C | PHE | 260 | 25.080 | -7.388 | 57.783 | 1.00 | 28.87 |
| | ATOM | 1952 | O | PHE | 260 | 24.487 | -7.576 | 58.849 | 1.00 | 27.08 |
| | ATOM | 1953 | N | GLY | 261 | 24.941 | -8.193 | 56.737 | 1.00 | 28.88 |
| | ATOM | 1954 | CA | GLY | 261 | 24.074 | -9.357 | 56.826 | 1.00 | 30.83 |
| 15 | ATOM | 1955 | C | GLY | 261 | 22.664 | -9.092 | 56.317 | 1.00 | 32.15 |
| | ATOM | 1956 | O | GLY | 261 | 21.905 | -10.021 | 56.043 | 1.00 | 34.22 |
| | ATOM | 1957 | N | ASP | 262 | 22.307 | -7.822 | 56.175 | 1.00 | 33.45 |
| | ATOM | 1958 | CA | ASP | 262 | 20.975 | -7.456 | 55.701 | 1.00 | 35.91 |
| | ATOM | 1959 | CB | ASP | 262 | 20.761 | -5.948 | 55.868 | 1.00 | 35.78 |
| 20 | ATOM | 1960 | CG | ASP | 262 | 20.674 | -5.541 | 57.323 | 1.00 | 35.93 |
| | ATOM | 1961 | OD1 | ASP | 262 | 20.903 | -6.415 | 58.182 | 1.00 | 37.70 |
| | ATOM | 1962 | OD2 | ASP | 262 | 20.382 | -4.364 | 57.615 | 1.00 | 35.14 |
| | ATOM | 1963 | C | ASP | 262 | 20.676 | -7.884 | 54.262 | 1.00 | 36.35 |
| | ATOM | 1964 | O | ASP | 262 | 19.546 | -7.758 | 53.799 | 1.00 | 37.40 |
| 25 | ATOM | 1965 | N | SER | 263 | 21.685 | -8.380 | 53.554 | 1.00 | 37.07 |
| | ATOM | 1966 | CA | SER | 263 | 21.488 | -8.863 | 52.189 | 1.00 | 37.53 |
| | ATOM | 1967 | CB | SER | 263 | 22.420 | -8.155 | 51.200 | 1.00 | 37.00 |
| | ATOM | 1968 | OG | SER | 263 | 22.028 | -6.815 | 50.991 | 1.00 | 38.85 |
| | ATOM | 1969 | C | SER | 263 | 21.770 | -10.359 | 52.161 | 1.00 | 37.06 |

- 84 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1970 | O | SER | 263 | 22. 062 | -10. 923 | 51. 107 | 1. 00 | 36. 90 |
| ATOM | 1971 | N | GLY | 264 | 21. 697 | -10. 988 | 53. 331 | 1. 00 | 36. 97 |
| ATOM | 1972 | CA | GLY | 264 | 21. 934 | -12. 418 | 53. 428 | 1. 00 | 37. 50 |
| ATOM | 1973 | C | GLY | 264 | 23. 370 | -12. 857 | 53. 663 | 1. 00 | 38. 59 |
| ATOM | 1974 | O | GLY | 264 | 23. 666 | -14. 050 | 53. 573 | 1. 00 | 40. 28 |
| ATOM | 1975 | N | GLU | 265 | 24. 263 | -11. 915 | 53. 961 | 1. 00 | 37. 52 |
| ATOM | 1976 | CA | GLU | 265 | 25. 671 | -12. 237 | 54. 199 | 1. 00 | 36. 34 |
| ATOM | 1977 | CB | GLU | 265 | 26. 488 | -10. 965 | 54. 438 | 1. 00 | 35. 82 |
| ATOM | 1978 | CG | GLU | 265 | 26. 535 | -9. 976 | 53. 289 | 1. 00 | 38. 57 |
| ATOM | 1979 | CD | GLU | 265 | 25. 270 | -9. 148 | 53. 158 | 1. 00 | 39. 55 |
| ATOM | 1980 | OE1 | GLU | 265 | 24. 600 | -8. 901 | 54. 173 | 1. 00 | 38. 51 |
| ATOM | 1981 | OE2 | GLU | 265 | 24. 953 | -8. 722 | 52. 031 | 1. 00 | 43. 82 |
| ATOM | 1982 | C | GLU | 265 | 25. 906 | -13. 171 | 55. 391 | 1. 00 | 36. 38 |
| ATOM | 1983 | O | GLU | 265 | 26. 899 | -13. 906 | 55. 425 | 1. 00 | 35. 35 |
| ATOM | 1984 | N | LEU | 266 | 24. 996 | -13. 140 | 56. 362 | 1. 00 | 34. 63 |
| ATOM | 1985 | CA | LEU | 266 | 25. 130 | -13. 955 | 57. 567 | 1. 00 | 35. 02 |
| ATOM | 1986 | CB | LEU | 266 | 25. 008 | -13. 054 | 58. 803 | 1. 00 | 31. 68 |
| ATOM | 1987 | CG | LEU | 266 | 26. 017 | -11. 914 | 58. 973 | 1. 00 | 33. 35 |
| ATOM | 1988 | CD1 | LEU | 266 | 25. 555 | -10. 975 | 60. 077 | 1. 00 | 32. 52 |
| ATOM | 1989 | CD2 | LEU | 266 | 27. 383 | -12. 480 | 59. 294 | 1. 00 | 32. 43 |
| ATOM | 1990 | C | LEU | 266 | 24. 108 | -15. 092 | 57. 674 | 1. 00 | 35. 37 |
| ATOM | 1991 | O | LEU | 266 | 24. 047 | -15. 779 | 58. 696 | 1. 00 | 35. 21 |
| ATOM | 1992 | N | ASP | 267 | 23. 321 | -15. 300 | 56. 627 | 1. 00 | 36. 35 |
| ATOM | 1993 | CA | ASP | 267 | 22. 286 | -16. 332 | 56. 643 | 1. 00 | 39. 50 |
| ATOM | 1994 | CB | ASP | 267 | 21. 664 | -16. 480 | 55. 248 | 1. 00 | 42. 21 |
| ATOM | 1995 | CG | ASP | 267 | 20. 666 | -15. 369 | 54. 921 | 1. 00 | 45. 43 |
| ATOM | 1996 | OD1 | ASP | 267 | 20. 205 | -15. 320 | 53. 759 | 1. 00 | 48. 41 |
| ATOM | 1997 | OD2 | ASP | 267 | 20. 332 | -14. 554 | 55. 813 | 1. 00 | 45. 57 |
| ATOM | 1998 | C | ASP | 267 | 22. 676 | -17. 715 | 57. 171 | 1. 00 | 38. 87 |

- 85 -

|    | ATOM | 1999 | O   | ASP | 267 | 21.888 | -18.353 | 57.867 | 1.00 | 39.64 |
|----|------|------|-----|-----|-----|--------|---------|--------|------|-------|
|    | ATOM | 2000 | N   | GLU | 268 | 23.879 | -18.179 | 56.860 | 1.00 | 38.72 |
|    | ATOM | 2001 | CA  | GLU | 268 | 24.301 | -19.502 | 57.313 | 1.00 | 39.91 |
|    | ATOM | 2002 | CB  | GLU | 268 | 25.510 | -19.971 | 56.495 | 1.00 | 40.60 |
| 5  | ATOM | 2003 | CG  | GLU | 268 | 26.847 | -19.444 | 56.976 | 1.00 | 43.85 |
|    | ATOM | 2004 | CD  | GLU | 268 | 27.969 | -19.710 | 55.981 | 1.00 | 47.64 |
|    | ATOM | 2005 | OE1 | GLU | 268 | 28.013 | -19.017 | 54.941 | 1.00 | 49.73 |
|    | ATOM | 2006 | OE2 | GLU | 268 | 28.802 | -20.612 | 56.232 | 1.00 | 48.40 |
|    | ATOM | 2007 | C   | GLU | 268 | 24.633 | -19.577 | 58.807 | 1.00 | 40.59 |
| 10 | ATOM | 2008 | O   | GLU | 268 | 24.790 | -20.667 | 59.360 | 1.00 | 41.43 |
|    | ATOM | 2009 | N   | PHE | 269 | 24.734 | -18.427 | 59.462 | 1.00 | 39.17 |
|    | ATOM | 2010 | CA  | PHE | 269 | 25.070 | -18.402 | 60.882 | 1.00 | 37.75 |
|    | ATOM | 2011 | CB  | PHE | 269 | 26.182 | -17.385 | 61.127 | 1.00 | 34.69 |
|    | ATOM | 2012 | CG  | PHE | 269 | 27.435 | -17.675 | 60.369 | 1.00 | 35.74 |
| 15 | ATOM | 2013 | CD1 | PHE | 269 | 28.144 | -18.853 | 60.599 | 1.00 | 35.94 |
|    | ATOM | 2014 | CD2 | PHE | 269 | 27.910 | -16.781 | 59.416 | 1.00 | 34.75 |
|    | ATOM | 2015 | CE1 | PHE | 269 | 29.306 | -19.136 | 59.891 | 1.00 | 34.71 |
|    | ATOM | 2016 | CE2 | PHE | 269 | 29.068 | -17.050 | 58.701 | 1.00 | 34.58 |
|    | ATOM | 2017 | CZ  | PHE | 269 | 29.770 | -18.233 | 58.939 | 1.00 | 35.80 |
| 20 | ATOM | 2018 | C   | PHE | 269 | 23.898 | -18.085 | 61.793 | 1.00 | 36.73 |
|    | ATOM | 2019 | O   | PHE | 269 | 23.932 | -18.384 | 62.984 | 1.00 | 36.59 |
|    | ATOM | 2020 | N   | LEU | 270 | 22.861 | -17.480 | 61.231 | 1.00 | 37.18 |
|    | ATOM | 2021 | CA  | LEU | 270 | 21.696 | -17.107 | 62.012 | 1.00 | 37.71 |
|    | ATOM | 2022 | CB  | LEU | 270 | 20.712 | -16.332 | 61.135 | 1.00 | 36.52 |
| 25 | ATOM | 2023 | CG  | LEU | 270 | 21.264 | -15.036 | 60.521 | 1.00 | 37.18 |
|    | ATOM | 2024 | CD1 | LEU | 270 | 20.299 | -14.516 | 59.466 | 1.00 | 38.72 |
|    | ATOM | 2025 | CD2 | LEU | 270 | 21.488 | -13.990 | 61.604 | 1.00 | 34.72 |
|    | ATOM | 2026 | C   | LEU | 270 | 21.010 | -18.312 | 62.644 | 1.00 | 38.27 |
|    | ATOM | 2027 | O   | LEU | 270 | 20.794 | -19.333 | 61.995 | 1.00 | 39.49 |

- 86 -

| ATOM | 2028 | N   | LEU | 271 | 20.685 | -18.176 | 63.924 | 1.00 | 37.92 |
|------|------|-----|-----|-----|--------|---------|--------|------|-------|
| ATOM | 2029 | CA  | LEU | 271 | 20.010 | -19.212 | 64.693 | 1.00 | 38.22 |
| ATOM | 2030 | CB  | LEU | 271 | 20.657 | -19.339 | 66.078 | 1.00 | 37.71 |
| ATOM | 2031 | CG  | LEU | 271 | 21.897 | -20.220 | 66.261 | 1.00 | 38.14 |
| ATOM | 2032 | CD1 | LEU | 271 | 22.827 | -20.111 | 65.075 | 1.00 | 39.09 |
| ATOM | 2033 | CD2 | LEU | 271 | 22.596 | -19.830 | 67.549 | 1.00 | 35.73 |
| ATOM | 2034 | C   | LEU | 271 | 18.536 | -18.845 | 64.855 | 1.00 | 39.78 |
| ATOM | 2035 | O   | LEU | 271 | 18.125 | -17.721 | 64.538 | 1.00 | 38.05 |
| ATOM | 2036 | N   | GLU | 272 | 17.751 | -19.794 | 65.358 | 1.00 | 39.69 |
| ATOM | 2037 | CA  | GLU | 272 | 16.322 | -19.590 | 65.575 | 1.00 | 41.03 |
| ATOM | 2038 | CB  | GLU | 272 | 15.697 | -20.842 | 66.219 | 1.00 | 43.64 |
| ATOM | 2039 | CG  | GLU | 272 | 16.221 | -21.179 | 67.627 | 1.00 | 47.44 |
| ATOM | 2040 | CD  | GLU | 272 | 15.685 | -22.509 | 68.182 | 1.00 | 49.81 |
| ATOM | 2041 | OE1 | GLU | 272 | 16.081 | -23.580 | 67.666 | 1.00 | 51.29 |
| ATOM | 2042 | OE2 | GLU | 272 | 14.869 | -22.484 | 69.134 | 1.00 | 47.60 |
| ATOM | 2043 | C   | GLU | 272 | 16.084 | -18.377 | 66.466 | 1.00 | 39.89 |
| ATOM | 2044 | O   | GLU | 272 | 15.151 | -17.602 | 66.250 | 1.00 | 40.35 |
| ATOM | 2045 | N   | TYR | 273 | 16.944 | -18.208 | 67.465 | 1.00 | 38.65 |
| ATOM | 2046 | CA  | TYR | 273 | 16.813 | -17.095 | 68.393 | 1.00 | 35.97 |
| ATOM | 2047 | CB  | TYR | 273 | 17.829 | -17.238 | 69.530 | 1.00 | 35.50 |
| ATOM | 2048 | CG  | TYR | 273 | 18.008 | -18.658 | 70.009 | 1.00 | 34.45 |
| ATOM | 2049 | CD1 | TYR | 273 | 19.109 | -19.416 | 69.611 | 1.00 | 32.53 |
| ATOM | 2050 | CE1 | TYR | 273 | 19.252 | -20.740 | 70.017 | 1.00 | 35.58 |
| ATOM | 2051 | CD2 | TYR | 273 | 17.053 | -19.258 | 70.830 | 1.00 | 34.35 |
| ATOM | 2052 | CE2 | TYR | 273 | 17.185 | -20.580 | 71.241 | 1.00 | 34.82 |
| ATOM | 2053 | CZ  | TYR | 273 | 18.281 | -21.314 | 70.830 | 1.00 | 35.96 |
| ATOM | 2054 | OH  | TYR | 273 | 18.381 | -22.626 | 71.208 | 1.00 | 38.31 |
| ATOM | 2055 | C   | TYR | 273 | 17.021 | -15.763 | 67.680 | 1.00 | 35.11 |
| ATOM | 2056 | O   | TYR | 273 | 16.404 | -14.752 | 68.031 | 1.00 | 34.85 |

- 87 -

```
    ATOM    2057  N   ASP  274    17.888 -15.763  66.676  1.00 36.47
    ATOM    2058  CA  ASP  274    18.164 -14.541  65.933  1.00 36.65
    ATOM    2059  CB  ASP  274    19.405 -14.718  65.059  1.00 32.36
    ATOM    2060  CG  ASP  274    20.627 -15.072  65.869  1.00 32.89
  5 ATOM    2061  OD1 ASP  274    20.949 -14.315  66.810  1.00 30.53
    ATOM    2062  OD2 ASP  274    21.265 -16.104  65.569  1.00 32.08
    ATOM    2063  C   ASP  274    16.968 -14.165  65.081  1.00 37.27
    ATOM    2064  O   ASP  274    16.571 -13.001  65.040  1.00 37.20
    ATOM    2065  N   ARG  275    16.380 -15.148  64.410  1.00 39.32
 10 ATOM    2066  CA  ARG  275    15.222 -14.866  63.574  1.00 41.70
    ATOM    2067  CB  ARG  275    14.803 -16.121  62.809  1.00 44.47
    ATOM    2068  CG  ARG  275    15.908 -16.666  61.914  1.00 49.05
    ATOM    2069  CD  ARG  275    15.516 -18.002  61.303  1.00 53.46
    ATOM    2070  NE  ARG  275    16.668 -18.740  60.779  1.00 57.36
 15 ATOM    2071  CZ  ARG  275    17.352 -18.408  59.685  1.00 58.81
    ATOM    2072  NH1 ARG  275    18.383 -19.148  59.296  1.00 60.43
    ATOM    2073  NH2 ARG  275    17.005 -17.341  58.976  1.00 61.75
    ATOM    2074  C   ARG  275    14.079 -14.353  64.446  1.00 41.43
    ATOM    2075  O   ARG  275    13.350 -13.444  64.059  1.00 40.04
 20 ATOM    2076  N   LEU  276    13.939 -14.927  65.637  1.00 40.97
    ATOM    2077  CA  LEU  276    12.888 -14.507  66.556  1.00 42.14
    ATOM    2078  CB  LEU  276    12.831 -15.450  67.761  1.00 44.12
    ATOM    2079  CG  LEU  276    12.315 -16.862  67.468  1.00 47.86
    ATOM    2080  CD1 LEU  276    12.662 -17.800  68.618  1.00 48.62
 25 ATOM    2081  CD2 LEU  276    10.808 -16.808  67.236  1.00 47.43
    ATOM    2082  C   LEU  276    13.094 -13.072  67.034  1.00 40.87
    ATOM    2083  O   LEU  276    12.152 -12.281  67.072  1.00 41.20
    ATOM    2084  N   VAL  277    14.322 -12.740  67.412  1.00 39.68
    ATOM    2085  CA  VAL  277    14.617 -11.390  67.876  1.00 40.86
```

- 88 -

|  | ATOM | 2086 | CB | VAL | 277 | 16.084 | -11.263 | 68.331 | 1.00 | 41.86 |
|---|------|------|-----|-----|-----|--------|---------|--------|------|-------|
|  | ATOM | 2087 | CG1 | VAL | 277 | 16.447 | -9.802 | 68.497 | 1.00 | 43.25 |
|  | ATOM | 2088 | CG2 | VAL | 277 | 16.290 | -12.012 | 69.647 | 1.00 | 41.47 |
|  | ATOM | 2089 | C | VAL | 277 | 14.363 | -10.381 | 66.761 | 1.00 | 40.10 |
| 5 | ATOM | 2090 | O | VAL | 277 | 13.813 | -9.305 | 66.993 | 1.00 | 41.12 |
|  | ATOM | 2091 | N | ASP | 278 | 14.767 | -10.738 | 65.550 | 1.00 | 39.42 |
|  | ATOM | 2092 | CA | ASP | 278 | 14.592 | -9.867 | 64.398 | 1.00 | 40.24 |
|  | ATOM | 2093 | CB | ASP | 278 | 15.356 | -10.434 | 63.195 | 1.00 | 38.24 |
|  | ATOM | 2094 | CG | ASP | 278 | 15.179 | -9.598 | 61.943 | 1.00 | 40.23 |
| 10 | ATOM | 2095 | OD1 | ASP | 278 | 15.260 | -8.351 | 62.043 | 1.00 | 39.72 |
|  | ATOM | 2096 | OD2 | ASP | 278 | 14.969 | -10.187 | 60.860 | 1.00 | 38.10 |
|  | ATOM | 2097 | C | ASP | 278 | 13.120 | -9.669 | 64.043 | 1.00 | 41.19 |
|  | ATOM | 2098 | O | ASP | 278 | 12.693 | -8.545 | 63.791 | 1.00 | 40.82 |
|  | ATOM | 2099 | N | GLU | 279 | 12.347 | -10.754 | 64.035 | 1.00 | 43.34 |
| 15 | ATOM | 2100 | CA | GLU | 279 | 10.922 | -10.688 | 63.696 | 1.00 | 46.81 |
|  | ATOM | 2101 | CB | GLU | 279 | 10.321 | -12.097 | 63.627 | 1.00 | 50.53 |
|  | ATOM | 2102 | CG | GLU | 279 | 10.870 | -12.965 | 62.496 | 1.00 | 56.10 |
|  | ATOM | 2103 | CD | GLU | 279 | 10.320 | -14.382 | 62.523 | 1.00 | 59.07 |
|  | ATOM | 2104 | OE1 | GLU | 279 | 10.336 | -15.006 | 63.607 | 1.00 | 60.28 |
| 20 | ATOM | 2105 | OE2 | GLU | 279 | 9.880 | -14.876 | 61.461 | 1.00 | 60.79 |
|  | ATOM | 2106 | C | GLU | 279 | 10.086 | -9.840 | 64.652 | 1.00 | 47.25 |
|  | ATOM | 2107 | O | GLU | 279 | 9.048 | -9.303 | 64.260 | 1.00 | 46.34 |
|  | ATOM | 2108 | N | SER | 280 | 10.535 | -9.722 | 65.899 | 1.00 | 46.87 |
|  | ATOM | 2109 | CA | SER | 280 | 9.809 | -8.948 | 66.900 | 1.00 | 47.53 |
| 25 | ATOM | 2110 | CB | SER | 280 | 9.769 | -9.708 | 68.228 | 1.00 | 49.98 |
|  | ATOM | 2111 | OG | SER | 280 | 9.043 | -10.919 | 68.093 | 1.00 | 52.36 |
|  | ATOM | 2112 | C | SER | 280 | 10.415 | -7.575 | 67.129 | 1.00 | 47.33 |
|  | ATOM | 2113 | O | SER | 280 | 9.909 | -6.788 | 67.936 | 1.00 | 45.86 |
|  | ATOM | 2114 | N | SER | 281 | 11.499 | -7.289 | 66.416 | 1.00 | 46.95 |

- 89 -

| | ATOM | 2115 | CA | SER | 281 | 12.172 | -6.004 | 66.552 | 1.00 | 46.75 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2116 | CB | SER | 281 | 13.581 | -6.081 | 65.971 | 1.00 | 47.24 |
| | ATOM | 2117 | OG | SER | 281 | 13.524 | -6.172 | 64.559 | 1.00 | 47.80 |
| | ATOM | 2118 | C | SER | 281 | 11.391 | -4.915 | 65.824 | 1.00 | 45.65 |
| 5 | ATOM | 2119 | O | SER | 281 | 10.514 | -5.199 | 65.013 | 1.00 | 45.10 |
| | ATOM | 2120 | N | ALA | 282 | 11.723 | -3.667 | 66.123 | 1.00 | 45.75 |
| | ATOM | 2121 | CA | ALA | 282 | 11.066 | -2.530 | 65.500 | 1.00 | 45.70 |
| | ATOM | 2122 | CB | ALA | 282 | 11.257 | -1.289 | 66.354 | 1.00 | 45.60 |
| | ATOM | 2123 | C | ALA | 282 | 11.617 | -2.286 | 64.100 | 1.00 | 46.48 |
| 10 | ATOM | 2124 | O | ALA | 282 | 11.252 | -1.303 | 63.449 | 1.00 | 48.61 |
| | ATOM | 2125 | N | ASN | 283 | 12.493 | -3.172 | 63.633 | 1.00 | 43.90 |
| | ATOM | 2126 | CA | ASN | 283 | 13.076 | -3.015 | 62.306 | 1.00 | 41.45 |
| | ATOM | 2127 | CB | ASN | 283 | 14.300 | -2.092 | 62.384 | 1.00 | 40.08 |
| | ATOM | 2128 | CG | ASN | 283 | 15.398 | -2.631 | 63.289 | 1.00 | 39.25 |
| 15 | ATOM | 2129 | OD1 | ASN | 283 | 15.136 | -3.308 | 64.289 | 1.00 | 37.65 |
| | ATOM | 2130 | ND2 | ASN | 283 | 16.641 | -2.310 | 62.950 | 1.00 | 37.96 |
| | ATOM | 2131 | C | ASN | 283 | 13.433 | -4.350 | 61.655 | 1.00 | 41.06 |
| | ATOM | 2132 | O | ASN | 283 | 14.585 | -4.606 | 61.318 | 1.00 | 40.48 |
| | ATOM | 2133 | N | PRO | 284 | 12.423 | -5.211 | 61.455 | 1.00 | 40.23 |
| 20 | ATOM | 2134 | CD | PRO | 284 | 11.013 | -4.898 | 61.751 | 1.00 | 40.75 |
| | ATOM | 2135 | CA | PRO | 284 | 12.534 | -6.540 | 60.851 | 1.00 | 40.08 |
| | ATOM | 2136 | CB | PRO | 284 | 11.080 | -6.914 | 60.581 | 1.00 | 40.52 |
| | ATOM | 2137 | CG | PRO | 284 | 10.364 | -6.260 | 61.712 | 1.00 | 41.21 |
| | ATOM | 2138 | C | PRO | 284 | 13.366 | -6.565 | 59.579 | 1.00 | 39.55 |
| 25 | ATOM | 2139 | O | PRO | 284 | 13.054 | -5.868 | 58.617 | 1.00 | 40.95 |
| | ATOM | 2140 | N | GLY | 285 | 14.416 | -7.382 | 59.576 | 1.00 | 38.56 |
| | ATOM | 2141 | CA | GLY | 285 | 15.266 | -7.491 | 58.407 | 1.00 | 35.73 |
| | ATOM | 2142 | C | GLY | 285 | 16.428 | -6.516 | 58.371 | 1.00 | 35.10 |
| | ATOM | 2143 | O | GLY | 285 | 17.288 | -6.624 | 57.500 | 1.00 | 36.22 |

- 90 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2144 | N | GLN | 286 | 16. 468 | −5. 573 | 59. 308 | 1. 00 | 34. 06 |
| ATOM | 2145 | CA | GLN | 286 | 17. 547 | −4. 584 | 59. 348 | 1. 00 | 34. 96 |
| ATOM | 2146 | CB | GLN | 286 | 16. 974 | −3. 166 | 59. 321 | 1. 00 | 39. 16 |
| ATOM | 2147 | CG | GLN | 286 | 16. 189 | −2. 825 | 58. 067 | 1. 00 | 45. 72 |
| ATOM | 2148 | CD | GLN | 286 | 15. 698 | −1. 384 | 58. 074 | 1. 00 | 51. 15 |
| ATOM | 2149 | OE1 | GLN | 286 | 14. 816 | −1. 018 | 58. 860 | 1. 00 | 52. 21 |
| ATOM | 2150 | NE2 | GLN | 286 | 16. 276 | −0. 555 | 57. 203 | 1. 00 | 50. 85 |
| ATOM | 2151 | C | GLN | 286 | 18. 439 | −4. 719 | 60. 573 | 1. 00 | 33. 59 |
| ATOM | 2152 | O | GLN | 286 | 17. 993 | −5. 157 | 61. 637 | 1. 00 | 33. 18 |
| ATOM | 2153 | N | GLN | 287 | 19. 701 | −4. 334 | 60. 408 | 1. 00 | 32. 85 |
| ATOM | 2154 | CA | GLN | 287 | 20. 691 | −4. 375 | 61. 484 | 1. 00 | 32. 45 |
| ATOM | 2155 | CB | GLN | 287 | 20. 248 | −3. 456 | 62. 636 | 1. 00 | 33. 34 |
| ATOM | 2156 | CG | GLN | 287 | 19. 955 | −1. 999 | 62. 251 | 1. 00 | 31. 48 |
| ATOM | 2157 | CD | GLN | 287 | 21. 188 | −1. 259 | 61. 743 | 1. 00 | 31. 78 |
| ATOM | 2158 | OE1 | GLN | 287 | 21. 330 | −1. 010 | 60. 544 | 1. 00 | 33. 25 |
| ATOM | 2159 | NE2 | GLN | 287 | 22. 090 | −0. 921 | 62. 652 | 1. 00 | 27. 51 |
| ATOM | 2160 | C | GLN | 287 | 20. 924 | −5. 788 | 62. 032 | 1. 00 | 30. 79 |
| ATOM | 2161 | O | GLN | 287 | 21. 120 | −5. 957 | 63. 229 | 1. 00 | 29. 31 |
| ATOM | 2162 | N | LEU | 288 | 20. 921 | −6. 791 | 61. 158 | 1. 00 | 29. 33 |
| ATOM | 2163 | CA | LEU | 288 | 21. 101 | −8. 181 | 61. 585 | 1. 00 | 27. 53 |
| ATOM | 2164 | CB | LEU | 288 | 20. 940 | −9. 129 | 60. 393 | 1. 00 | 28. 13 |
| ATOM | 2165 | CG | LEU | 288 | 19. 599 | −9. 090 | 59. 647 | 1. 00 | 29. 14 |
| ATOM | 2166 | CD1 | LEU | 288 | 19. 390 | −10. 418 | 58. 922 | 1. 00 | 27. 60 |
| ATOM | 2167 | CD2 | LEU | 288 | 18. 453 | −8. 844 | 60. 621 | 1. 00 | 27. 42 |
| ATOM | 2168 | C | LEU | 288 | 22. 418 | −8. 476 | 62. 297 | 1. 00 | 27. 92 |
| ATOM | 2169 | O | LEU | 288 | 22. 438 | −9. 184 | 63. 303 | 1. 00 | 28. 24 |
| ATOM | 2170 | N | TYR | 289 | 23. 520 | −7. 946 | 61. 776 | 1. 00 | 27. 17 |
| ATOM | 2171 | CA | TYR | 289 | 24. 819 | −8. 153 | 62. 399 | 1. 00 | 24. 83 |
| ATOM | 2172 | CB | TYR | 289 | 25. 899 | −7. 458 | 61. 583 | 1. 00 | 24. 32 |

| ATOM | 2173 | CG | TYR | 289 | 27.303 | -7.575 | 62.137 | 1.00 | 21.26 |
|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| ATOM | 2174 | CD1 | TYR | 289 | 27.951 | -8.814 | 62.208 | 1.00 | 20.00 |
| ATOM | 2175 | CE1 | TYR | 289 | 29.281 | -8.909 | 62.616 | 1.00 | 18.43 |
| ATOM | 2176 | CD2 | TYR | 289 | 28.013 | -6.441 | 62.503 | 1.00 | 18.12 |
| ATOM | 2177 | CE2 | TYR | 289 | 29.338 | -6.520 | 62.918 | 1.00 | 20.65 |
| ATOM | 2178 | CZ | TYR | 289 | 29.976 | -7.762 | 62.966 | 1.00 | 21.27 |
| ATOM | 2179 | OH | TYR | 289 | 31.314 | -7.833 | 63.326 | 1.00 | 19.02 |
| ATOM | 2180 | C | TYR | 289 | 24.771 | -7.566 | 63.799 | 1.00 | 26.94 |
| ATOM | 2181 | O | TYR | 289 | 25.221 | -8.175 | 64.776 | 1.00 | 27.95 |
| ATOM | 2182 | N | GLU | 290 | 24.198 | -6.374 | 63.892 | 1.00 | 27.68 |
| ATOM | 2183 | CA | GLU | 290 | 24.078 | -5.686 | 65.165 | 1.00 | 26.41 |
| ATOM | 2184 | CB | GLU | 290 | 23.484 | -4.309 | 64.927 | 1.00 | 26.55 |
| ATOM | 2185 | CG | GLU | 290 | 23.059 | -3.595 | 66.180 | 1.00 | 27.05 |
| ATOM | 2186 | CD | GLU | 290 | 22.815 | -2.142 | 65.913 | 1.00 | 25.47 |
| ATOM | 2187 | OE1 | GLU | 290 | 23.716 | -1.336 | 66.204 | 1.00 | 27.17 |
| ATOM | 2188 | OE2 | GLU | 290 | 21.731 | -1.815 | 65.398 | 1.00 | 29.09 |
| ATOM | 2189 | C | GLU | 290 | 23.218 | -6.463 | 66.159 | 1.00 | 26.59 |
| ATOM | 2190 | O | GLU | 290 | 23.458 | -6.430 | 67.371 | 1.00 | 25.62 |
| ATOM | 2191 | N | LYS | 291 | 22.216 | -7.166 | 65.646 | 1.00 | 26.31 |
| ATOM | 2192 | CA | LYS | 291 | 21.343 | -7.942 | 66.509 | 1.00 | 27.77 |
| ATOM | 2193 | CB | LYS | 291 | 20.110 | -8.394 | 65.722 | 1.00 | 28.30 |
| ATOM | 2194 | CG | LYS | 291 | 19.096 | -7.263 | 65.585 | 1.00 | 33.35 |
| ATOM | 2195 | CD | LYS | 291 | 18.005 | -7.529 | 64.555 | 1.00 | 33.56 |
| ATOM | 2196 | CE | LYS | 291 | 17.038 | -6.330 | 64.522 | 1.00 | 36.46 |
| ATOM | 2197 | NZ | LYS | 291 | 16.150 | -6.319 | 63.327 | 1.00 | 36.55 |
| ATOM | 2198 | C | LYS | 291 | 22.073 | -9.123 | 67.138 | 1.00 | 26.53 |
| ATOM | 2199 | O | LYS | 291 | 21.584 | -9.736 | 68.084 | 1.00 | 27.81 |
| ATOM | 2200 | N | LEU | 292 | 23.261 | -9.426 | 66.628 | 1.00 | 26.02 |
| ATOM | 2201 | CA | LEU | 292 | 24.043 | -10.523 | 67.168 | 1.00 | 25.35 |

- 92 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2202 | CB | LEU | 292 | 24.922 | -11.140 | 66.079 | 1.00 25.16 |
| | ATOM | 2203 | CG | LEU | 292 | 24.229 | -11.746 | 64.856 | 1.00 26.25 |
| | ATOM | 2204 | CD1 | LEU | 292 | 25.274 | -12.190 | 63.827 | 1.00 23.09 |
| | ATOM | 2205 | CD2 | LEU | 292 | 23.359 | -12.912 | 65.297 | 1.00 24.40 |
| 5 | ATOM | 2206 | C | LEU | 292 | 24.942 | -10.030 | 68.283 | 1.00 25.18 |
| | ATOM | 2207 | O | LEU | 292 | 25.392 | -10.808 | 69.120 | 1.00 23.84 |
| | ATOM | 2208 | N | ILE | 293 | 25.179 | -8.723 | 68.308 | 1.00 24.94 |
| | ATOM | 2209 | CA | ILE | 293 | 26.107 | -8.140 | 69.267 | 1.00 23.59 |
| | ATOM | 2210 | CB | ILE | 293 | 27.259 | -7.468 | 68.476 | 1.00 24.66 |
| 10 | ATOM | 2211 | CG2 | ILE | 293 | 28.233 | -6.762 | 69.409 | 1.00 21.05 |
| | ATOM | 2212 | CG1 | ILE | 293 | 27.952 | -8.527 | 67.618 | 1.00 24.42 |
| | ATOM | 2213 | CD1 | ILE | 293 | 28.715 | -7.965 | 66.441 | 1.00 25.64 |
| | ATOM | 2214 | C | ILE | 293 | 25.560 | -7.148 | 70.278 | 1.00 25.10 |
| | ATOM | 2215 | O | ILE | 293 | 25.797 | -7.289 | 71.474 | 1.00 23.79 |
| 15 | ATOM | 2216 | N | GLY | 294 | 24.845 | -6.136 | 69.781 | 1.00 28.83 |
| | ATOM | 2217 | CA | GLY | 294 | 24.302 | -5.071 | 70.615 | 1.00 26.73 |
| | ATOM | 2218 | C | GLY | 294 | 23.551 | -5.379 | 71.898 | 1.00 29.79 |
| | ATOM | 2219 | O | GLY | 294 | 22.757 | -6.318 | 71.964 | 1.00 27.85 |
| | ATOM | 2220 | N | GLY | 295 | 23.794 | -4.553 | 72.918 | 1.00 30.56 |
| 20 | ATOM | 2221 | CA | GLY | 295 | 23.136 | -4.722 | 74.204 | 1.00 33.01 |
| | ATOM | 2222 | C | GLY | 295 | 21.628 | -4.539 | 74.144 | 1.00 34.05 |
| | ATOM | 2223 | O | GLY | 295 | 20.927 | -4.810 | 75.107 | 1.00 34.93 |
| | ATOM | 2224 | N | LYS | 296 | 21.124 | -4.058 | 73.016 | 1.00 35.19 |
| | ATOM | 2225 | CA | LYS | 296 | 19.690 | -3.868 | 72.851 | 1.00 36.24 |
| 25 | ATOM | 2226 | CB | LYS | 296 | 19.419 | -2.988 | 71.626 | 1.00 38.05 |
| | ATOM | 2227 | CG | LYS | 296 | 17.961 | -2.910 | 71.181 | 1.00 40.26 |
| | ATOM | 2228 | CD | LYS | 296 | 17.122 | -2.093 | 72.141 | 1.00 43.32 |
| | ATOM | 2229 | CE | LYS | 296 | 15.730 | -1.862 | 71.579 | 1.00 44.42 |
| | ATOM | 2230 | NZ | LYS | 296 | 14.842 | -1.175 | 72.562 | 1.00 44.77 |

- 93 -

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2231 | C | LYS | 296 | 19.045 | -5.235 | 72.654 | 1.00 | 36.63 |
| ATOM | 2232 | O | LYS | 296 | 17.867 | -5.420 | 72.963 | 1.00 | 38.56 |
| ATOM | 2233 | N | TYR | 297 | 19.836 | -6.193 | 72.168 | 1.00 | 34.63 |
| ATOM | 2234 | CA | TYR | 297 | 19.346 | -7.539 | 71.890 | 1.00 | 33.22 |
| ATOM | 2235 | CB | TYR | 297 | 19.487 | -7.810 | 70.389 | 1.00 | 34.65 |
| ATOM | 2236 | CG | TYR | 297 | 19.073 | -6.631 | 69.535 | 1.00 | 36.28 |
| ATOM | 2237 | CD1 | TYR | 297 | 20.010 | -5.677 | 69.125 | 1.00 | 34.21 |
| ATOM | 2238 | CE1 | TYR | 297 | 19.622 | -4.548 | 68.404 | 1.00 | 36.22 |
| ATOM | 2239 | CD2 | TYR | 297 | 17.732 | -6.431 | 69.195 | 1.00 | 34.24 |
| ATOM | 2240 | CE2 | TYR | 297 | 17.330 | -5.305 | 68.476 | 1.00 | 35.71 |
| ATOM | 2241 | CZ | TYR | 297 | 18.280 | -4.368 | 68.082 | 1.00 | 37.38 |
| ATOM | 2242 | OH | TYR | 297 | 17.887 | -3.258 | 67.375 | 1.00 | 35.33 |
| ATOM | 2243 | C | TYR | 297 | 19.968 | -8.713 | 72.670 | 1.00 | 33.21 |
| ATOM | 2244 | O | TYR | 297 | 19.392 | -9.800 | 72.716 | 1.00 | 33.78 |
| ATOM | 2245 | N | MET | 298 | 21.126 | -8.504 | 73.283 | 1.00 | 31.19 |
| ATOM | 2246 | CA | MET | 298 | 21.803 | -9.576 | 74.005 | 1.00 | 30.16 |
| ATOM | 2247 | CB | MET | 298 | 23.075 | -9.038 | 74.644 | 1.00 | 30.05 |
| ATOM | 2248 | CG | MET | 298 | 23.957 | -10.104 | 75.231 | 1.00 | 26.86 |
| ATOM | 2249 | SD | MET | 298 | 25.486 | -9.405 | 75.850 | 1.00 | 32.83 |
| ATOM | 2250 | CE | MET | 298 | 26.409 | -9.201 | 74.338 | 1.00 | 29.59 |
| ATOM | 2251 | C | MET | 298 | 20.963 | -10.296 | 75.066 | 1.00 | 31.27 |
| ATOM | 2252 | O | MET | 298 | 20.882 | -11.529 | 75.077 | 1.00 | 29.78 |
| ATOM | 2253 | N | GLY | 299 | 20.353 | -9.530 | 75.963 | 1.00 | 30.40 |
| ATOM | 2254 | CA | GLY | 299 | 19.534 | -10.132 | 76.998 | 1.00 | 31.32 |
| ATOM | 2255 | C | GLY | 299 | 18.354 | -10.869 | 76.393 | 1.00 | 33.32 |
| ATOM | 2256 | O | GLY | 299 | 17.988 | -11.962 | 76.831 | 1.00 | 33.97 |
| ATOM | 2257 | N | GLU | 300 | 17.752 | -10.265 | 75.377 | 1.00 | 31.78 |
| ATOM | 2258 | CA | GLU | 300 | 16.617 | -10.874 | 74.707 | 1.00 | 31.93 |
| ATOM | 2259 | CB | GLU | 300 | 16.080 | -9.937 | 73.621 | 1.00 | 29.00 |

- 94 -

| ATOM | 2260 | CG | GLU | 300 | 14.877 | -10.486 | 72.881 | 1.00 | 32.60 |
|------|------|-----|-----|-----|--------|---------|--------|------|-------|
| ATOM | 2261 | CD | GLU | 300 | 13.655 | -10.655 | 73.769 | 1.00 | 31.13 |
| ATOM | 2262 | OE1 | GLU | 300 | 12.629 | -11.144 | 73.265 | 1.00 | 34.55 |
| ATOM | 2263 | OE2 | GLU | 300 | 13.714 | -10.299 | 74.963 | 1.00 | 33.16 |
| ATOM | 2264 | C | GLU | 300 | 17.013 | -12.215 | 74.092 | 1.00 | 30.90 |
| ATOM | 2265 | O | GLU | 300 | 16.225 | -13.156 | 74.090 | 1.00 | 32.89 |
| ATOM | 2266 | N | LEU | 301 | 18.234 | -12.301 | 73.570 | 1.00 | 31.16 |
| ATOM | 2267 | CA | LEU | 301 | 18.714 | -13.546 | 72.973 | 1.00 | 28.93 |
| ATOM | 2268 | CB | LEU | 301 | 20.085 | -13.339 | 72.325 | 1.00 | 24.69 |
| ATOM | 2269 | CG | LEU | 301 | 20.152 | -12.667 | 70.952 | 1.00 | 24.17 |
| ATOM | 2270 | CD1 | LEU | 301 | 21.607 | -12.326 | 70.628 | 1.00 | 23.70 |
| ATOM | 2271 | CD2 | LEU | 301 | 19.560 | -13.598 | 69.886 | 1.00 | 23.13 |
| ATOM | 2272 | C | LEU | 301 | 18.814 | -14.616 | 74.056 | 1.00 | 29.42 |
| ATOM | 2273 | O | LEU | 301 | 18.408 | -15.761 | 73.853 | 1.00 | 32.03 |
| ATOM | 2274 | N | VAL | 302 | 19.365 | -14.239 | 75.204 | 1.00 | 28.73 |
| ATOM | 2275 | CA | VAL | 302 | 19.505 | -15.164 | 76.317 | 1.00 | 29.42 |
| ATOM | 2276 | CB | VAL | 302 | 20.265 | -14.510 | 77.497 | 1.00 | 26.51 |
| ATOM | 2277 | CG1 | VAL | 302 | 20.172 | -15.395 | 78.740 | 1.00 | 25.63 |
| ATOM | 2278 | CG2 | VAL | 302 | 21.731 | -14.301 | 77.117 | 1.00 | 25.98 |
| ATOM | 2279 | C | VAL | 302 | 18.127 | -15.624 | 76.795 | 1.00 | 31.88 |
| ATOM | 2280 | O | VAL | 302 | 17.934 | -16.795 | 77.112 | 1.00 | 32.71 |
| ATOM | 2281 | N | ARG | 303 | 17.171 | -14.703 | 76.835 | 1.00 | 32.91 |
| ATOM | 2282 | CA | ARG | 303 | 15.818 | -15.039 | 77.270 | 1.00 | 36.08 |
| ATOM | 2283 | CB | ARG | 303 | 14.910 | -13.802 | 77.250 | 1.00 | 35.86 |
| ATOM | 2284 | CG | ARG | 303 | 13.524 | -14.055 | 77.847 | 1.00 | 36.97 |
| ATOM | 2285 | CD | ARG | 303 | 12.660 | -12.802 | 77.833 | 1.00 | 39.15 |
| ATOM | 2286 | NE | ARG | 303 | 12.105 | -12.529 | 76.511 | 1.00 | 41.95 |
| ATOM | 2287 | CZ | ARG | 303 | 11.090 | -13.197 | 75.968 | 1.00 | 43.84 |
| ATOM | 2288 | NH1 | ARG | 303 | 10.502 | -14.182 | 76.631 | 1.00 | 42.47 |

– 95 –

| | ATOM | 2289 | NH2 | ARG | 303 | 10.666 | −12.885 | 74.750 | 1.00 | 43.86 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2290 | C | ARG | 303 | 15.215 | −16.110 | 76.373 | 1.00 | 36.97 |
| | ATOM | 2291 | O | ARG | 303 | 14.554 | −17.032 | 76.851 | 1.00 | 37.22 |
| | ATOM | 2292 | N | LEU | 304 | 15.432 | −15.970 | 75.068 | 1.00 | 37.86 |
| 5 | ATOM | 2293 | CA | LEU | 304 | 14.914 | −16.924 | 74.103 | 1.00 | 37.63 |
| | ATOM | 2294 | CB | LEU | 304 | 15.113 | −16.387 | 72.687 | 1.00 | 38.69 |
| | ATOM | 2295 | CG | LEU | 304 | 13.944 | −15.590 | 72.104 | 1.00 | 40.35 |
| | ATOM | 2296 | CD1 | LEU | 304 | 13.486 | −14.516 | 73.062 | 1.00 | 40.85 |
| | ATOM | 2297 | CD2 | LEU | 304 | 14.378 | −14.986 | 70.785 | 1.00 | 42.07 |
| 10 | ATOM | 2298 | C | LEU | 304 | 15.602 | −18.272 | 74.262 | 1.00 | 37.69 |
| | ATOM | 2299 | O | LEU | 304 | 14.978 | −19.324 | 74.120 | 1.00 | 38.84 |
| | ATOM | 2300 | N | VAL | 305 | 16.893 | −18.238 | 74.558 | 1.00 | 36.28 |
| | ATOM | 2301 | CA | VAL | 305 | 17.647 | −19.466 | 74.753 | 1.00 | 34.31 |
| | ATOM | 2302 | CB | VAL | 305 | 19.148 | −19.184 | 74.908 | 1.00 | 32.24 |
| 15 | ATOM | 2303 | CG1 | VAL | 305 | 19.868 | −20.438 | 75.390 | 1.00 | 28.85 |
| | ATOM | 2304 | CG2 | VAL | 305 | 19.717 | −18.713 | 73.578 | 1.00 | 29.80 |
| | ATOM | 2305 | C | VAL | 305 | 17.153 | −20.158 | 76.012 | 1.00 | 35.48 |
| | ATOM | 2306 | O | VAL | 305 | 17.079 | −21.389 | 76.070 | 1.00 | 34.47 |
| | ATOM | 2307 | N | LEU | 306 | 16.820 | −19.362 | 77.023 | 1.00 | 34.14 |
| 20 | ATOM | 2308 | CA | LEU | 306 | 16.328 | −19.921 | 78.273 | 1.00 | 35.52 |
| | ATOM | 2309 | CB | LEU | 306 | 16.257 | −18.841 | 79.353 | 1.00 | 32.11 |
| | ATOM | 2310 | CG | LEU | 306 | 17.601 | −18.289 | 79.829 | 1.00 | 32.53 |
| | ATOM | 2311 | CD1 | LEU | 306 | 17.359 | −17.326 | 80.964 | 1.00 | 33.54 |
| | ATOM | 2312 | CD2 | LEU | 306 | 18.515 | −19.420 | 80.287 | 1.00 | 30.60 |
| 25 | ATOM | 2313 | C | LEU | 306 | 14.948 | −20.532 | 78.049 | 1.00 | 37.53 |
| | ATOM | 2314 | O | LEU | 306 | 14.637 | −21.608 | 78.566 | 1.00 | 33.87 |
| | ATOM | 2315 | N | LEU | 307 | 14.129 | −19.850 | 77.257 | 1.00 | 39.39 |
| | ATOM | 2316 | CA | LEU | 307 | 12.787 | −20.336 | 76.971 | 1.00 | 41.43 |
| | ATOM | 2317 | CB | LEU | 307 | 12.011 | −19.296 | 76.165 | 1.00 | 40.84 |

- 96 -

| | ATOM | 2318 | CG | LEU | 307 | 10.932 | -18.527 | 76.935 | 1.00 | 43.43 |
|---|------|------|-----|-----|-----|--------|---------|--------|------|-------|
| | ATOM | 2319 | CD1 | LEU | 307 | 11.389 | -18.243 | 78.356 | 1.00 | 43.36 |
| | ATOM | 2320 | CD2 | LEU | 307 | 10.610 | -17.233 | 76.197 | 1.00 | 41.75 |
| | ATOM | 2321 | C | LEU | 307 | 12.802 | -21.674 | 76.239 | 1.00 | 42.39 |
| 5 | ATOM | 2322 | 0 | LEU | 307 | 11.974 | -22.537 | 76.514 | 1.00 | 42.90 |
| | ATOM | 2323 | N | ARG | 308 | 13.729 | -21.860 | 75.306 | 1.00 | 42.02 |
| | ATOM | 2324 | CA | ARG | 308 | 13.771 | -23.132 | 74.605 | 1.00 | 42.88 |
| | ATOM | 2325 | CB | ARG | 308 | 14.765 | -23.125 | 73.445 | 1.00 | 43.55 |
| | ATOM | 2326 | CG | ARG | 308 | 14.891 | -24.514 | 72.837 | 1.00 | 47.00 |
| 10 | ATOM | 2327 | CD | ARG | 308 | 15.908 | -24.626 | 71.729 | 1.00 | 49.25 |
| | ATOM | 2328 | NE | ARG | 308 | 16.079 | -26.026 | 71.349 | 1.00 | 52.10 |
| | ATOM | 2329 | CZ | ARG | 308 | 16.915 | -26.456 | 70.410 | 1.00 | 52.45 |
| | ATOM | 2330 | NH1 | ARG | 308 | 17.663 | -25.591 | 69.739 | 1.00 | 54.77 |
| | ATOM | 2331 | NH2 | ARG | 308 | 17.016 | -27.756 | 70.154 | 1.00 | 51.73 |
| 15 | ATOM | 2332 | C | ARG | 308 | 14.181 | -24.222 | 75.582 | 1.00 | 43.27 |
| | ATOM | 2333 | 0 | ARG | 308 | 13.654 | -25.333 | 75.540 | 1.00 | 42.09 |
| | ATOM | 2334 | N | LEU | 309 | 15.135 | -23.895 | 76.452 | 1.00 | 42.54 |
| | ATOM | 2335 | CA | LEU | 309 | 15.627 | -24.837 | 77.447 | 1.00 | 42.29 |
| | ATOM | 2336 | CB | LEU | 309 | 16.771 | -24.207 | 78.248 | 1.00 | 40.55 |
| 20 | ATOM | 2337 | CG | LEU | 309 | 18.193 | -24.656 | 77.886 | 1.00 | 39.65 |
| | ATOM | 2338 | CD1 | LEU | 309 | 18.313 | -24.973 | 76.416 | 1.00 | 38.56 |
| | ATOM | 2339 | CD2 | LEU | 309 | 19.171 | -23.569 | 78.284 | 1.00 | 37.67 |
| | ATOM | 2340 | C | LEU | 309 | 14.515 | -25.302 | 78.379 | 1.00 | 42.66 |
| | ATOM | 2341 | 0 | LEU | 309 | 14.509 | -26.450 | 78.818 | 1.00 | 41.33 |
| 25 | ATOM | 2342 | N | VAL | 310 | 13.570 | -24.416 | 78.676 | 1.00 | 44.27 |
| | ATOM | 2343 | CA | VAL | 310 | 12.464 | -24.789 | 79.543 | 1.00 | 46.40 |
| | ATOM | 2344 | CB | VAL | 310 | 11.711 | -23.546 | 80.111 | 1.00 | 46.06 |
| | ATOM | 2345 | CG1 | VAL | 310 | 12.682 | -22.613 | 80.807 | 1.00 | 45.43 |
| | ATOM | 2346 | CG2 | VAL | 310 | 10.976 | -22.825 | 79.014 | 1.00 | 48.29 |

- 97 -

| | ATOM | 2347 | C | VAL | 310 | 11.479 | -25.666 | 78.769 | 1.00 | 48.00 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2348 | O | VAL | 310 | 10.952 | -26.638 | 79.311 | 1.00 | 47.71 |
| | ATOM | 2349 | N | ASP | 311 | 11.242 | -25.333 | 77.501 | 1.00 | 49.58 |
| | ATOM | 2350 | CA | ASP | 311 | 10.313 | -26.104 | 76.683 | 1.00 | 52.37 |
| 5 | ATOM | 2351 | CB | ASP | 311 | 9.978 | -25.365 | 75.382 | 1.00 | 54.70 |
| | ATOM | 2352 | CG | ASP | 311 | 9.318 | -24.014 | 75.626 | 1.00 | 58.89 |
| | ATOM | 2353 | OD1 | ASP | 311 | 8.742 | -23.808 | 76.719 | 1.00 | 60.74 |
| | ATOM | 2354 | OD2 | ASP | 311 | 9.364 | -23.158 | 74.713 | 1.00 | 60.54 |
| | ATOM | 2355 | C | ASP | 311 | 10.872 | -27.485 | 76.365 | 1.00 | 52.35 |
| 10 | ATOM | 2356 | O | ASP | 311 | 10.131 | -28.388 | 75.982 | 1.00 | 55.07 |
| | ATOM | 2357 | N | GLU | 312 | 12.180 | -27.642 | 76.515 | 1.00 | 51.23 |
| | ATOM | 2358 | CA | GLU | 312 | 12.828 | -28.926 | 76.279 | 1.00 | 51.12 |
| | ATOM | 2359 | CB | GLU | 312 | 14.277 | -28.729 | 75.834 | 1.00 | 52.62 |
| | ATOM | 2360 | CG | GLU | 312 | 14.445 | -28.141 | 74.448 | 1.00 | 57.13 |
| 15 | ATOM | 2361 | CD | GLU | 312 | 14.187 | -29.153 | 73.358 | 1.00 | 58.40 |
| | ATOM | 2362 | OE1 | GLU | 312 | 14.831 | -30.222 | 73.385 | 1.00 | 59.31 |
| | ATOM | 2363 | OE2 | GLU | 312 | 13.346 | -28.879 | 72.476 | 1.00 | 60.41 |
| | ATOM | 2364 | C | GLU | 312 | 12.810 | -29.660 | 77.611 | 1.00 | 50.76 |
| | ATOM | 2365 | O | GLU | 312 | 13.292 | -30.787 | 77.720 | 1.00 | 50.64 |
| 20 | ATOM | 2366 | N | ASN | 313 | 12.265 | -28.989 | 78.624 | 1.00 | 50.08 |
| | ATOM | 2367 | CA | ASN | 313 | 12.154 | -29.533 | 79.974 | 1.00 | 51.37 |
| | ATOM | 2368 | CB | ASN | 313 | 11.428 | -30.886 | 79.932 | 1.00 | 53.51 |
| | ATOM | 2369 | CG | ASN | 313 | 10.846 | -31.275 | 81.271 | 1.00 | 55.73 |
| | ATOM | 2370 | OD1 | ASN | 313 | 10.011 | -30.560 | 81.824 | 1.00 | 58.95 |
| 25 | ATOM | 2371 | ND2 | ASN | 313 | 11.281 | -32.415 | 81.803 | 1.00 | 59.16 |
| | ATOM | 2372 | C | ASN | 313 | 13.524 | -29.693 | 80.635 | 1.00 | 50.00 |
| | ATOM | 2373 | O | ASN | 313 | 13.733 | -30.595 | 81.447 | 1.00 | 50.40 |
| | ATOM | 2374 | N | LEU | 314 | 14.449 | -28.799 | 80.296 | 1.00 | 48.35 |
| | ATOM | 2375 | CA | LEU | 314 | 15.805 | -28.843 | 80.835 | 1.00 | 45.12 |

- 98 -

|  | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2376 | CB | LEU | 314 | 16.819 | -28.785 | 79.688 | 1.00 | 44.25 |
|  | ATOM | 2377 | CG | LEU | 314 | 16.759 | -29.872 | 78.611 | 1.00 | 45.98 |
|  | ATOM | 2378 | CD1 | LEU | 314 | 17.619 | -29.465 | 77.416 | 1.00 | 43.63 |
|  | ATOM | 2379 | CD2 | LEU | 314 | 17.232 | -31.201 | 79.196 | 1.00 | 45.09 |
| 5 | ATOM | 2380 | C | LEU | 314 | 16.119 | -27.724 | 81.829 | 1.00 | 43.38 |
|  | ATOM | 2381 | O | LEU | 314 | 17.180 | -27.732 | 82.449 | 1.00 | 41.90 |
|  | ATOM | 2382 | N | LEU | 315 | 15.211 | -26.765 | 81.982 | 1.00 | 41.74 |
|  | ATOM | 2383 | CA | LEU | 315 | 15.446 | -25.645 | 82.899 | 1.00 | 42.39 |
|  | ATOM | 2384 | CB | LEU | 315 | 15.907 | -24.407 | 82.116 | 1.00 | 40.17 |
| 10 | ATOM | 2385 | CG | LEU | 315 | 17.243 | -23.721 | 82.428 | 1.00 | 39.81 |
|  | ATOM | 2386 | CD1 | LEU | 315 | 17.262 | -22.383 | 81.689 | 1.00 | 41.89 |
|  | ATOM | 2387 | CD2 | LEU | 315 | 17.421 | -23.482 | 83.920 | 1.00 | 37.58 |
|  | ATOM | 2388 | C | LEU | 315 | 14.198 | -25.278 | 83.694 | 1.00 | 42.28 |
|  | ATOM | 2389 | O | LEU | 315 | 13.103 | -25.214 | 83.144 | 1.00 | 40.83 |
| 15 | ATOM | 2390 | N | PHE | 316 | 14.377 | -25.021 | 84.986 | 1.00 | 43.70 |
|  | ATOM | 2391 | CA | PHE | 316 | 13.271 | -24.648 | 85.863 | 1.00 | 46.70 |
|  | ATOM | 2392 | CB | PHE | 316 | 12.717 | -23.278 | 85.459 | 1.00 | 47.06 |
|  | ATOM | 2393 | CG | PHE | 316 | 13.776 | -22.247 | 85.187 | 1.00 | 47.07 |
|  | ATOM | 2394 | CD1 | PHE | 316 | 14.824 | -22.051 | 86.082 | 1.00 | 47.24 |
| 20 | ATOM | 2395 | CD2 | PHE | 316 | 13.722 | -21.467 | 84.037 | 1.00 | 47.25 |
|  | ATOM | 2396 | CE1 | PHE | 316 | 15.803 | -21.094 | 85.835 | 1.00 | 46.12 |
|  | ATOM | 2397 | CE2 | PHE | 316 | 14.695 | -20.507 | 83.782 | 1.00 | 47.70 |
|  | ATOM | 2398 | CZ | PHE | 316 | 15.738 | -20.321 | 84.683 | 1.00 | 47.68 |
|  | ATOM | 2399 | C | PHE | 316 | 12.131 | -25.672 | 85.857 | 1.00 | 48.45 |
| 25 | ATOM | 2400 | O | PHE | 316 | 10.960 | -25.306 | 85.967 | 1.00 | 48.86 |
|  | ATOM | 2401 | N | HIS | 317 | 12.473 | -26.950 | 85.725 | 1.00 | 50.80 |
|  | ATOM | 2402 | CA | HIS | 317 | 11.469 | -28.009 | 85.712 | 1.00 | 53.83 |
|  | ATOM | 2403 | CB | HIS | 317 | 10.655 | -27.986 | 87.010 | 1.00 | 57.67 |
|  | ATOM | 2404 | CG | HIS | 317 | 11.496 | -27.985 | 88.246 | 1.00 | 61.10 |

- 99 -

| | ATOM | 2405 | CD2 | HIS | 317 | 11. 558 | -27. 116 | 89. 282 | 1. 00 | 63. 07 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2406 | ND1 | HIS | 317 | 12. 430 | -28. 965 | 88. 509 | 1. 00 | 62. 35 |
| | ATOM | 2407 | CE1 | HIS | 317 | 13. 032 | -28. 699 | 89. 655 | 1. 00 | 64. 77 |
| | ATOM | 2408 | NE2 | HIS | 317 | 12. 521 | -27. 582 | 90. 144 | 1. 00 | 65. 99 |
| 5 | ATOM | 2409 | C | HIS | 317 | 10. 521 | -27. 859 | 84. 534 | 1. 00 | 53. 57 |
| | ATOM | 2410 | 0 | HIS | 317 | 9. 429 | -28. 425 | 84. 537 | 1. 00 | 53. 60 |
| | ATOM | 2411 | N | GLY | 318 | 10. 939 | -27. 090 | 83. 534 | 1. 00 | 52. 50 |
| | ATOM | 2412 | CA | GLY | 318 | 10. 113 | -26. 881 | 82. 358 | 1. 00 | 51. 83 |
| | ATOM | 2413 | C | GLY | 318 | 8. 940 | -25. 958 | 82. 615 | 1. 00 | 51. 72 |
| 10 | ATOM | 2414 | 0 | GLY | 318 | 7. 939 | -25. 999 | 81. 904 | 1. 00 | 50. 88 |
| | ATOM | 2415 | N | GLU | 319 | 9. 073 | -25. 110 | 83. 627 | 1. 00 | 53. 43 |
| | ATOM | 2416 | CA | GLU | 319 | 8. 014 | -24. 182 | 83. 996 | 1. 00 | 55. 73 |
| | ATOM | 2417 | CB | GLU | 319 | 7. 510 | -24. 544 | 85. 392 | 1. 00 | 58. 85 |
| | ATOM | 2418 | CG | GLU | 319 | 6. 145 | -23. 998 | 85. 761 | 1. 00 | 63. 60 |
| 15 | ATOM | 2419 | CD | GLU | 319 | 5. 590 | -24. 664 | 87. 016 | 1. 00 | 66. 32 |
| | ATOM | 2420 | OE1 | GLU | 319 | 6. 206 | -24. 527 | 88. 100 | 1. 00 | 65. 47 |
| | ATOM | 2421 | OE2 | GLU | 319 | 4. 540 | -25. 335 | 86. 913 | 1. 00 | 67. 45 |
| | ATOM | 2422 | C | GLU | 319 | 8. 538 | -22. 748 | 83. 966 | 1. 00 | 55. 18 |
| | ATOM | 2423 | 0 | GLU | 319 | 9. 278 | -22. 324 | 84. 851 | 1. 00 | 55. 23 |
| 20 | ATOM | 2424 | N | ALA | 320 | 8. 145 | -22. 006 | 82. 938 | 1. 00 | 55. 14 |
| | ATOM | 2425 | CA | ALA | 320 | 8. 585 | -20. 630 | 82. 780 | 1. 00 | 55. 95 |
| | ATOM | 2426 | CB | ALA | 320 | 8. 609 | -20. 265 | 81. 304 | 1. 00 | 55. 13 |
| | ATOM | 2427 | C | ALA | 320 | 7. 708 | -19. 649 | 83. 544 | 1. 00 | 56. 88 |
| | ATOM | 2428 | 0 | ALA | 320 | 6. 487 | -19. 789 | 83. 584 | 1. 00 | 58. 58 |
| 25 | ATOM | 2429 | N | SER | 321 | 8. 344 | -18. 648 | 84. 141 | 1. 00 | 57. 00 |
| | ATOM | 2430 | CA | SER | 321 | 7. 644 | -17. 625 | 84. 902 | 1. 00 | 56. 57 |
| | ATOM | 2431 | CB | SER | 321 | 8. 649 | -16. 808 | 85. 705 | 1. 00 | 56. 74 |
| | ATOM | 2432 | OG | SER | 321 | 8. 013 | -15. 725 | 86. 349 | 1. 00 | 57. 41 |
| | ATOM | 2433 | C | SER | 321 | 6. 853 | -16. 689 | 83. 995 | 1. 00 | 58. 61 |

- 100 -

|  |  |  |  |  |  |  |  |  |  |
|------|------|-----|-----|-----|---------|---------|--------|------|--------|
| ATOM | 2434 | O | SER | 321 | 7.054 | -16.665 | 82.783 | 1.00 | 58.41 |
| ATOM | 2435 | N | GLU | 322 | 5.955 | -15.914 | 84.595 | 1.00 | 60.41 |
| ATOM | 2436 | CA | GLU | 322 | 5.133 | -14.960 | 83.858 | 1.00 | 62.09 |
| ATOM | 2437 | CB | GLU | 322 | 4.171 | -14.254 | 84.819 | 1.00 | 65.34 |
| ATOM | 2438 | CG | GLU | 322 | 3.185 | -13.299 | 84.165 | 1.00 | 69.70 |
| ATOM | 2439 | CD | GLU | 322 | 2.075 | -14.020 | 83.418 | 1.00 | 73.68 |
| ATOM | 2440 | OE1 | GLU | 322 | 1.379 | -14.851 | 84.046 | 1.00 | 74.78 |
| ATOM | 2441 | OE2 | GLU | 322 | 1.896 | -13.751 | 82.208 | 1.00 | 75.02 |
| ATOM | 2442 | C | GLU | 322 | 6.047 | -13.929 | 83.204 | 1.00 | 61.24 |
| ATOM | 2443 | O | GLU | 322 | 5.913 | -13.612 | 82.022 | 1.00 | 60.81 |
| ATOM | 2444 | N | GLN | 323 | 6.987 | -13.420 | 83.991 | 1.00 | 60.42 |
| ATOM | 2445 | CA | GLN | 323 | 7.935 | -12.422 | 83.521 | 1.00 | 58.63 |
| ATOM | 2446 | CB | GLN | 323 | 8.729 | -11.863 | 84.700 | 1.00 | 59.77 |
| ATOM | 2447 | CG | GLN | 323 | 7.902 | -11.039 | 85.658 | 1.00 | 61.20 |
| ATOM | 2448 | CD | GLN | 323 | 8.690 | -10.608 | 86.873 | 1.00 | 63.03 |
| ATOM | 2449 | OE1 | GLN | 323 | 9.672 | -9.866 | 86.767 | 1.00 | 63.70 |
| ATOM | 2450 | NE2 | GLN | 323 | 8.266 | -11.074 | 88.044 | 1.00 | 64.05 |
| ATOM | 2451 | C | GLN | 323 | 8.904 | -12.955 | 82.478 | 1.00 | 56.96 |
| ATOM | 2452 | O | GLN | 323 | 9.244 | -12.255 | 81.526 | 1.00 | 56.89 |
| ATOM | 2453 | N | LEU | 324 | 9.351 | -14.190 | 82.652 | 1.00 | 53.93 |
| ATOM | 2454 | CA | LEU | 324 | 10.298 | -14.763 | 81.713 | 1.00 | 52.62 |
| ATOM | 2455 | CB | LEU | 324 | 10.745 | -16.151 | 82.180 | 1.00 | 51.22 |
| ATOM | 2456 | CG | LEU | 324 | 11.830 | -16.826 | 81.334 | 1.00 | 50.58 |
| ATOM | 2457 | CD1 | LEU | 324 | 13.076 | -15.952 | 81.299 | 1.00 | 49.50 |
| ATOM | 2458 | CD2 | LEU | 324 | 12.160 | -18.192 | 81.909 | 1.00 | 49.35 |
| ATOM | 2459 | C | LEU | 324 | 9.730 | -14.855 | 80.306 | 1.00 | 52.38 |
| ATOM | 2460 | O | LEU | 324 | 10.485 | -14.870 | 79.337 | 1.00 | 51.83 |
| ATOM | 2461 | N | ARG | 325 | 8.405 | -14.902 | 80.193 | 1.00 | 52.63 |
| ATOM | 2462 | CA | ARG | 325 | 7.759 | -15.015 | 78.887 | 1.00 | 53.00 |

| | ATOM | 2463 | CB | ARG | 325 | 6. 477 | -15. 848 | 79. 000 | 1. 00 | 54. 77 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2464 | CG | ARG | 325 | 6. 585 | -17. 005 | 79. 985 | 1. 00 | 58. 57 |
| | ATOM | 2465 | CD | ARG | 325 | 6. 013 | -18. 330 | 79. 458 | 1. 00 | 60. 34 |
| | ATOM | 2466 | NE | ARG | 325 | 6. 881 | -18. 961 | 78. 464 | 1. 00 | 62. 28 |
| 5 | ATOM | 2467 | CZ | ARG | 325 | 6. 953 | -20. 273 | 78. 249 | 1. 00 | 62. 81 |
| | ATOM | 2468 | NH1 | ARG | 325 | 6. 208 | -21. 109 | 78. 963 | 1. 00 | 62. 98 |
| | ATOM | 2469 | NH2 | ARG | 325 | 7. 769 | -20. 752 | 77. 317 | 1. 00 | 62. 50 |
| | ATOM | 2470 | C | ARG | 325 | 7. 430 | -13. 663 | 78. 266 | 1. 00 | 52. 20 |
| | ATOM | 2471 | O | ARG | 325 | 6. 835 | -13. 595 | 77. 194 | 1. 00 | 51. 65 |
| 10 | ATOM | 2472 | N | THR | 326 | 7. 820 | -12. 589 | 78. 940 | 1. 00 | 51. 52 |
| | ATOM | 2473 | CA | THR | 326 | 7. 562 | -11. 248 | 78. 438 | 1. 00 | 53. 54 |
| | ATOM | 2474 | CB | THR | 326 | 7. 031 | -10. 343 | 79. 570 | 1. 00 | 54. 40 |
| | ATOM | 2475 | OG1 | THR | 326 | 8. 068 | -10. 120 | 80. 534 | 1. 00 | 56. 68 |
| | ATOM | 2476 | CG2 | THR | 326 | 5. 858 | -11. 012 | 80. 274 | 1. 00 | 53. 00 |
| 15 | ATOM | 2477 | C | THR | 326 | 8. 853 | -10. 655 | 77. 850 | 1. 00 | 54. 00 |
| | ATOM | 2478 | O | THR | 326 | 9. 891 | -10. 626 | 78. 515 | 1. 00 | 53. 48 |
| | ATOM | 2479 | N | ARG | 327 | 8. 782 | -10. 191 | 76. 604 | 1. 00 | 54. 30 |
| | ATOM | 2480 | CA | ARG | 327 | 9. 948 | -9. 628 | 75. 923 | 1. 00 | 55. 25 |
| | ATOM | 2481 | CB | ARG | 327 | 9. 568 | -9. 074 | 74. 550 | 1. 00 | 58. 73 |
| 20 | ATOM | 2482 | CG | ARG | 327 | 9. 050 | -10. 101 | 73. 572 | 1. 00 | 62. 94 |
| | ATOM | 2483 | CD | ARG | 327 | 9. 189 | -9. 599 | 72. 143 | 1. 00 | 66. 63 |
| | ATOM | 2484 | NE | ARG | 327 | 8. 462 | -10. 454 | 71. 213 | 1. 00 | 70. 25 |
| | ATOM | 2485 | CZ | ARG | 327 | 7. 136 | -10. 522 | 71. 154 | 1. 00 | 72. 29 |
| | ATOM | 2486 | NH1 | ARG | 327 | 6. 399 | -9. 778 | 71. 969 | 1. 00 | 72. 86 |
| 25 | ATOM | 2487 | NH2 | ARG | 327 | 6. 546 | -11. 338 | 70. 288 | 1. 00 | 73. 24 |
| | ATOM | 2488 | C | ARG | 327 | 10. 660 | -8. 529 | 76. 688 | 1. 00 | 53. 79 |
| | ATOM | 2489 | O | ARG | 327 | 10. 027 | -7. 690 | 77. 326 | 1. 00 | 55. 10 |
| | ATOM | 2490 | N | GLY | 328 | 11. 986 | -8. 535 | 76. 604 | 1. 00 | 50. 97 |
| | ATOM | 2491 | CA | GLY | 328 | 12. 773 | -7. 520 | 77. 276 | 1. 00 | 50. 03 |

- 102 -

|   | ATOM | 2492 | C | GLY | 328 | 12.922 | -7.715 | 78.770 | 1.00 | 49.36 |
|---|------|------|------|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 2493 | O | GLY | 328 | 13.622 | -6.942 | 79.426 | 1.00 | 49.68 |
|   | ATOM | 2494 | N | ALA | 329 | 12.274 | -8.740 | 79.315 | 1.00 | 47.47 |
|   | ATOM | 2495 | CA | ALA | 329 | 12.354 | -9.007 | 80.749 | 1.00 | 46.93 |
| 5 | ATOM | 2496 | CB | ALA | 329 | 11.468 | -10.184 | 81.115 | 1.00 | 48.23 |
|   | ATOM | 2497 | C | ALA | 329 | 13.786 | -9.287 | 81.173 | 1.00 | 45.48 |
|   | ATOM | 2498 | O | ALA | 329 | 14.247 | -8.794 | 82.203 | 1.00 | 44.91 |
|   | ATOM | 2499 | N | PHE | 330 | 14.490 | -10.088 | 80.383 | 1.00 | 43.75 |
|   | ATOM | 2500 | CA | PHE | 330 | 15.870 | -10.392 | 80.710 | 1.00 | 42.95 |
| 10 | ATOM | 2501 | CB | PHE | 330 | 16.271 | -11.760 | 80.156 | 1.00 | 39.40 |
|   | ATOM | 2502 | CG | PHE | 330 | 17.478 | -12.350 | 80.829 | 1.00 | 36.90 |
|   | ATOM | 2503 | CD1 | PHE | 330 | 18.761 | -11.985 | 80.436 | 1.00 | 35.73 |
|   | ATOM | 2504 | CD2 | PHE | 330 | 17.330 | -13.241 | 81.893 | 1.00 | 35.23 |
|   | ATOM | 2505 | CE1 | PHE | 330 | 19.878 | -12.496 | 81.093 | 1.00 | 33.48 |
| 15 | ATOM | 2506 | CE2 | PHE | 330 | 18.443 | -13.759 | 82.558 | 1.00 | 31.61 |
|   | ATOM | 2507 | CZ | PHE | 330 | 19.716 | -13.387 | 82.160 | 1.00 | 33.39 |
|   | ATOM | 2508 | C | PHE | 330 | 16.752 | -9.292 | 80.130 | 1.00 | 43.51 |
|   | ATOM | 2509 | O | PHE | 330 | 17.202 | -9.373 | 78.986 | 1.00 | 44.11 |
|   | ATOM | 2510 | N | GLU | 331 | 16.962 | -8.254 | 80.935 | 1.00 | 43.95 |
| 20 | ATOM | 2511 | CA | GLU | 331 | 17.777 | -7.099 | 80.569 | 1.00 | 43.11 |
|   | ATOM | 2512 | CB | GLU | 331 | 17.767 | -6.068 | 81.697 | 1.00 | 46.19 |
|   | ATOM | 2513 | CG | GLU | 331 | 16.393 | -5.551 | 82.092 | 1.00 | 50.13 |
|   | ATOM | 2514 | CD | GLU | 331 | 16.458 | -4.651 | 83.316 | 1.00 | 53.54 |
|   | ATOM | 2515 | OE1 | GLU | 331 | 17.324 | -3.745 | 83.343 | 1.00 | 55.03 |
| 25 | ATOM | 2516 | OE2 | GLU | 331 | 15.646 | -4.846 | 84.247 | 1.00 | 53.56 |
|   | ATOM | 2517 | C | GLU | 331 | 19.216 | -7.511 | 80.310 | 1.00 | 42.02 |
|   | ATOM | 2518 | O | GLU | 331 | 19.742 | -8.411 | 80.968 | 1.00 | 42.05 |
|   | ATOM | 2519 | N | THR | 332 | 19.855 | -6.830 | 79.365 | 1.00 | 39.23 |
|   | ATOM | 2520 | CA | THR | 332 | 21.235 | -7.122 | 79.017 | 1.00 | 36.08 |

- 103 -

|  | ATOM | 2521 | CB | THR | 332 | 21. 713 | -6. 200 | 77. 869 | 1. 00 | 36. 47 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2522 | OG1 | THR | 332 | 21. 297 | -6. 762 | 76. 618 | 1. 00 | 33. 61 |
|  | ATOM | 2523 | CG2 | THR | 332 | 23. 235 | -6. 030 | 77. 884 | 1. 00 | 31. 36 |
|  | ATOM | 2524 | C | THR | 332 | 22. 159 | -6. 987 | 80. 219 | 1. 00 | 35. 73 |
| 5 | ATOM | 2525 | O | THR | 332 | 23. 209 | -7. 634 | 80. 280 | 1. 00 | 35. 30 |
|  | ATOM | 2526 | N | ARG | 333 | 21. 782 | -6. 151 | 81. 180 | 1. 00 | 34. 21 |
|  | ATOM | 2527 | CA | ARG | 333 | 22. 632 | -6. 003 | 82. 353 | 1. 00 | 34. 18 |
|  | ATOM | 2528 | CB | ARG | 333 | 22. 211 | -4. 786 | 83. 193 | 1. 00 | 36. 60 |
|  | ATOM | 2529 | CG | ARG | 333 | 20. 830 | -4. 854 | 83. 835 | 1. 00 | 39. 58 |
| 10 | ATOM | 2530 | CD | ARG | 333 | 20. 488 | -3. 518 | 84. 520 | 1. 00 | 42. 78 |
|  | ATOM | 2531 | NE | ARG | 333 | 19. 264 | -3. 590 | 85. 316 | 1. 00 | 45. 29 |
|  | ATOM | 2532 | CZ | ARG | 333 | 19. 205 | -4. 039 | 86. 567 | 1. 00 | 47. 32 |
|  | ATOM | 2533 | NH1 | ARG | 333 | 20. 305 | -4. 455 | 87. 182 | 1. 00 | 49. 55 |
|  | ATOM | 2534 | NH2 | ARG | 333 | 18. 042 | -4. 080 | 87. 205 | 1. 00 | 48. 70 |
| 15 | ATOM | 2535 | C | ARG | 333 | 22. 609 | -7. 298 | 83. 181 | 1. 00 | 31. 65 |
|  | ATOM | 2536 | O | ARG | 333 | 23. 584 | -7. 625 | 83. 863 | 1. 00 | 31. 61 |
|  | ATOM | 2537 | N | PHE | 334 | 21. 513 | -8. 049 | 83. 105 | 1. 00 | 31. 01 |
|  | ATOM | 2538 | CA | PHE | 334 | 21. 431 | -9. 317 | 83. 835 | 1. 00 | 30. 67 |
|  | ATOM | 2539 | CB | PHE | 334 | 20. 048 | -9. 967 | 83. 678 | 1. 00 | 30. 39 |
| 20 | ATOM | 2540 | CG | PHE | 334 | 18. 923 | -9. 210 | 84. 330 | 1. 00 | 30. 58 |
|  | ATOM | 2541 | CD1 | PHE | 334 | 19. 170 | -8. 214 | 85. 269 | 1. 00 | 29. 37 |
|  | ATOM | 2542 | CD2 | PHE | 334 | 17. 600 | -9. 522 | 84. 019 | 1. 00 | 31. 94 |
|  | ATOM | 2543 | CE1 | PHE | 334 | 18. 113 | -7. 539 | 85. 891 | 1. 00 | 31. 67 |
|  | ATOM | 2544 | CE2 | PHE | 334 | 16. 535 | -8. 851 | 84. 636 | 1. 00 | 32. 25 |
| 25 | ATOM | 2545 | CZ | PHE | 334 | 16. 796 | -7. 857 | 85. 575 | 1. 00 | 28. 89 |
|  | ATOM | 2546 | C | PHE | 334 | 22. 496 | -10. 287 | 83. 295 | 1. 00 | 30. 73 |
|  | ATOM | 2547 | O | PHE | 334 | 23. 136 | -11. 016 | 84. 064 | 1. 00 | 30. 77 |
|  | ATOM | 2548 | N | VAL | 335 | 22. 685 | -10. 290 | 81. 973 | 1. 00 | 29. 44 |
|  | ATOM | 2549 | CA | VAL | 335 | 23. 672 | -11. 165 | 81. 350 | 1. 00 | 30. 61 |

- 104 -

|   | ATOM | 2550 | CB | VAL | 335 | 23. 777 | -10. 921 | 79. 831 | 1. 00 | 30. 75 |
|---|------|------|-----|-----|-----|---------|----------|---------|-------|--------|
|   | ATOM | 2551 | CG1 | VAL | 335 | 24. 774 | -11. 898 | 79. 216 | 1. 00 | 32. 48 |
|   | ATOM | 2552 | CG2 | VAL | 335 | 22. 424 | -11. 078 | 79. 181 | 1. 00 | 29. 80 |
|   | ATOM | 2553 | C | VAL | 335 | 25. 041 | -10. 904 | 81. 964 | 1. 00 | 31. 64 |
| 5 | ATOM | 2554 | 0 | VAL | 335 | 25. 759 | -11. 830 | 82. 356 | 1. 00 | 31. 87 |
|   | ATOM | 2555 | N | SER | 336 | 25. 382 | -9. 623 | 82. 048 | 1. 00 | 33. 23 |
|   | ATOM | 2556 | CA | SER | 336 | 26. 655 | -9. 173 | 82. 593 | 1. 00 | 32. 42 |
|   | ATOM | 2557 | CB | SER | 336 | 26. 778 | -7. 660 | 82. 384 | 1. 00 | 33. 94 |
|   | ATOM | 2558 | OG | SER | 336 | 28. 080 | -7. 204 | 82. 682 | 1. 00 | 38. 27 |
| 10 | ATOM | 2559 | C | SER | 336 | 26. 793 | -9. 524 | 84. 078 | 1. 00 | 32. 82 |
|   | ATOM | 2560 | 0 | SER | 336 | 27. 863 | -9. 917 | 84. 529 | 1. 00 | 33. 76 |
|   | ATOM | 2561 | N | GLN | 337 | 25. 711 | -9. 389 | 84. 839 | 1. 00 | 32. 64 |
|   | ATOM | 2562 | CA | GLN | 337 | 25. 753 | -9. 715 | 86. 260 | 1. 00 | 34. 83 |
|   | ATOM | 2563 | CB | GLN | 337 | 24. 480 | -9. 233 | 86. 958 | 1. 00 | 37. 43 |
| 15 | ATOM | 2564 | CG | GLN | 337 | 24. 339 | -7. 721 | 86. 972 | 1. 00 | 42. 29 |
|   | ATOM | 2565 | CD | GLN | 337 | 22. 984 | -7. 260 | 87. 471 | 1. 00 | 44. 59 |
|   | ATOM | 2566 | OE1 | GLN | 337 | 22. 710 | -6. 062 | 87. 525 | 1. 00 | 46. 49 |
|   | ATOM | 2567 | NE2 | GLN | 337 | 22. 128 | -8. 209 | 87. 835 | 1. 00 | 43. 79 |
|   | ATOM | 2568 | C | GLN | 337 | 25. 899 | -11. 217 | 86. 447 | 1. 00 | 33. 66 |
| 20 | ATOM | 2569 | 0 | GLN | 337 | 26. 663 | -11. 674 | 87. 297 | 1. 00 | 35. 28 |
|   | ATOM | 2570 | N | VAL | 338 | 25. 159 | -11. 983 | 85. 655 | 1. 00 | 31. 29 |
|   | ATOM | 2571 | CA | VAL | 338 | 25. 236 | -13. 432 | 85. 743 | 1. 00 | 29. 21 |
|   | ATOM | 2572 | CB | VAL | 338 | 24. 326 | -14. 102 | 84. 690 | 1. 00 | 28. 27 |
|   | ATOM | 2573 | CG1 | VAL | 338 | 24. 687 | -15. 571 | 84. 525 | 1. 00 | 27. 17 |
| 25 | ATOM | 2574 | CG2 | VAL | 338 | 22. 877 | -13. 984 | 85. 129 | 1. 00 | 26. 99 |
|   | ATOM | 2575 | C | VAL | 338 | 26. 678 | -13. 877 | 85. 547 | 1. 00 | 27. 35 |
|   | ATOM | 2576 | 0 | VAL | 338 | 27. 176 | -14. 722 | 86. 284 | 1. 00 | 26. 69 |
|   | ATOM | 2577 | N | GLU | 339 | 27. 361 | -13. 283 | 84. 576 | 1. 00 | 27. 29 |
|   | ATOM | 2578 | CA | GLU | 339 | 28. 747 | -13. 657 | 84. 314 | 1. 00 | 27. 15 |

- 105 -

| | ATOM | 2579 | CB | GLU | 339 | 29.136 | -13.303 | 82.871 | 1.00 | 27.02 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2580 | CG | GLU | 339 | 28.404 | -14.185 | 81.843 | 1.00 | 30.73 |
| | ATOM | 2581 | CD | GLU | 339 | 28.942 | -14.063 | 80.425 | 1.00 | 30.33 |
| | ATOM | 2582 | OE1 | GLU | 339 | 30.121 | -14.414 | 80.185 | 1.00 | 34.73 |
| 5 | ATOM | 2583 | OE2 | GLU | 339 | 28.179 | -13.619 | 79.548 | 1.00 | 29.50 |
| | ATOM | 2584 | C | GLU | 339 | 29.749 | -13.085 | 85.311 | 1.00 | 26.93 |
| | ATOM | 2585 | O | GLU | 339 | 30.940 | -13.345 | 85.209 | 1.00 | 27.69 |
| | ATOM | 2586 | N | SER | 340 | 29.264 | -12.320 | 86.285 | 1.00 | 27.55 |
| | ATOM | 2587 | CA | SER | 340 | 30.140 | -11.763 | 87.318 | 1.00 | 28.61 |
| 10 | ATOM | 2588 | CB | SER | 340 | 29.741 | -10.323 | 87.667 | 1.00 | 29.40 |
| | ATOM | 2589 | OG | SER | 340 | 29.800 | -9.485 | 86.528 | 1.00 | 35.97 |
| | ATOM | 2590 | C | SER | 340 | 30.029 | -12.615 | 88.583 | 1.00 | 27.94 |
| | ATOM | 2591 | O | SER | 340 | 30.811 | -12.448 | 89.526 | 1.00 | 24.04 |
| | ATOM | 2592 | N | ASP | 341 | 29.042 | -13.511 | 88.600 | 1.00 | 28.02 |
| 15 | ATOM | 2593 | CA | ASP | 341 | 28.812 | -14.387 | 89.748 | 1.00 | 29.66 |
| | ATOM | 2594 | CB | ASP | 341 | 27.808 | -15.490 | 89.393 | 1.00 | 30.94 |
| | ATOM | 2595 | CG | ASP | 341 | 27.296 | -16.227 | 90.620 | 1.00 | 33.11 |
| | ATOM | 2596 | OD1 | ASP | 341 | 26.289 | -15.778 | 91.217 | 1.00 | 28.78 |
| | ATOM | 2597 | OD2 | ASP | 341 | 27.918 | -17.247 | 90.991 | 1.00 | 32.82 |
| 20 | ATOM | 2598 | C | ASP | 341 | 30.137 | -15.003 | 90.163 | 1.00 | 30.38 |
| | ATOM | 2599 | O | ASP | 341 | 30.853 | -15.564 | 89.342 | 1.00 | 30.59 |
| | ATOM | 2600 | N | THR | 342 | 30.466 | -14.886 | 91.443 | 1.00 | 33.59 |
| | ATOM | 2601 | CA | THR | 342 | 31.729 | -15.405 | 91.953 | 1.00 | 37.01 |
| | ATOM | 2602 | CB | THR | 342 | 32.013 | -14.836 | 93.350 | 1.00 | 38.81 |
| 25 | ATOM | 2603 | OG1 | THR | 342 | 31.012 | -15.304 | 94.265 | 1.00 | 43.90 |
| | ATOM | 2604 | CG2 | THR | 342 | 31.972 | -13.316 | 93.317 | 1.00 | 35.79 |
| | ATOM | 2605 | C | THR | 342 | 31.780 | -16.929 | 92.027 | 1.00 | 37.87 |
| | ATOM | 2606 | O | THR | 342 | 32.853 | -17.514 | 92.191 | 1.00 | 39.64 |
| | ATOM | 2607 | N | GLY | 343 | 30.625 | -17.568 | 91.894 | 1.00 | 36.81 |

- 106 -

|   | ATOM | 2608 | CA | GLY | 343 | 30.578 | -19.018 | 91.970 | 1.00 | 39.26 |
|---|------|------|-----|-----|-----|--------|---------|--------|------|-------|
|   | ATOM | 2609 | C | GLY | 343 | 29.631 | -19.515 | 93.053 | 1.00 | 38.98 |
|   | ATOM | 2610 | O | GLY | 343 | 29.293 | -20.695 | 93.090 | 1.00 | 39.46 |
|   | ATOM | 2611 | N | ASP | 344 | 29.204 | -18.615 | 93.935 | 1.00 | 38.20 |
| 5 | ATOM | 2612 | CA | ASP | 344 | 28.287 | -18.980 | 95.005 | 1.00 | 39.74 |
|   | ATOM | 2613 | CB | ASP | 344 | 28.480 | -18.071 | 96.231 | 1.00 | 39.14 |
|   | ATOM | 2614 | CG | ASP | 344 | 28.267 | -16.595 | 95.928 | 1.00 | 41.19 |
|   | ATOM | 2615 | OD1 | ASP | 344 | 27.733 | -16.256 | 94.848 | 1.00 | 39.57 |
|   | ATOM | 2616 | OD2 | ASP | 344 | 28.627 | -15.767 | 96.794 | 1.00 | 42.27 |
| 10 | ATOM | 2617 | C | ASP | 344 | 26.842 | -18.926 | 94.516 | 1.00 | 40.25 |
|   | ATOM | 2618 | O | ASP | 344 | 25.904 | -19.235 | 95.257 | 1.00 | 39.36 |
|   | ATOM | 2619 | N | ARG | 345 | 26.680 | -18.525 | 93.259 | 1.00 | 38.45 |
|   | ATOM | 2620 | CA | ARG | 345 | 25.374 | -18.449 | 92.618 | 1.00 | 37.30 |
|   | ATOM | 2621 | CB | ARG | 345 | 24.738 | -19.847 | 92.587 | 1.00 | 37.49 |
| 15 | ATOM | 2622 | CG | ARG | 345 | 25.657 | -20.935 | 92.044 | 1.00 | 38.81 |
|   | ATOM | 2623 | CD | ARG | 345 | 24.976 | -22.301 | 92.046 | 1.00 | 40.19 |
|   | ATOM | 2624 | NE | ARG | 345 | 25.790 | -23.327 | 91.397 | 1.00 | 42.18 |
|   | ATOM | 2625 | CZ | ARG | 345 | 26.730 | -24.051 | 91.999 | 1.00 | 43.19 |
|   | ATOM | 2626 | NH1 | ARG | 345 | 26.990 | -23.880 | 93.288 | 1.00 | 43.31 |
| 20 | ATOM | 2627 | NH2 | ARG | 345 | 27.421 | -24.947 | 91.302 | 1.00 | 40.56 |
|   | ATOM | 2628 | C | ARG | 345 | 24.397 | -17.456 | 93.246 | 1.00 | 37.06 |
|   | ATOM | 2629 | O | ARG | 345 | 23.231 | -17.395 | 92.837 | 1.00 | 35.44 |
|   | ATOM | 2630 | N | LYS | 346 | 24.855 | -16.681 | 94.228 | 1.00 | 37.09 |
|   | ATOM | 2631 | CA | LYS | 346 | 23.977 | -15.704 | 94.876 | 1.00 | 39.61 |
| 25 | ATOM | 2632 | CB | LYS | 346 | 24.710 | -14.964 | 96.005 | 1.00 | 43.18 |
|   | ATOM | 2633 | CG | LYS | 346 | 25.084 | -15.826 | 97.214 | 1.00 | 47.92 |
|   | ATOM | 2634 | CD | LYS | 346 | 25.835 | -15.009 | 98.285 | 1.00 | 50.48 |
|   | ATOM | 2635 | CE | LYS | 346 | 26.274 | -15.887 | 99.466 | 1.00 | 53.20 |
|   | ATOM | 2636 | NZ | LYS | 346 | 27.039 | -15.136 | 100.520 | 1.00 | 54.15 |

- 107 -

|   |      |      |     |     |     |         |         |        |      |        |
|---|------|------|-----|-----|-----|---------|---------|--------|------|--------|
|    | ATOM | 2637 | C   | LYS | 346 | 23.467  | -14.690 | 93.858 | 1.00 | 39.25  |
|    | ATOM | 2638 | O   | LYS | 346 | 22.271  | -14.400 | 93.795 | 1.00 | 38.51  |
|    | ATOM | 2639 | N   | GLN | 347 | 24.384  | -14.158 | 93.055 | 1.00 | 40.01  |
|    | ATOM | 2640 | CA  | GLN | 347 | 24.036  | -13.169 | 92.037 | 1.00 | 39.62  |
| 5  | ATOM | 2641 | CB  | GLN | 347 | 25.301  | -12.725 | 91.290 | 1.00 | 44.30  |
|    | ATOM | 2642 | CG  | GLN | 347 | 25.117  | -11.507 | 90.403 | 1.00 | 50.12  |
|    | ATOM | 2643 | CD  | GLN | 347 | 24.996  | -10.214 | 91.196 | 1.00 | 54.40  |
|    | ATOM | 2644 | OE1 | GLN | 347 | 24.699  | -9.153  | 90.637 | 1.00 | 57.36  |
|    | ATOM | 2645 | NE2 | GLN | 347 | 25.234  | -10.295 | 92.501 | 1.00 | 55.02  |
| 10 | ATOM | 2646 | C   | GLN | 347 | 23.015  | -13.735 | 91.046 | 1.00 | 36.71  |
|    | ATOM | 2647 | O   | GLN | 347 | 22.012  | -13.087 | 90.732 | 1.00 | 35.38  |
|    | ATOM | 2648 | N   | ILE | 348 | 23.264  | -14.949 | 90.563 | 1.00 | 33.61  |
|    | ATOM | 2649 | CA  | ILE | 348 | 22.360  | -15.579 | 89.610 | 1.00 | 30.26  |
|    | ATOM | 2650 | CB  | ILE | 348 | 22.946  | -16.906 | 89.103 | 1.00 | 31.09  |
| 15 | ATOM | 2651 | CG2 | ILE | 348 | 21.983  | -17.561 | 88.102 | 1.00 | 24.14  |
|    | ATOM | 2652 | CG1 | ILE | 348 | 24.315  | -16.641 | 88.467 | 1.00 | 24.89  |
|    | ATOM | 2653 | CD1 | ILE | 348 | 25.016  | -17.870 | 87.989 | 1.00 | 26.20  |
|    | ATOM | 2654 | C   | ILE | 348 | 20.990  | -15.836 | 90.231 | 1.00 | 32.47  |
|    | ATOM | 2655 | O   | ILE | 348 | 19.946  | -15.578 | 89.607 | 1.00 | 28.48  |
| 20 | ATOM | 2656 | N   | TYR | 349 | 20.996  | -16.330 | 91.468 | 1.00 | 33.64  |
|    | ATOM | 2657 | CA  | TYR | 349 | 19.757  | -16.622 | 92.173 | 1.00 | 33.94  |
|    | ATOM | 2658 | CB  | TYR | 349 | 20.023  | -17.189 | 93.566 | 1.00 | 35.19  |
|    | ATOM | 2659 | CG  | TYR | 349 | 18.728  | -17.513 | 94.273 | 1.00 | 35.54  |
|    | ATOM | 2660 | CD1 | TYR | 349 | 18.085  | -18.737 | 94.064 | 1.00 | 35.44  |
| 25 | ATOM | 2661 | CE1 | TYR | 349 | 16.847  | -19.009 | 94.647 | 1.00 | 35.96  |
|    | ATOM | 2662 | CD2 | TYR | 349 | 18.100  | -16.569 | 95.083 | 1.00 | 34.28  |
|    | ATOM | 2663 | CE2 | TYR | 349 | 16.860  | -16.833 | 95.665 | 1.00 | 34.50  |
|    | ATOM | 2664 | CZ  | TYR | 349 | 16.242  | -18.053 | 95.441 | 1.00 | 34.82  |
|    | ATOM | 2665 | OH  | TYR | 349 | 15.007  | -18.305 | 95.990 | 1.00 | 39.44  |

- 108 -

| | ATOM | 2666 | C | TYR | 349 | 18.888 | -15.390 | 92.339 | 1.00 | 35.45 |
|---|------|------|----|-----|-----|--------|---------|--------|------|-------|
| | ATOM | 2667 | O | TYR | 349 | 17.698 | -15.419 | 92.042 | 1.00 | 37.11 |
| | ATOM | 2668 | N | ASN | 350 | 19.475 | -14.312 | 92.846 | 1.00 | 37.18 |
| | ATOM | 2669 | CA | ASN | 350 | 18.722 | -13.082 | 93.049 | 1.00 | 38.47 |
| 5 | ATOM | 2670 | CB | ASN | 350 | 19.617 | -11.985 | 93.630 | 1.00 | 40.65 |
| | ATOM | 2671 | CG | ASN | 350 | 20.014 | -12.263 | 95.065 | 1.00 | 45.75 |
| | ATOM | 2672 | OD1 | ASN | 350 | 19.176 | -12.638 | 95.893 | 1.00 | 45.11 |
| | ATOM | 2673 | ND2 | ASN | 350 | 21.298 | -12.075 | 95.373 | 1.00 | 46.81 |
| | ATOM | 2674 | C | ASN | 350 | 18.085 | -12.585 | 91.768 | 1.00 | 37.56 |
| 10 | ATOM | 2675 | O | ASN | 350 | 16.924 | -12.186 | 91.769 | 1.00 | 40.92 |
| | ATOM | 2676 | N | ILE | 351 | 18.839 | -12.601 | 90.673 | 1.00 | 37.62 |
| | ATOM | 2677 | CA | ILE | 351 | 18.310 | -12.139 | 89.395 | 1.00 | 37.09 |
| | ATOM | 2678 | CB | ILE | 351 | 19.401 | -12.130 | 88.308 | 1.00 | 38.11 |
| | ATOM | 2679 | CG2 | ILE | 351 | 18.771 | -11.955 | 86.938 | 1.00 | 37.56 |
| 15 | ATOM | 2680 | CG1 | ILE | 351 | 20.400 | -11.004 | 88.588 | 1.00 | 38.11 |
| | ATOM | 2681 | CD1 | ILE | 351 | 21.726 | -11.178 | 87.879 | 1.00 | 36.24 |
| | ATOM | 2682 | C | ILE | 351 | 17.144 | -12.997 | 88.921 | 1.00 | 36.57 |
| | ATOM | 2683 | O | ILE | 351 | 16.120 | -12.474 | 88.479 | 1.00 | 38.22 |
| | ATOM | 2684 | N | LEU | 352 | 17.291 | -14.314 | 89.012 | 1.00 | 35.96 |
| 20 | ATOM | 2685 | CA | LEU | 352 | 16.219 | -15.206 | 88.577 | 1.00 | 36.28 |
| | ATOM | 2686 | CB | LEU | 352 | 16.740 | -16.640 | 88.443 | 1.00 | 32.41 |
| | ATOM | 2687 | CG | LEU | 352 | 17.845 | -16.828 | 87.395 | 1.00 | 30.66 |
| | ATOM | 2688 | CD1 | LEU | 352 | 18.465 | -18.226 | 87.496 | 1.00 | 25.83 |
| | ATOM | 2689 | CD2 | LEU | 352 | 17.262 | -16.597 | 86.025 | 1.00 | 27.66 |
| 25 | ATOM | 2690 | C | LEU | 352 | 15.039 | -15.156 | 89.547 | 1.00 | 37.27 |
| | ATOM | 2691 | O | LEU | 352 | 13.896 | -15.356 | 89.145 | 1.00 | 38.32 |
| | ATOM | 2692 | N | SER | 353 | 15.322 | -14.888 | 90.819 | 1.00 | 39.41 |
| | ATOM | 2693 | CA | SER | 353 | 14.279 | -14.794 | 91.838 | 1.00 | 42.13 |
| | ATOM | 2694 | CB | SER | 353 | 14.893 | -14.708 | 93.237 | 1.00 | 43.72 |

- 109 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2695 | OG | SER | 353 | 13. 883 | −14. 546 | 94. 224 | 1. 00 | 48. 17 |
| ATOM | 2696 | C | SER | 353 | 13. 431 | −13. 557 | 91. 590 | 1. 00 | 43. 61 |
| ATOM | 2697 | O | SER | 353 | 12. 229 | −13. 552 | 91. 858 | 1. 00 | 42. 99 |
| ATOM | 2698 | N | THR | 354 | 14. 066 | −12. 506 | 91. 081 | 1. 00 | 44. 80 |
| ATOM | 2699 | CA | THR | 354 | 13. 363 | −11. 267 | 90. 785 | 1. 00 | 46. 06 |
| ATOM | 2700 | CB | THR | 354 | 14. 356 | −10. 122 | 90. 497 | 1. 00 | 47. 48 |
| ATOM | 2701 | OG1 | THR | 354 | 15. 100 | −9. 820 | 91. 687 | 1. 00 | 47. 39 |
| ATOM | 2702 | CG2 | THR | 354 | 13. 615 | −8. 877 | 90. 034 | 1. 00 | 47. 87 |
| ATOM | 2703 | C | THR | 354 | 12. 446 | −11. 455 | 89. 579 | 1. 00 | 46. 06 |
| ATOM | 2704 | O | THR | 354 | 11. 443 | −10. 757 | 89. 436 | 1. 00 | 47. 23 |
| ATOM | 2705 | N | LEU | 355 | 12. 788 | −12. 406 | 88. 717 | 1. 00 | 46. 03 |
| ATOM | 2706 | CA | LEU | 355 | 11. 983 | −12. 679 | 87. 533 | 1. 00 | 46. 26 |
| ATOM | 2707 | CB | LEU | 355 | 12. 875 | −13. 157 | 86. 390 | 1. 00 | 46. 43 |
| ATOM | 2708 | CG | LEU | 355 | 14. 030 | −12. 210 | 86. 063 | 1. 00 | 46. 85 |
| ATOM | 2709 | CD1 | LEU | 355 | 14. 861 | −12. 813 | 84. 950 | 1. 00 | 47. 00 |
| ATOM | 2710 | CD2 | LEU | 355 | 13. 497 | −10. 844 | 85. 660 | 1. 00 | 45. 99 |
| ATOM | 2711 | C | LEU | 355 | 10. 908 | −13. 722 | 87. 821 | 1. 00 | 46. 88 |
| ATOM | 2712 | O | LEU | 355 | 10. 370 | −14. 346 | 86. 902 | 1. 00 | 47. 28 |
| ATOM | 2713 | N | GLY | 356 | 10. 609 | −13. 912 | 89. 105 | 1. 00 | 47. 29 |
| ATOM | 2714 | CA | GLY | 356 | 9. 586 | −14. 858 | 89. 511 | 1. 00 | 44. 74 |
| ATOM | 2715 | C | GLY | 356 | 9. 959 | −16. 321 | 89. 396 | 1. 00 | 44. 45 |
| ATOM | 2716 | O | GLY | 356 | 9. 097 | −17. 163 | 89. 146 | 1. 00 | 45. 09 |
| ATOM | 2717 | N | LEU | 357 | 11. 235 | −16. 635 | 89. 575 | 1. 00 | 43. 26 |
| ATOM | 2718 | CA | LEU | 357 | 11. 681 | −18. 018 | 89. 485 | 1. 00 | 41. 29 |
| ATOM | 2719 | CB | LEU | 357 | 12. 653 | −18. 187 | 88. 310 | 1. 00 | 42. 15 |
| ATOM | 2720 | CG | LEU | 357 | 12. 171 | −17. 833 | 86. 896 | 1. 00 | 41. 21 |
| ATOM | 2721 | CD1 | LEU | 357 | 13. 366 | −17. 781 | 85. 972 | 1. 00 | 39. 61 |
| ATOM | 2722 | CD2 | LEU | 357 | 11. 153 | −18. 849 | 86. 393 | 1. 00 | 39. 50 |
| ATOM | 2723 | C | LEU | 357 | 12. 361 | −18. 455 | 90. 780 | 1. 00 | 40. 57 |

- 110 -

| | ATOM | 2724 | O | LEU | 357 | 12.780 | -17.627 | 91.590 | 1.00 | 38.53 |
|---|------|------|------|-----|-----|--------|---------|--------|------|-------|
| | ATOM | 2725 | N | ARG | 358 | 12.448 | -19.766 | 90.970 | 1.00 | 39.68 |
| | ATOM | 2726 | CA | ARG | 358 | 13.092 | -20.355 | 92.139 | 1.00 | 40.04 |
| | ATOM | 2727 | CB | ARG | 358 | 12.048 | -20.916 | 93.112 | 1.00 | 42.61 |
| 5 | ATOM | 2728 | CG | ARG | 358 | 11.172 | -19.845 | 93.760 | 1.00 | 46.08 |
| | ATOM | 2729 | CD | ARG | 358 | 12.019 | -18.871 | 94.560 | 1.00 | 49.74 |
| | ATOM | 2730 | NE | ARG | 358 | 11.355 | -17.588 | 94.772 | 1.00 | 55.41 |
| | ATOM | 2731 | CZ | ARG | 358 | 10.588 | -17.293 | 95.816 | 1.00 | 58.08 |
| | ATOM | 2732 | NH1 | ARG | 358 | 10.376 | -18.195 | 96.771 | 1.00 | 59.09 |
| 10 | ATOM | 2733 | NH2 | ARG | 358 | 10.035 | -16.087 | 95.906 | 1.00 | 58.98 |
| | ATOM | 2734 | C | ARG | 358 | 13.954 | -21.471 | 91.576 | 1.00 | 38.39 |
| | ATOM | 2735 | O | ARG | 358 | 13.569 | -22.641 | 91.586 | 1.00 | 37.47 |
| | ATOM | 2736 | N | PRO | 359 | 15.140 | -21.109 | 91.065 | 1.00 | 36.51 |
| | ATOM | 2737 | CD | PRO | 359 | 15.664 | -19.728 | 91.087 | 1.00 | 36.88 |
| 15 | ATOM | 2738 | CA | PRO | 359 | 16.123 | -22.006 | 90.461 | 1.00 | 34.17 |
| | ATOM | 2739 | CB | PRO | 359 | 17.035 | -21.039 | 89.722 | 1.00 | 35.29 |
| | ATOM | 2740 | CG | PRO | 359 | 17.135 | -19.925 | 90.703 | 1.00 | 34.03 |
| | ATOM | 2741 | C | PRO | 359 | 16.915 | -22.872 | 91.416 | 1.00 | 33.10 |
| | ATOM | 2742 | O | PRO | 359 | 17.140 | -22.520 | 92.566 | 1.00 | 31.20 |
| 20 | ATOM | 2743 | N | SER | 360 | 17.365 | -24.004 | 90.899 | 1.00 | 33.97 |
| | ATOM | 2744 | CA | SER | 360 | 18.183 | -24.931 | 91.658 | 1.00 | 34.21 |
| | ATOM | 2745 | CB | SER | 360 | 17.912 | -26.363 | 91.210 | 1.00 | 34.53 |
| | ATOM | 2746 | OG | SER | 360 | 18.287 | -26.530 | 89.851 | 1.00 | 33.54 |
| | ATOM | 2747 | C | SER | 360 | 19.618 | -24.568 | 91.307 | 1.00 | 34.99 |
| 25 | ATOM | 2748 | O | SER | 360 | 19.855 | -23.673 | 90.495 | 1.00 | 35.49 |
| | ATOM | 2749 | N | THR | 361 | 20.564 | -25.267 | 91.920 | 1.00 | 34.70 |
| | ATOM | 2750 | CA | THR | 361 | 21.977 | -25.048 | 91.673 | 1.00 | 36.89 |
| | ATOM | 2751 | CB | THR | 361 | 22.838 | -26.003 | 92.535 | 1.00 | 36.99 |
| | ATOM | 2752 | OG1 | THR | 361 | 22.828 | -25.558 | 93.898 | 1.00 | 38.93 |

- 111 -

| | ATOM | 2753 | CG2 | THR | 361 | 24. 260 | -26. 041 | 92. 033 | 1. 00 | 38. 24 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2754 | C | THR | 361 | 22. 303 | -25. 291 | 90. 201 | 1. 00 | 37. 14 |
| | ATOM | 2755 | 0 | THR | 361 | 23. 142 | -24. 606 | 89. 616 | 1. 00 | 37. 81 |
| | ATOM | 2756 | N | THR | 362 | 21. 635 | -26. 273 | 89. 612 | 1. 00 | 35. 92 |
| 5 | ATOM | 2757 | CA | THR | 362 | 21. 865 | -26. 614 | 88. 223 | 1. 00 | 34. 91 |
| | ATOM | 2758 | CB | THR | 362 | 21. 369 | -28. 037 | 87. 914 | 1. 00 | 36. 12 |
| | ATOM | 2759 | OG1 | THR | 362 | 19. 969 | -28. 117 | 88. 199 | 1. 00 | 40. 45 |
| | ATOM | 2760 | CG2 | THR | 362 | 22. 113 | -29. 063 | 88. 771 | 1. 00 | 34. 62 |
| | ATOM | 2761 | C | THR | 362 | 21. 181 | -25. 626 | 87. 292 | 1. 00 | 33. 53 |
| 10 | ATOM | 2762 | 0 | THR | 362 | 21. 684 | -25. 360 | 86. 205 | 1. 00 | 33. 46 |
| | ATOM | 2763 | N | ASP | 363 | 20. 034 | -25. 091 | 87. 698 | 1. 00 | 31. 06 |
| | ATOM | 2764 | CA | ASP | 363 | 19. 355 | -24. 115 | 86. 860 | 1. 00 | 32. 46 |
| | ATOM | 2765 | CB | ASP | 363 | 18. 018 | -23. 690 | 87. 468 | 1. 00 | 34. 45 |
| | ATOM | 2766 | CG | ASP | 363 | 16. 964 | -24. 783 | 87. 409 | 1. 00 | 37. 91 |
| 15 | ATOM | 2767 | OD1 | ASP | 363 | 16. 889 | -25. 504 | 86. 388 | 1. 00 | 38. 99 |
| | ATOM | 2768 | OD2 | ASP | 363 | 16. 194 | -24. 907 | 88. 385 | 1. 00 | 38. 23 |
| | ATOM | 2769 | C | ASP | 363 | 20. 254 | -22. 878 | 86. 718 | 1. 00 | 32. 88 |
| | ATOM | 2770 | 0 | ASP | 363 | 20. 419 | -22. 331 | 85. 629 | 1. 00 | 30. 65 |
| | ATOM | 2771 | N | CYS | 364 | 20. 833 | -22. 451 | 87. 836 | 1. 00 | 33. 86 |
| 20 | ATOM | 2772 | CA | CYS | 364 | 21. 712 | -21. 292 | 87. 860 | 1. 00 | 32. 22 |
| | ATOM | 2773 | CB | CYS | 364 | 22. 186 | -21. 015 | 89. 289 | 1. 00 | 31. 35 |
| | ATOM | 2774 | SG | CYS | 364 | 20. 915 | -20. 338 | 90. 389 | 1. 00 | 31. 77 |
| | ATOM | 2775 | C | CYS | 364 | 22. 914 | -21. 493 | 86. 950 | 1. 00 | 30. 91 |
| | ATOM | 2776 | 0 | CYS | 364 | 23. 207 | -20. 645 | 86. 119 | 1. 00 | 30. 71 |
| 25 | ATOM | 2777 | N | ASP | 365 | 23. 608 | -22. 614 | 87. 107 | 1. 00 | 31. 25 |
| | ATOM | 2778 | CA | ASP | 365 | 24. 774 | -22. 894 | 86. 280 | 1. 00 | 32. 00 |
| | ATOM | 2779 | CB | ASP | 365 | 25. 389 | -24. 243 | 86. 659 | 1. 00 | 32. 78 |
| | ATOM | 2780 | CG | ASP | 365 | 26. 037 | -24. 211 | 88. 023 | 1. 00 | 35. 48 |
| | ATOM | 2781 | OD1 | ASP | 365 | 26. 017 | -23. 127 | 88. 650 | 1. 00 | 37. 01 |

- 112 -

|   | ATOM | 2782 | OD2 | ASP | 365 | 26.564 | -25.251 | 88.466 | 1.00 | 35.21 |
|---|------|------|-----|-----|-----|--------|---------|--------|------|-------|
|   | ATOM | 2783 | C   | ASP | 365 | 24.405 | -22.886 | 84.810 | 1.00 | 30.41 |
|   | ATOM | 2784 | O   | ASP | 365 | 25.166 | -22.407 | 83.966 | 1.00 | 31.73 |
|   | ATOM | 2785 | N   | ILE | 366 | 23.225 | -23.408 | 84.514 | 1.00 | 29.17 |
| 5 | ATOM | 2786 | CA  | ILE | 366 | 22.739 | -23.462 | 83.148 | 1.00 | 30.58 |
|   | ATOM | 2787 | CB  | ILE | 366 | 21.456 | -24.318 | 83.058 | 1.00 | 30.61 |
|   | ATOM | 2788 | CG2 | ILE | 366 | 20.779 | -24.118 | 81.712 | 1.00 | 28.15 |
|   | ATOM | 2789 | CG1 | ILE | 366 | 21.808 | -25.797 | 83.261 | 1.00 | 33.09 |
|   | ATOM | 2790 | CD1 | ILE | 366 | 20.577 | -26.702 | 83.405 | 1.00 | 32.69 |
| 10 | ATOM | 2791 | C   | ILE | 366 | 22.462 | -22.066 | 82.576 | 1.00 | 29.08 |
|   | ATOM | 2792 | O   | ILE | 366 | 22.729 | -21.815 | 81.405 | 1.00 | 28.78 |
|   | ATOM | 2793 | N   | VAL | 367 | 21.906 | -21.170 | 83.386 | 1.00 | 27.52 |
|   | ATOM | 2794 | CA  | VAL | 367 | 21.632 | -19.817 | 82.910 | 1.00 | 27.71 |
|   | ATOM | 2795 | CB  | VAL | 367 | 20.803 | -19.021 | 83.943 | 1.00 | 26.66 |
| 15 | ATOM | 2796 | CG1 | VAL | 367 | 20.812 | -17.531 | 83.609 | 1.00 | 24.57 |
|   | ATOM | 2797 | CG2 | VAL | 367 | 19.373 | -19.535 | 83.928 | 1.00 | 26.09 |
|   | ATOM | 2798 | C   | VAL | 367 | 22.979 | -19.143 | 82.643 | 1.00 | 28.05 |
|   | ATOM | 2799 | O   | VAL | 367 | 23.144 | -18.409 | 81.670 | 1.00 | 28.53 |
|   | ATOM | 2800 | N   | ARG | 368 | 23.940 | -19.436 | 83.508 | 1.00 | 27.74 |
| 20 | ATOM | 2801 | CA  | ARG | 368 | 25.300 | -18.927 | 83.386 | 1.00 | 30.76 |
|   | ATOM | 2802 | CB  | ARG | 368 | 26.172 | -19.575 | 84.458 | 1.00 | 31.66 |
|   | ATOM | 2803 | CG  | ARG | 368 | 27.023 | -18.648 | 85.269 | 1.00 | 38.26 |
|   | ATOM | 2804 | CD  | ARG | 368 | 28.312 | -18.282 | 84.579 | 1.00 | 41.00 |
|   | ATOM | 2805 | NE  | ARG | 368 | 29.272 | -17.763 | 85.547 | 1.00 | 43.72 |
| 25 | ATOM | 2806 | CZ  | ARG | 368 | 30.397 | -17.135 | 85.226 | 1.00 | 46.75 |
|   | ATOM | 2807 | NH1 | ARG | 368 | 30.710 | -16.938 | 83.954 | 1.00 | 48.06 |
|   | ATOM | 2808 | NH2 | ARG | 368 | 31.212 | -16.708 | 86.179 | 1.00 | 47.96 |
|   | ATOM | 2809 | C   | ARG | 368 | 25.841 | -19.317 | 82.003 | 1.00 | 30.63 |
|   | ATOM | 2810 | O   | ARG | 368 | 26.343 | -18.469 | 81.256 | 1.00 | 27.84 |

- 113 -

| | ATOM | 2811 | N | ARG | 369 | 25. 735 | -20. 606 | 81. 677 | 1. 00 | 27. 70 |
|---|------|------|-----|-----|-----|---------|----------|---------|-------|--------|
| | ATOM | 2812 | CA | ARG | 369 | 26. 228 | -21. 115 | 80. 399 | 1. 00 | 28. 24 |
| | ATOM | 2813 | CB | ARG | 369 | 26. 077 | -22. 645 | 80. 327 | 1. 00 | 26. 69 |
| | ATOM | 2814 | CG | ARG | 369 | 27. 044 | -23. 429 | 81. 224 | 1. 00 | 29. 04 |
| 5 | ATOM | 2815 | CD | ARG | 369 | 28. 506 | -23. 228 | 80. 815 | 1. 00 | 31. 91 |
| | ATOM | 2816 | NE | ARG | 369 | 28. 752 | -23. 683 | 79. 445 | 1. 00 | 35. 74 |
| | ATOM | 2817 | CZ | ARG | 369 | 29. 117 | -22. 892 | 78. 439 | 1. 00 | 36. 75 |
| | ATOM | 2818 | NH1 | ARG | 369 | 29. 291 | -21. 590 | 78. 638 | 1. 00 | 36. 65 |
| | ATOM | 2819 | NH2 | ARG | 369 | 29. 291 | -23. 400 | 77. 225 | 1. 00 | 36. 11 |
| 10 | ATOM | 2820 | C | ARG | 369 | 25. 528 | -20. 472 | 79. 208 | 1. 00 | 27. 14 |
| | ATOM | 2821 | O | ARG | 369 | 26. 160 | -20. 188 | 78. 189 | 1. 00 | 28. 06 |
| | ATOM | 2822 | N | ALA | 370 | 24. 224 | -20. 252 | 79. 327 | 1. 00 | 25. 64 |
| | ATOM | 2823 | CA | ALA | 370 | 23. 480 | -19. 634 | 78. 238 | 1. 00 | 25. 08 |
| | ATOM | 2824 | CB | ALA | 370 | 21. 991 | -19. 587 | 78. 574 | 1. 00 | 25. 47 |
| 15 | ATOM | 2825 | C | ALA | 370 | 24. 015 | -18. 218 | 78. 006 | 1. 00 | 25. 14 |
| | ATOM | 2826 | O | ALA | 370 | 24. 196 | -17. 793 | 76. 870 | 1. 00 | 25. 23 |
| | ATOM | 2827 | N | CYS | 371 | 24. 268 | -17. 491 | 79. 087 | 1. 00 | 24. 15 |
| | ATOM | 2828 | CA | CYS | 371 | 24. 785 | -16. 135 | 78. 965 | 1. 00 | 25. 09 |
| | ATOM | 2829 | CB | CYS | 371 | 24. 855 | -15. 467 | 80. 338 | 1. 00 | 22. 74 |
| 20 | ATOM | 2830 | SG | CYS | 371 | 23. 239 | -15. 076 | 81. 033 | 1. 00 | 25. 40 |
| | ATOM | 2831 | C | CYS | 371 | 26. 161 | -16. 127 | 78. 300 | 1. 00 | 24. 93 |
| | ATOM | 2832 | O | CYS | 371 | 26. 392 | -15. 358 | 77. 367 | 1. 00 | 25. 49 |
| | ATOM | 2833 | N | GLU | 372 | 27. 062 | -16. 991 | 78. 765 | 1. 00 | 24. 70 |
| | ATOM | 2834 | CA | GLU | 372 | 28. 411 | -17. 073 | 78. 207 | 1. 00 | 26. 69 |
| 25 | ATOM | 2835 | CB | GLU | 372 | 29. 247 | -18. 105 | 78. 975 | 1. 00 | 27. 07 |
| | ATOM | 2836 | CG | GLU | 372 | 29. 232 | -17. 890 | 80. 481 | 1. 00 | 32. 77 |
| | ATOM | 2837 | CD | GLU | 372 | 30. 016 | -18. 945 | 81. 243 | 1. 00 | 33. 87 |
| | ATOM | 2838 | OE1 | GLU | 372 | 29. 905 | -20. 139 | 80. 892 | 1. 00 | 36. 95 |
| | ATOM | 2839 | OE2 | GLU | 372 | 30. 733 | -18. 583 | 82. 200 | 1. 00 | 35. 18 |

- 114 -

| | ATOM | 2840 | C | GLU | 372 | 28. 418 | -17. 420 | 76. 718 | 1. 00 | 27. 23 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2841 | O | GLU | 372 | 29. 259 | -16. 922 | 75. 966 | 1. 00 | 29. 09 |
| | ATOM | 2842 | N | SER | 373 | 27. 489 | -18. 273 | 76. 296 | 1. 00 | 25. 93 |
| | ATOM | 2843 | CA | SER | 373 | 27. 403 | -18. 664 | 74. 894 | 1. 00 | 27. 07 |
| 5 | ATOM | 2844 | CB | SER | 373 | 26. 393 | -19. 803 | 74. 718 | 1. 00 | 25. 93 |
| | ATOM | 2845 | OG | SER | 373 | 26. 784 | -20. 951 | 75. 457 | 1. 00 | 32. 56 |
| | ATOM | 2846 | C | SER | 373 | 26. 988 | -17. 471 | 74. 034 | 1. 00 | 25. 31 |
| | ATOM | 2847 | O | SER | 373 | 27. 585 | -17. 207 | 72. 998 | 1. 00 | 24. 49 |
| | ATOM | 2848 | N | VAL | 374 | 25. 962 | -16. 754 | 74. 475 | 1. 00 | 25. 87 |
| 10 | ATOM | 2849 | CA | VAL | 374 | 25. 473 | -15. 596 | 73. 743 | 1. 00 | 25. 12 |
| | ATOM | 2850 | CB | VAL | 374 | 24. 139 | -15. 103 | 74. 319 | 1. 00 | 26. 07 |
| | ATOM | 2851 | CG1 | VAL | 374 | 23. 754 | -13. 766 | 73. 682 | 1. 00 | 29. 29 |
| | ATOM | 2852 | CG2 | VAL | 374 | 23. 055 | -16. 127 | 74. 061 | 1. 00 | 25. 56 |
| | ATOM | 2853 | C | VAL | 374 | 26. 465 | -14. 429 | 73. 742 | 1. 00 | 24. 54 |
| 15 | ATOM | 2854 | O | VAL | 374 | 26. 657 | -13. 792 | 72. 714 | 1. 00 | 25. 64 |
| | ATOM | 2855 | N | SER | 375 | 27. 094 | -14. 144 | 74. 878 | 1. 00 | 21. 70 |
| | ATOM | 2856 | CA | SER | 375 | 28. 029 | -13. 034 | 74. 922 | 1. 00 | 23. 89 |
| | ATOM | 2857 | CB | SER | 375 | 28. 298 | -12. 585 | 76. 365 | 1. 00 | 23. 28 |
| | ATOM | 2858 | OG | SER | 375 | 28. 986 | -13. 565 | 77. 120 | 1. 00 | 29. 71 |
| 20 | ATOM | 2859 | C | SER | 375 | 29. 324 | -13. 391 | 74. 210 | 1. 00 | 24. 77 |
| | ATOM | 2860 | O | SER | 375 | 29. 873 | -12. 560 | 73. 490 | 1. 00 | 23. 61 |
| | ATOM | 2861 | N | THR | 376 | 29. 805 | -14. 623 | 74. 386 | 1. 00 | 23. 54 |
| | ATOM | 2862 | CA | THR | 376 | 31. 029 | -15. 052 | 73. 707 | 1. 00 | 23. 38 |
| | ATOM | 2863 | CB | THR | 376 | 31. 444 | -16. 501 | 74. 096 | 1. 00 | 23. 76 |
| 25 | ATOM | 2864 | OG1 | THR | 376 | 31. 874 | -16. 527 | 75. 458 | 1. 00 | 26. 36 |
| | ATOM | 2865 | CG2 | THR | 376 | 32. 594 | -16. 987 | 73. 222 | 1. 00 | 21. 48 |
| | ATOM | 2866 | C | THR | 376 | 30. 859 | -14. 996 | 72. 189 | 1. 00 | 22. 33 |
| | ATOM | 2867 | O | THR | 376 | 31. 810 | -14. 694 | 71. 465 | 1. 00 | 23. 88 |
| | ATOM | 2868 | N | ARG | 377 | 29. 660 | -15. 293 | 71. 695 | 1. 00 | 20. 80 |

| | ATOM | 2869 | CA | ARG | 377 | 29. 452 | -15. 239 | 70. 253 | 1. 00 | 21. 46 |
|---|------|------|-----|-----|-----|---------|----------|---------|-------|--------|
| | ATOM | 2870 | CB | ARG | 377 | 28. 141 | -15. 918 | 69. 839 | 1. 00 | 22. 21 |
| | ATOM | 2871 | CG | ARG | 377 | 27. 958 | -15. 875 | 68. 312 | 1. 00 | 25. 01 |
| | ATOM | 2872 | CD | ARG | 377 | 26. 601 | -16. 377 | 67. 827 | 1. 00 | 27. 70 |
| 5 | ATOM | 2873 | NE | ARG | 377 | 25. 491 | -15. 558 | 68. 302 | 1. 00 | 25. 17 |
| | ATOM | 2874 | CZ | ARG | 377 | 24. 255 | -15. 637 | 67. 825 | 1. 00 | 26. 42 |
| | ATOM | 2875 | NH1 | ARG | 377 | 23. 973 | -16. 492 | 66. 850 | 1. 00 | 25. 23 |
| | ATOM | 2876 | NH2 | ARG | 377 | 23. 294 | -14. 877 | 68. 339 | 1. 00 | 26. 96 |
| | ATOM | 2877 | C | ARG | 377 | 29. 439 | -13. 773 | 69. 787 | 1. 00 | 21. 55 |
| 10 | ATOM | 2878 | O | ARG | 377 | 29. 856 | -13. 462 | 68. 670 | 1. 00 | 20. 80 |
| | ATOM | 2879 | N | ALA | 378 | 28. 951 | -12. 879 | 70. 639 | 1. 00 | 19. 46 |
| | ATOM | 2880 | CA | ALA | 378 | 28. 927 | -11. 463 | 70. 302 | 1. 00 | 21. 17 |
| | ATOM | 2881 | CB | ALA | 378 | 28. 239 | -10. 653 | 71. 412 | 1. 00 | 20. 68 |
| | ATOM | 2882 | C | ALA | 378 | 30. 374 | -11. 015 | 70. 151 | 1. 00 | 20. 18 |
| 15 | ATOM | 2883 | O | ALA | 378 | 30. 747 | -10. 420 | 69. 145 | 1. 00 | 20. 36 |
| | ATOM | 2884 | N | ALA | 379 | 31. 191 | -11. 326 | 71. 153 | 1. 00 | 19. 41 |
| | ATOM | 2885 | CA | ALA | 379 | 32. 600 | -10. 950 | 71. 138 | 1. 00 | 20. 64 |
| | ATOM | 2886 | CB | ALA | 379 | 33. 296 | -11. 515 | 72. 371 | 1. 00 | 20. 04 |
| | ATOM | 2887 | C | ALA | 379 | 33. 332 | -11. 405 | 69. 869 | 1. 00 | 22. 79 |
| 20 | ATOM | 2888 | O | ALA | 379 | 34. 054 | -10. 620 | 69. 234 | 1. 00 | 21. 82 |
| | ATOM | 2889 | N | HIS | 380 | 33. 139 | -12. 666 | 69. 489 | 1. 00 | 22. 45 |
| | ATOM | 2890 | CA | HIS | 380 | 33. 803 | -13. 208 | 68. 305 | 1. 00 | 22. 78 |
| | ATOM | 2891 | CB | HIS | 380 | 33. 726 | -14. 745 | 68. 314 | 1. 00 | 22. 80 |
| | ATOM | 2892 | CG | HIS | 380 | 34. 584 | -15. 384 | 69. 364 | 1. 00 | 26. 52 |
| 25 | ATOM | 2893 | CD2 | HIS | 380 | 35. 557 | -14. 870 | 70. 152 | 1. 00 | 27. 81 |
| | ATOM | 2894 | ND1 | HIS | 380 | 34. 499 | -16. 720 | 69. 687 | 1. 00 | 28. 99 |
| | ATOM | 2895 | CE1 | HIS | 380 | 35. 383 | -17. 002 | 70. 627 | 1. 00 | 28. 15 |
| | ATOM | 2896 | NE2 | HIS | 380 | 36. 039 | -15. 896 | 70. 927 | 1. 00 | 28. 70 |
| | ATOM | 2897 | C | HIS | 380 | 33. 242 | -12. 657 | 66. 994 | 1. 00 | 22. 38 |

- 116 -

|   | ATOM | 2898 | O | HIS | 380 | 33.988 | -12.368 | 66.073 | 1.00 | 20.71 |
|---|------|------|------|-----|-----|--------|---------|--------|------|-------|
|   | ATOM | 2899 | N | MET | 381 | 31.926 | -12.524 | 66.915 | 1.00 | 23.83 |
|   | ATOM | 2900 | CA | MET | 381 | 31.285 | -12.018 | 65.713 | 1.00 | 26.66 |
|   | ATOM | 2901 | CB | MET | 381 | 29.760 | -12.086 | 65.899 | 1.00 | 29.06 |
| 5 | ATOM | 2902 | CG | MET | 381 | 28.926 | -12.031 | 64.622 | 1.00 | 34.34 |
|   | ATOM | 2903 | SD | MET | 381 | 29.456 | -13.157 | 63.312 | 1.00 | 33.69 |
|   | ATOM | 2904 | CE | MET | 381 | 28.228 | -14.472 | 63.429 | 1.00 | 34.64 |
|   | ATOM | 2905 | C | MET | 381 | 31.781 | -10.580 | 65.509 | 1.00 | 27.50 |
|   | ATOM | 2906 | O | MET | 381 | 32.153 | -10.188 | 64.406 | 1.00 | 26.70 |
| 10 | ATOM | 2907 | N | CYS | 382 | 31.830 | -9.813 | 66.595 | 1.00 | 26.32 |
|   | ATOM | 2908 | CA | CYS | 382 | 32.302 | -8.441 | 66.536 | 1.00 | 24.87 |
|   | ATOM | 2909 | CB | CYS | 382 | 32.102 | -7.769 | 67.896 | 1.00 | 26.05 |
|   | ATOM | 2910 | SG | CYS | 382 | 32.389 | -5.962 | 67.931 | 1.00 | 26.70 |
|   | ATOM | 2911 | C | CYS | 382 | 33.785 | -8.355 | 66.122 | 1.00 | 24.60 |
| 15 | ATOM | 2912 | O | CYS | 382 | 34.187 | -7.457 | 65.360 | 1.00 | 19.92 |
|   | ATOM | 2913 | N | SER | 383 | 34.590 | -9.288 | 66.623 | 1.00 | 22.62 |
|   | ATOM | 2914 | CA | SER | 383 | 36.017 | -9.302 | 66.327 | 1.00 | 22.35 |
|   | ATOM | 2915 | CB | SER | 383 | 36.716 | -10.439 | 67.096 | 1.00 | 23.03 |
|   | ATOM | 2916 | OG | SER | 383 | 36.361 | -11.712 | 66.571 | 1.00 | 24.25 |
| 20 | ATOM | 2917 | C | SER | 383 | 36.272 | -9.463 | 64.834 | 1.00 | 23.77 |
|   | ATOM | 2918 | O | SER | 383 | 37.202 | -8.875 | 64.288 | 1.00 | 24.79 |
|   | ATOM | 2919 | N | ALA | 384 | 35.448 | -10.269 | 64.173 | 1.00 | 24.03 |
|   | ATOM | 2920 | CA | ALA | 384 | 35.612 | -10.480 | 62.743 | 1.00 | 25.52 |
|   | ATOM | 2921 | CB | ALA | 384 | 34.649 | -11.552 | 62.256 | 1.00 | 22.05 |
| 25 | ATOM | 2922 | C | ALA | 384 | 35.369 | -9.182 | 61.980 | 1.00 | 25.61 |
|   | ATOM | 2923 | O | ALA | 384 | 35.990 | -8.942 | 60.947 | 1.00 | 25.37 |
|   | ATOM | 2924 | N | GLY | 385 | 34.450 | -8.360 | 62.490 | 1.00 | 25.67 |
|   | ATOM | 2925 | CA | GLY | 385 | 34.134 | -7.098 | 61.842 | 1.00 | 23.86 |
|   | ATOM | 2926 | C | GLY | 385 | 35.289 | -6.128 | 61.944 | 1.00 | 20.99 |

- 117 -

|    | ATOM | 2927 | O   | GLY | 385 | 35.702 | -5.531 | 60.960 | 1.00 | 22.47 |
|----|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|    | ATOM | 2928 | N   | LEU | 386 | 35.811 | -5.962 | 63.148 | 1.00 | 22.82 |
|    | ATOM | 2929 | CA  | LEU | 386 | 36.937 | -5.065 | 63.364 | 1.00 | 25.33 |
|    | ATOM | 2930 | CB  | LEU | 386 | 37.259 | -4.971 | 64.850 | 1.00 | 23.48 |
| 5  | ATOM | 2931 | CG  | LEU | 386 | 37.800 | -3.658 | 65.425 | 1.00 | 27.75 |
|    | ATOM | 2932 | CD1 | LEU | 386 | 38.641 | -4.007 | 66.641 | 1.00 | 26.18 |
|    | ATOM | 2933 | CD2 | LEU | 386 | 38.621 | -2.865 | 64.428 | 1.00 | 25.52 |
|    | ATOM | 2934 | C   | LEU | 386 | 38.172 | -5.584 | 62.616 | 1.00 | 26.01 |
|    | ATOM | 2935 | O   | LEU | 386 | 38.953 | -4.794 | 62.067 | 1.00 | 26.60 |
| 10 | ATOM | 2936 | N   | ALA | 387 | 38.356 | -6.904 | 62.601 | 1.00 | 23.95 |
|    | ATOM | 2937 | CA  | ALA | 387 | 39.509 | -7.482 | 61.902 | 1.00 | 24.13 |
|    | ATOM | 2938 | CB  | ALA | 387 | 39.585 | -8.989 | 62.135 | 1.00 | 20.59 |
|    | ATOM | 2939 | C   | ALA | 387 | 39.405 | -7.181 | 60.411 | 1.00 | 24.07 |
|    | ATOM | 2940 | O   | ALA | 387 | 40.419 | -6.990 | 59.730 | 1.00 | 22.59 |
| 15 | ATOM | 2941 | N   | GLY | 388 | 38.175 | -7.141 | 59.904 | 1.00 | 24.30 |
|    | ATOM | 2942 | CA  | GLY | 388 | 37.975 | -6.838 | 58.497 | 1.00 | 24.40 |
|    | ATOM | 2943 | C   | GLY | 388 | 38.380 | -5.398 | 58.203 | 1.00 | 25.62 |
|    | ATOM | 2944 | O   | GLY | 388 | 39.048 | -5.114 | 57.205 | 1.00 | 25.24 |
|    | ATOM | 2945 | N   | VAL | 389 | 37.974 | -4.488 | 59.084 | 1.00 | 25.15 |
| 20 | ATOM | 2946 | CA  | VAL | 389 | 38.294 | -3.072 | 58.950 | 1.00 | 23.08 |
|    | ATOM | 2947 | CB  | VAL | 389 | 37.581 | -2.259 | 60.057 | 1.00 | 21.38 |
|    | ATOM | 2948 | CG1 | VAL | 389 | 38.083 | -0.820 | 60.076 | 1.00 | 21.90 |
|    | ATOM | 2949 | CG2 | VAL | 389 | 36.078 | -2.303 | 59.819 | 1.00 | 20.64 |
|    | ATOM | 2950 | C   | VAL | 389 | 39.802 | -2.858 | 59.034 | 1.00 | 24.13 |
| 25 | ATOM | 2951 | O   | VAL | 389 | 40.402 | -2.198 | 58.178 | 1.00 | 25.99 |
|    | ATOM | 2952 | N   | ILE | 390 | 40.424 | -3.429 | 60.054 | 1.00 | 24.21 |
|    | ATOM | 2953 | CA  | ILE | 390 | 41.866 | -3.289 | 60.209 | 1.00 | 25.31 |
|    | ATOM | 2954 | CB  | ILE | 390 | 42.317 | -3.883 | 61.576 | 1.00 | 25.21 |
|    | ATOM | 2955 | CG2 | ILE | 390 | 43.831 | -3.962 | 61.661 | 1.00 | 27.92 |

- 118 -

| | ATOM | 2956 | CG1 | ILE | 390 | 41.778 | -2.993 | 62.708 | 1.00 | 26.03 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2957 | CD1 | ILE | 390 | 42.091 | -3.476 | 64.094 | 1.00 | 27.41 |
| | ATOM | 2958 | C | ILE | 390 | 42.668 | -3.899 | 59.040 | 1.00 | 26.27 |
| | ATOM | 2959 | O | ILE | 390 | 43.622 | -3.287 | 58.563 | 1.00 | 25.08 |
| 5 | ATOM | 2960 | N | ASN | 391 | 42.286 | -5.082 | 58.561 | 1.00 | 27.72 |
| | ATOM | 2961 | CA | ASN | 391 | 43.026 | -5.689 | 57.448 | 1.00 | 29.87 |
| | ATOM | 2962 | CB | ASN | 391 | 42.649 | -7.162 | 57.250 | 1.00 | 27.74 |
| | ATOM | 2963 | CG | ASN | 391 | 43.147 | -8.044 | 58.375 | 1.00 | 29.54 |
| | ATOM | 2964 | OD1 | ASN | 391 | 44.216 | -7.804 | 58.939 | 1.00 | 28.68 |
| 10 | ATOM | 2965 | ND2 | ASN | 391 | 42.383 | -9.079 | 58.699 | 1.00 | 26.84 |
| | ATOM | 2966 | C | ASN | 391 | 42.805 | -4.930 | 56.144 | 1.00 | 31.14 |
| | ATOM | 2967 | O | ASN | 391 | 43.688 | -4.903 | 55.281 | 1.00 | 29.49 |
| | ATOM | 2968 | N | ARG | 392 | 41.627 | -4.331 | 55.991 | 1.00 | 31.07 |
| | ATOM | 2969 | CA | ARG | 392 | 41.358 | -3.553 | 54.795 | 1.00 | 33.43 |
| 15 | ATOM | 2970 | CB | ARG | 392 | 39.921 | -3.018 | 54.780 | 1.00 | 35.04 |
| | ATOM | 2971 | CG | ARG | 392 | 39.597 | -2.307 | 53.483 | 1.00 | 35.84 |
| | ATOM | 2972 | CD | ARG | 392 | 38.614 | -1.173 | 53.650 | 1.00 | 37.18 |
| | ATOM | 2973 | NE | ARG | 392 | 38.804 | -0.186 | 52.589 | 1.00 | 35.89 |
| | ATOM | 2974 | CZ | ARG | 392 | 38.518 | -0.390 | 51.309 | 1.00 | 36.67 |
| 20 | ATOM | 2975 | NH1 | ARG | 392 | 38.006 | -1.550 | 50.911 | 1.00 | 38.42 |
| | ATOM | 2976 | NH2 | ARG | 392 | 38.788 | 0.553 | 50.417 | 1.00 | 37.33 |
| | ATOM | 2977 | C | ARG | 392 | 42.335 | -2.377 | 54.831 | 1.00 | 33.73 |
| | ATOM | 2978 | O | ARG | 392 | 43.028 | -2.107 | 53.858 | 1.00 | 34.52 |
| | ATOM | 2979 | N | MET | 393 | 42.396 | -1.691 | 55.967 | 1.00 | 34.05 |
| 25 | ATOM | 2980 | CA | MET | 393 | 43.298 | -0.554 | 56.126 | 1.00 | 35.93 |
| | ATOM | 2981 | CB | MET | 393 | 43.119 | 0.073 | 57.517 | 1.00 | 32.21 |
| | ATOM | 2982 | CG | MET | 393 | 41.801 | 0.834 | 57.692 | 1.00 | 28.72 |
| | ATOM | 2983 | SD | MET | 393 | 41.530 | 1.348 | 59.400 | 1.00 | 27.28 |
| | ATOM | 2984 | CE | MET | 393 | 42.652 | 2.753 | 59.533 | 1.00 | 24.26 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2985 | C | MET | 393 | 44.751 | -0.979 | 55.947 | 1.00 | 39.48 |
| ATOM | 2986 | O | MET | 393 | 45.579 | -0.216 | 55.448 | 1.00 | 39.63 |
| ATOM | 2987 | N | ARG | 394 | 45.049 | -2.205 | 56.364 | 1.00 | 43.20 |
| ATOM | 2988 | CA | ARG | 394 | 46.391 | -2.766 | 56.277 | 1.00 | 45.79 |
| ATOM | 2989 | CB | ARG | 394 | 46.381 | -4.180 | 56.870 | 1.00 | 49.86 |
| ATOM | 2990 | CG | ARG | 394 | 47.670 | -4.595 | 57.551 | 1.00 | 53.76 |
| ATOM | 2991 | CD | ARG | 394 | 48.587 | -5.335 | 56.612 | 1.00 | 56.09 |
| ATOM | 2992 | NE | ARG | 394 | 49.896 | -5.554 | 57.217 | 1.00 | 60.36 |
| ATOM | 2993 | CZ | ARG | 394 | 50.797 | -4.596 | 57.411 | 1.00 | 60.35 |
| ATOM | 2994 | NH1 | ARG | 394 | 50.528 | -3.353 | 57.042 | 1.00 | 61.48 |
| ATOM | 2995 | NH2 | ARG | 394 | 51.964 | -4.878 | 57.978 | 1.00 | 60.51 |
| ATOM | 2996 | C | ARG | 394 | 46.912 | -2.792 | 54.835 | 1.00 | 46.90 |
| ATOM | 2997 | O | ARG | 394 | 48.117 | -2.697 | 54.606 | 1.00 | 44.95 |
| ATOM | 2998 | N | GLU | 395 | 46.005 | -2.906 | 53.869 | 1.00 | 48.68 |
| ATOM | 2999 | CA | GLU | 395 | 46.387 | -2.943 | 52.459 | 1.00 | 52.84 |
| ATOM | 3000 | CB | GLU | 395 | 45.165 | -3.275 | 51.590 | 1.00 | 54.51 |
| ATOM | 3001 | CG | GLU | 395 | 44.388 | -4.508 | 52.051 | 1.00 | 60.85 |
| ATOM | 3002 | CD | GLU | 395 | 43.310 | -4.952 | 51.061 | 1.00 | 64.84 |
| ATOM | 3003 | OE1 | GLU | 395 | 42.485 | -4.105 | 50.642 | 1.00 | 65.83 |
| ATOM | 3004 | OE2 | GLU | 395 | 43.286 | -6.155 | 50.708 | 1.00 | 66.43 |
| ATOM | 3005 | C | GLU | 395 | 47.008 | -1.621 | 51.991 | 1.00 | 54.64 |
| ATOM | 3006 | O | GLU | 395 | 47.791 | -1.594 | 51.039 | 1.00 | 53.71 |
| ATOM | 3007 | N | SER | 396 | 46.660 | -0.528 | 52.666 | 1.00 | 56.54 |
| ATOM | 3008 | CA | SER | 396 | 47.179 | 0.794 | 52.313 | 1.00 | 58.22 |
| ATOM | 3009 | CB | SER | 396 | 46.037 | 1.808 | 52.266 | 1.00 | 57.21 |
| ATOM | 3010 | OG | SER | 396 | 44.980 | 1.340 | 51.448 | 1.00 | 59.52 |
| ATOM | 3011 | C | SER | 396 | 48.221 | 1.268 | 53.318 | 1.00 | 60.22 |
| ATOM | 3012 | O | SER | 396 | 48.394 | 2.468 | 53.527 | 1.00 | 60.38 |
| ATOM | 3013 | N | ARG | 397 | 48.915 | 0.324 | 53.941 | 1.00 | 62.22 |

- 120 -

| | ATOM | 3014 | CA | ARG | 397 | 49. 924 | 0. 663 | 54. 933 | 1. 00 64. 67 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3015 | CB | ARG | 397 | 49. 430 | 0. 260 | 56. 324 | 1. 00 65. 24 |
| | ATOM | 3016 | CG | ARG | 397 | 49. 798 | 1. 218 | 57. 444 | 1. 00 67. 16 |
| | ATOM | 3017 | CD | ARG | 397 | 49. 178 | 2. 596 | 57. 244 | 1. 00 68. 03 |
| 5 | ATOM | 3018 | NE | ARG | 397 | 48. 803 | 3. 208 | 58. 516 | 1. 00 69. 13 |
| | ATOM | 3019 | CZ | ARG | 397 | 47. 681 | 2. 933 | 59. 178 | 1. 00 70. 58 |
| | ATOM | 3020 | NH1 | ARG | 397 | 46. 813 | 2. 059 | 58. 687 | 1. 00 71. 37 |
| | ATOM | 3021 | NH2 | ARG | 397 | 47. 429 | 3. 521 | 60. 340 | 1. 00 70. 29 |
| | ATOM | 3022 | C | ARG | 397 | 51. 222 | -0. 063 | 54. 611 | 1. 00 65. 54 |
| 10 | ATOM | 3023 | 0 | ARG | 397 | 51. 416 | -1. 215 | 54. 998 | 1. 00 66. 75 |
| | ATOM | 3024 | N | SER | 398 | 52. 106 | 0. 621 | 53. 894 | 1. 00 66. 86 |
| | ATOM | 3025 | CA | SER | 398 | 53. 388 | 0. 052 | 53. 508 | 1. 00 67. 48 |
| | ATOM | 3026 | CB | SER | 398 | 53. 980 | 0. 832 | 52. 331 | 1. 00 67. 48 |
| | ATOM | 3027 | OG | SER | 398 | 53. 155 | 0. 725 | 51. 181 | 1. 00 66. 93 |
| 15 | ATOM | 3028 | C | SER | 398 | 54. 358 | 0. 063 | 54. 679 | 1. 00 68. 36 |
| | ATOM | 3029 | 0 | SER | 398 | 55. 036 | 1. 063 | 54. 934 | 1. 00 69. 35 |
| | ATOM | 3030 | N | GLU | 399 | 54. 413 | -1. 059 | 55. 388 | 1. 00 67. 90 |
| | ATOM | 3031 | CA | GLU | 399 | 55. 297 | -1. 206 | 56. 533 | 1. 00 68. 16 |
| | ATOM | 3032 | CB | GLU | 399 | 55. 002 | -0. 126 | 57. 564 | 1. 00 68. 95 |
| 20 | ATOM | 3033 | CG | GLU | 399 | 53. 540 | 0. 020 | 57. 889 | 1. 00 71. 05 |
| | ATOM | 3034 | CD | GLU | 399 | 53. 261 | 1. 318 | 58. 598 | 1. 00 71. 37 |
| | ATOM | 3035 | OE1 | GLU | 399 | 53. 871 | 1. 545 | 59. 662 | 1. 00 72. 25 |
| | ATOM | 3036 | OE2 | GLU | 399 | 52. 443 | 2. 111 | 58. 089 | 1. 00 71. 32 |
| | ATOM | 3037 | C | GLU | 399 | 55. 167 | -2. 581 | 57. 168 | 1. 00 67. 57 |
| 25 | ATOM | 3038 | 0 | GLU | 399 | 54. 078 | -3. 155 | 57. 232 | 1. 00 67. 34 |
| | ATOM | 3039 | N | ASP | 400 | 56. 301 | -3. 091 | 57. 635 | 1. 00 66. 86 |
| | ATOM | 3040 | CA | ASP | 400 | 56. 397 | -4. 400 | 58. 265 | 1. 00 65. 75 |
| | ATOM | 3041 | CB | ASP | 400 | 57. 739 | -4. 507 | 58. 989 | 1. 00 68. 55 |
| | ATOM | 3042 | CG | ASP | 400 | 58. 892 | -3. 961 | 58. 157 | 1. 00 71. 49 |

- 121 -

| ATOM | 3043 | OD1 | ASP | 400 | 59.015 | -4.356 | 56.976 | 1.00 | 72.29 |
|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| ATOM | 3044 | OD2 | ASP | 400 | 59.675 | -3.136 | 58.682 | 1.00 | 72.38 |
| ATOM | 3045 | C | ASP | 400 | 55.247 | -4.676 | 59.233 | 1.00 | 63.41 |
| ATOM | 3046 | O | ASP | 400 | 54.385 | -5.514 | 58.962 | 1.00 | 63.27 |
| ATOM | 3047 | N | VAL | 401 | 55.241 | -3.973 | 60.361 | 1.00 | 59.50 |
| ATOM | 3048 | CA | VAL | 401 | 54.193 | -4.138 | 61.360 | 1.00 | 55.59 |
| ATOM | 3049 | CB | VAL | 401 | 54.789 | -4.439 | 62.757 | 1.00 | 55.81 |
| ATOM | 3050 | CG1 | VAL | 401 | 53.698 | -4.375 | 63.818 | 1.00 | 54.69 |
| ATOM | 3051 | CG2 | VAL | 401 | 55.442 | -5.817 | 62.757 | 1.00 | 54.18 |
| ATOM | 3052 | C | VAL | 401 | 53.345 | -2.876 | 61.454 | 1.00 | 53.78 |
| ATOM | 3053 | O | VAL | 401 | 53.841 | -1.807 | 61.820 | 1.00 | 53.39 |
| ATOM | 3054 | N | MET | 402 | 52.065 | -2.991 | 61.114 | 1.00 | 50.91 |
| ATOM | 3055 | CA | MET | 402 | 51.190 | -1.834 | 61.194 | 1.00 | 47.59 |
| ATOM | 3056 | CB | MET | 402 | 49.992 | -1.958 | 60.250 | 1.00 | 46.98 |
| ATOM | 3057 | CG | MET | 402 | 49.043 | -0.768 | 60.387 | 1.00 | 47.22 |
| ATOM | 3058 | SD | MET | 402 | 47.505 | -0.874 | 59.461 | 1.00 | 48.69 |
| ATOM | 3059 | CE | MET | 402 | 46.622 | -2.099 | 60.439 | 1.00 | 48.15 |
| ATOM | 3060 | C | MET | 402 | 50.670 | -1.643 | 62.605 | 1.00 | 44.98 |
| ATOM | 3061 | O | MET | 402 | 49.945 | -2.483 | 63.134 | 1.00 | 43.92 |
| ATOM | 3062 | N | ARG | 403 | 51.054 | -0.533 | 63.219 | 1.00 | 43.27 |
| ATOM | 3063 | CA | ARG | 403 | 50.587 | -0.229 | 64.556 | 1.00 | 41.71 |
| ATOM | 3064 | CB | ARG | 403 | 51.673 | 0.484 | 65.350 | 1.00 | 45.65 |
| ATOM | 3065 | CG | ARG | 403 | 52.903 | -0.356 | 65.596 | 1.00 | 52.20 |
| ATOM | 3066 | CD | ARG | 403 | 53.973 | 0.474 | 66.262 | 1.00 | 57.99 |
| ATOM | 3067 | NE | ARG | 403 | 55.137 | -0.324 | 66.630 | 1.00 | 65.47 |
| ATOM | 3068 | CZ | ARG | 403 | 56.251 | 0.184 | 67.149 | 1.00 | 68.76 |
| ATOM | 3069 | NH1 | ARG | 403 | 56.349 | 1.493 | 67.357 | 1.00 | 69.34 |
| ATOM | 3070 | NH2 | ARG | 403 | 57.265 | -0.615 | 67.468 | 1.00 | 69.59 |
| ATOM | 3071 | C | ARG | 403 | 49.388 | 0.685 | 64.372 | 1.00 | 37.99 |

- 122 -

|  | ATOM | 3072 | O | ARG | 403 | 49.471 | 1.692 | 63.679 | 1.00 | 37.13 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|  | ATOM | 3073 | N | ILE | 404 | 48.267 | 0.322 | 64.975 | 1.00 | 34.39 |
|  | ATOM | 3074 | CA | ILE | 404 | 47.069 | 1.129 | 64.854 | 1.00 | 31.53 |
|  | ATOM | 3075 | CB | ILE | 404 | 46.161 | 0.577 | 63.735 | 1.00 | 33.38 |
| 5 | ATOM | 3076 | CG2 | ILE | 404 | 45.681 | -0.829 | 64.096 | 1.00 | 32.57 |
|  | ATOM | 3077 | CG1 | ILE | 404 | 44.987 | 1.524 | 63.500 | 1.00 | 35.77 |
|  | ATOM | 3078 | CD1 | ILE | 404 | 44.144 | 1.153 | 62.300 | 1.00 | 38.45 |
|  | ATOM | 3079 | C | ILE | 404 | 46.322 | 1.152 | 66.179 | 1.00 | 28.96 |
|  | ATOM | 3080 | O | ILE | 404 | 46.393 | 0.204 | 66.956 | 1.00 | 29.35 |
| 10 | ATOM | 3081 | N | THR | 405 | 45.632 | 2.250 | 66.453 | 1.00 | 28.84 |
|  | ATOM | 3082 | CA | THR | 405 | 44.874 | 2.359 | 67.693 | 1.00 | 27.84 |
|  | ATOM | 3083 | CB | THR | 405 | 45.323 | 3.558 | 68.535 | 1.00 | 26.65 |
|  | ATOM | 3084 | OG1 | THR | 405 | 46.663 | 3.335 | 68.990 | 1.00 | 30.48 |
|  | ATOM | 3085 | CG2 | THR | 405 | 44.428 | 3.715 | 69.749 | 1.00 | 27.32 |
| 15 | ATOM | 3086 | C | THR | 405 | 43.387 | 2.460 | 67.408 | 1.00 | 27.13 |
|  | ATOM | 3087 | O | THR | 405 | 42.964 | 3.127 | 66.462 | 1.00 | 24.36 |
|  | ATOM | 3088 | N | VAL | 406 | 42.604 | 1.786 | 68.245 | 1.00 | 25.61 |
|  | ATOM | 3089 | CA | VAL | 406 | 41.160 | 1.737 | 68.107 | 1.00 | 23.67 |
|  | ATOM | 3090 | CB | VAL | 406 | 40.705 | 0.244 | 67.973 | 1.00 | 23.64 |
| 20 | ATOM | 3091 | CG1 | VAL | 406 | 39.189 | 0.138 | 67.798 | 1.00 | 24.19 |
|  | ATOM | 3092 | CG2 | VAL | 406 | 41.405 | -0.399 | 66.783 | 1.00 | 21.36 |
|  | ATOM | 3093 | C | VAL | 406 | 40.493 | 2.392 | 69.320 | 1.00 | 26.21 |
|  | ATOM | 3094 | O | VAL | 406 | 40.763 | 2.018 | 70.469 | 1.00 | 26.86 |
|  | ATOM | 3095 | N | GLY | 407 | 39.644 | 3.389 | 69.072 | 1.00 | 25.61 |
| 25 | ATOM | 3096 | CA | GLY | 407 | 38.943 | 4.044 | 70.168 | 1.00 | 23.09 |
|  | ATOM | 3097 | C | GLY | 407 | 37.645 | 3.285 | 70.387 | 1.00 | 21.77 |
|  | ATOM | 3098 | O | GLY | 407 | 36.919 | 3.011 | 69.426 | 1.00 | 23.17 |
|  | ATOM | 3099 | N | VAL | 408 | 37.334 | 2.943 | 71.632 | 1.00 | 20.52 |
|  | ATOM | 3100 | CA | VAL | 408 | 36.128 | 2.167 | 71.907 | 1.00 | 21.51 |

| | ATOM | 3101 | CB | VAL | 408 | 36.500 | 0.684 | 72.252 | 1.00 | 23.04 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 3102 | CG1 | VAL | 408 | 35.237 | -0.176 | 72.351 | 1.00 | 19.52 |
| | ATOM | 3103 | CG2 | VAL | 408 | 37.436 | 0.121 | 71.201 | 1.00 | 20.49 |
| | ATOM | 3104 | C | VAL | 408 | 35.282 | 2.704 | 73.060 | 1.00 | 23.66 |
| 5 | ATOM | 3105 | O | VAL | 408 | 35.814 | 3.223 | 74.045 | 1.00 | 23.60 |
| | ATOM | 3106 | N | ASP | 409 | 33.963 | 2.580 | 72.923 | 1.00 | 24.58 |
| | ATOM | 3107 | CA | ASP | 409 | 33.040 | 2.992 | 73.975 | 1.00 | 26.70 |
| | ATOM | 3108 | CB | ASP | 409 | 32.612 | 4.455 | 73.803 | 1.00 | 30.78 |
| | ATOM | 3109 | CG | ASP | 409 | 31.909 | 4.998 | 75.041 | 1.00 | 31.51 |
| 10 | ATOM | 3110 | OD1 | ASP | 409 | 32.322 | 4.625 | 76.156 | 1.00 | 31.70 |
| | ATOM | 3111 | OD2 | ASP | 409 | 30.955 | 5.794 | 74.910 | 1.00 | 35.70 |
| | ATOM | 3112 | C | ASP | 409 | 31.824 | 2.083 | 73.898 | 1.00 | 25.68 |
| | ATOM | 3113 | O | ASP | 409 | 31.639 | 1.396 | 72.901 | 1.00 | 27.99 |
| | ATOM | 3114 | N | GLY | 410 | 30.999 | 2.079 | 74.943 | 1.00 | 28.67 |
| 15 | ATOM | 3115 | CA | GLY | 410 | 29.807 | 1.233 | 74.964 | 1.00 | 29.54 |
| | ATOM | 3116 | C | GLY | 410 | 29.755 | 0.355 | 76.212 | 1.00 | 30.09 |
| | ATOM | 3117 | O | GLY | 410 | 30.787 | -0.138 | 76.657 | 1.00 | 28.57 |
| | ATOM | 3118 | N | SER | 411 | 28.560 | 0.150 | 76.767 | 1.00 | 30.89 |
| | ATOM | 3119 | CA | SER | 411 | 28.392 | -0.649 | 77.983 | 1.00 | 32.71 |
| 20 | ATOM | 3120 | CB | SER | 411 | 26.941 | -0.554 | 78.490 | 1.00 | 32.88 |
| | ATOM | 3121 | OG | SER | 411 | 26.011 | -0.884 | 77.473 | 1.00 | 36.82 |
| | ATOM | 3122 | C | SER | 411 | 28.804 | -2.121 | 77.840 | 1.00 | 31.25 |
| | ATOM | 3123 | O | SER | 411 | 29.480 | -2.661 | 78.712 | 1.00 | 29.96 |
| | ATOM | 3124 | N | VAL | 412 | 28.398 | -2.768 | 76.754 | 1.00 | 29.78 |
| 25 | ATOM | 3125 | CA | VAL | 412 | 28.780 | -4.158 | 76.535 | 1.00 | 28.59 |
| | ATOM | 3126 | CB | VAL | 412 | 28.264 | -4.665 | 75.174 | 1.00 | 29.68 |
| | ATOM | 3127 | CG1 | VAL | 412 | 28.772 | -6.088 | 74.908 | 1.00 | 27.25 |
| | ATOM | 3128 | CG2 | VAL | 412 | 26.739 | -4.642 | 75.173 | 1.00 | 29.93 |
| | ATOM | 3129 | C | VAL | 412 | 30.307 | -4.320 | 76.584 | 1.00 | 29.24 |

- 124 -

| ATOM | 3130 | O | VAL | 412 | 30.831 | -5.145 | 77.340 | 1.00 | 28.78 |
|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| ATOM | 3131 | N | TYR | 413 | 31.023 | -3.522 | 75.796 | 1.00 | 27.57 |
| ATOM | 3132 | CA | TYR | 413 | 32.482 | -3.602 | 75.763 | 1.00 | 24.60 |
| ATOM | 3133 | CB | TYR | 413 | 33.049 | -2.730 | 74.645 | 1.00 | 19.87 |
| ATOM | 3134 | CG | TYR | 413 | 34.568 | -2.710 | 74.587 | 1.00 | 20.22 |
| ATOM | 3135 | CD1 | TYR | 413 | 35.270 | -3.566 | 73.735 | 1.00 | 21.52 |
| ATOM | 3136 | CE1 | TYR | 413 | 36.667 | -3.519 | 73.655 | 1.00 | 19.93 |
| ATOM | 3137 | CD2 | TYR | 413 | 35.300 | -1.819 | 75.363 | 1.00 | 14.63 |
| ATOM | 3138 | CE2 | TYR | 413 | 36.690 | -1.770 | 75.294 | 1.00 | 17.31 |
| ATOM | 3139 | CZ | TYR | 413 | 37.364 | -2.616 | 74.439 | 1.00 | 19.92 |
| ATOM | 3140 | OH | TYR | 413 | 38.737 | -2.547 | 74.362 | 1.00 | 23.08 |
| ATOM | 3141 | C | TYR | 413 | 33.151 | -3.193 | 77.072 | 1.00 | 26.48 |
| ATOM | 3142 | O | TYR | 413 | 34.085 | -3.849 | 77.534 | 1.00 | 26.86 |
| ATOM | 3143 | N | LYS | 414 | 32.690 | -2.108 | 77.669 | 1.00 | 26.13 |
| ATOM | 3144 | CA | LYS | 414 | 33.309 | -1.640 | 78.902 | 1.00 | 29.80 |
| ATOM | 3145 | CB | LYS | 414 | 33.001 | -0.147 | 79.117 | 1.00 | 29.42 |
| ATOM | 3146 | CG | LYS | 414 | 33.882 | 0.802 | 78.302 | 1.00 | 32.94 |
| ATOM | 3147 | CD | LYS | 414 | 33.558 | 2.275 | 78.559 | 1.00 | 34.12 |
| ATOM | 3148 | CE | LYS | 414 | 34.553 | 3.179 | 77.833 | 1.00 | 36.09 |
| ATOM | 3149 | NZ | LYS | 414 | 34.170 | 4.626 | 77.859 | 1.00 | 35.28 |
| ATOM | 3150 | C | LYS | 414 | 32.966 | -2.400 | 80.181 | 1.00 | 29.74 |
| ATOM | 3151 | O | LYS | 414 | 33.850 | -2.677 | 80.988 | 1.00 | 28.77 |
| ATOM | 3152 | N | LEU | 415 | 31.696 | -2.749 | 80.357 | 1.00 | 30.99 |
| ATOM | 3153 | CA | LEU | 415 | 31.255 | -3.395 | 81.591 | 1.00 | 34.39 |
| ATOM | 3154 | CB | LEU | 415 | 29.942 | -2.738 | 82.041 | 1.00 | 34.94 |
| ATOM | 3155 | CG | LEU | 415 | 29.964 | -1.195 | 82.012 | 1.00 | 38.17 |
| ATOM | 3156 | CD1 | LEU | 415 | 28.610 | -0.647 | 82.469 | 1.00 | 38.59 |
| ATOM | 3157 | CD2 | LEU | 415 | 31.080 | -0.660 | 82.901 | 1.00 | 34.42 |
| ATOM | 3158 | C | LEU | 415 | 31.113 | -4.923 | 81.657 | 1.00 | 34.46 |

- 125 -

| | ATOM | 3159 | O | LEU | 415 | 31.202 | -5.493 | 82.741 | 1.00 33.89 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3160 | N | HIS | 416 | 30.886 | -5.586 | 80.531 | 1.00 34.56 |
| | ATOM | 3161 | CA | HIS | 416 | 30.746 | -7.041 | 80.561 | 1.00 36.94 |
| | ATOM | 3162 | CB | HIS | 416 | 30.394 | -7.572 | 79.175 | 1.00 39.81 |
| 5 | ATOM | 3163 | CG | HIS | 416 | 29.811 | -8.949 | 79.192 | 1.00 44.04 |
| | ATOM | 3164 | CD2 | HIS | 416 | 28.536 | -9.375 | 79.038 | 1.00 43.02 |
| | ATOM | 3165 | ND1 | HIS | 416 | 30.573 | -10.080 | 79.402 | 1.00 44.57 |
| | ATOM | 3166 | CE1 | HIS | 416 | 29.791 | -11.144 | 79.374 | 1.00 44.76 |
| | ATOM | 3167 | NE2 | HIS | 416 | 28.550 | -10.744 | 79.156 | 1.00 46.14 |
| 10 | ATOM | 3168 | C | HIS | 416 | 32.046 | -7.673 | 81.060 | 1.00 35.57 |
| | ATOM | 3169 | O | HIS | 416 | 33.103 | -7.483 | 80.471 | 1.00 37.06 |
| | ATOM | 3170 | N | PRO | 417 | 31.973 | -8.445 | 82.153 | 1.00 33.55 |
| | ATOM | 3171 | CD | PRO | 417 | 30.727 | -8.999 | 82.700 | 1.00 32.04 |
| | ATOM | 3172 | CA | PRO | 417 | 33.134 | -9.109 | 82.757 | 1.00 33.47 |
| 15 | ATOM | 3173 | CB | PRO | 417 | 32.504 | -10.219 | 83.614 | 1.00 31.67 |
| | ATOM | 3174 | CG | PRO | 417 | 31.142 | -10.410 | 83.016 | 1.00 32.88 |
| | ATOM | 3175 | C | PRO | 417 | 34.252 | -9.628 | 81.849 | 1.00 32.70 |
| | ATOM | 3176 | O | PRO | 417 | 35.428 | -9.411 | 82.146 | 1.00 36.28 |
| | ATOM | 3177 | N | SER | 418 | 33.929 | -10.302 | 80.752 | 1.00 29.70 |
| 20 | ATOM | 3178 | CA | SER | 418 | 35.015 | -10.808 | 79.915 | 1.00 28.37 |
| | ATOM | 3179 | CB | SER | 418 | 35.215 | -12.314 | 80.163 | 1.00 30.65 |
| | ATOM | 3180 | OG | SER | 418 | 35.798 | -12.555 | 81.439 | 1.00 35.61 |
| | ATOM | 3181 | C | SER | 418 | 34.895 | -10.560 | 78.418 | 1.00 25.27 |
| | ATOM | 3182 | O | SER | 418 | 35.730 | -11.028 | 77.648 | 1.00 23.69 |
| 25 | ATOM | 3183 | N | PHE | 419 | 33.856 | -9.846 | 78.004 | 1.00 21.86 |
| | ATOM | 3184 | CA | PHE | 419 | 33.673 | -9.543 | 76.587 | 1.00 24.13 |
| | ATOM | 3185 | CB | PHE | 419 | 32.551 | -8.522 | 76.407 | 1.00 22.03 |
| | ATOM | 3186 | CG | PHE | 419 | 32.270 | -8.187 | 74.978 | 1.00 24.42 |
| | ATOM | 3187 | CD1 | PHE | 419 | 31.273 | -8.860 | 74.276 | 1.00 23.32 |

- 126 -

| ATOM | 3188 | CD2 | PHE | 419 | 33.033 | -7.231 | 74.312 | 1.00 | 22.16 |
|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| ATOM | 3189 | CE1 | PHE | 419 | 31.038 | -8.593 | 72.932 | 1.00 | 23.49 |
| ATOM | 3190 | CE2 | PHE | 419 | 32.808 | -6.961 | 72.967 | 1.00 | 25.91 |
| ATOM | 3191 | CZ | PHE | 419 | 31.806 | -7.645 | 72.275 | 1.00 | 24.70 |
| ATOM | 3192 | C | PHE | 419 | 34.961 | -8.965 | 76.000 | 1.00 | 24.09 |
| ATOM | 3193 | O | PHE | 419 | 35.491 | -9.455 | 75.009 | 1.00 | 26.51 |
| ATOM | 3194 | N | LYS | 420 | 35.432 | -7.899 | 76.628 | 1.00 | 25.00 |
| ATOM | 3195 | CA | LYS | 420 | 36.641 | -7.179 | 76.238 | 1.00 | 26.79 |
| ATOM | 3196 | CB | LYS | 420 | 36.984 | -6.207 | 77.370 | 1.00 | 28.35 |
| ATOM | 3197 | CG | LYS | 420 | 38.241 | -5.396 | 77.229 | 1.00 | 30.04 |
| ATOM | 3198 | CD | LYS | 420 | 38.433 | -4.537 | 78.497 | 1.00 | 33.98 |
| ATOM | 3199 | CE | LYS | 420 | 37.170 | -3.740 | 78.832 | 1.00 | 31.09 |
| ATOM | 3200 | NZ | LYS | 420 | 37.322 | -2.923 | 80.067 | 1.00 | 36.69 |
| ATOM | 3201 | C | LYS | 420 | 37.819 | -8.118 | 75.968 | 1.00 | 25.76 |
| ATOM | 3202 | O | LYS | 420 | 38.446 | -8.064 | 74.911 | 1.00 | 25.94 |
| ATOM | 3203 | N | GLU | 421 | 38.111 | -8.961 | 76.951 | 1.00 | 24.13 |
| ATOM | 3204 | CA | GLU | 421 | 39.195 | -9.929 | 76.887 | 1.00 | 26.26 |
| ATOM | 3205 | CB | GLU | 421 | 39.204 | -10.781 | 78.155 | 1.00 | 32.38 |
| ATOM | 3206 | CG | GLU | 421 | 39.547 | -10.043 | 79.417 | 1.00 | 38.45 |
| ATOM | 3207 | CD | GLU | 421 | 38.700 | -8.798 | 79.664 | 1.00 | 41.54 |
| ATOM | 3208 | OE1 | GLU | 421 | 37.458 | -8.844 | 79.501 | 1.00 | 42.17 |
| ATOM | 3209 | OE2 | GLU | 421 | 39.300 | -7.767 | 80.053 | 1.00 | 42.62 |
| ATOM | 3210 | C | GLU | 421 | 39.075 | -10.864 | 75.699 | 1.00 | 24.57 |
| ATOM | 3211 | O | GLU | 421 | 40.017 | -11.023 | 74.930 | 1.00 | 25.86 |
| ATOM | 3212 | N | ARG | 422 | 37.921 | -11.509 | 75.576 | 1.00 | 24.00 |
| ATOM | 3213 | CA | ARG | 422 | 37.682 | -12.439 | 74.480 | 1.00 | 26.01 |
| ATOM | 3214 | CB | ARG | 422 | 36.284 | -13.063 | 74.610 | 1.00 | 27.36 |
| ATOM | 3215 | CG | ARG | 422 | 36.076 | -13.878 | 75.887 | 1.00 | 31.58 |
| ATOM | 3216 | CD | ARG | 422 | 34.600 | -14.053 | 76.188 | 1.00 | 35.39 |

- 127 -

| | ATOM | 3217 | NE | ARG | 422 | 34.390 | -14.834 | 77.397 | 1.00 | 40.58 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3218 | CZ | ARG | 422 | 33.232 | -14.911 | 78.046 | 1.00 | 44.53 |
| | ATOM | 3219 | NH1 | ARG | 422 | 32.171 | -14.243 | 77.596 | 1.00 | 41.79 |
| | ATOM | 3220 | NH2 | ARG | 422 | 33.141 | -15.651 | 79.150 | 1.00 | 41.67 |
| 5 | ATOM | 3221 | C | ARG | 422 | 37.794 | -11.691 | 73.160 | 1.00 | 24.48 |
| | ATOM | 3222 | O | ARG | 422 | 38.439 | -12.148 | 72.221 | 1.00 | 22.97 |
| | ATOM | 3223 | N | PHE | 423 | 37.153 | -10.531 | 73.094 | 1.00 | 24.48 |
| | ATOM | 3224 | CA | PHE | 423 | 37.189 | -9.737 | 71.879 | 1.00 | 22.97 |
| | ATOM | 3225 | CB | PHE | 423 | 36.403 | -8.442 | 72.089 | 1.00 | 24.98 |
| 10 | ATOM | 3226 | CG | PHE | 423 | 36.494 | -7.484 | 70.939 | 1.00 | 25.21 |
| | ATOM | 3227 | CD1 | PHE | 423 | 37.468 | -6.490 | 70.926 | 1.00 | 25.04 |
| | ATOM | 3228 | CD2 | PHE | 423 | 35.618 | -7.584 | 69.861 | 1.00 | 23.47 |
| | ATOM | 3229 | CE1 | PHE | 423 | 37.568 | -5.607 | 69.857 | 1.00 | 24.77 |
| | ATOM | 3230 | CE2 | PHE | 423 | 35.710 | -6.708 | 68.784 | 1.00 | 25.48 |
| 15 | ATOM | 3231 | CZ | PHE | 423 | 36.684 | -5.715 | 68.780 | 1.00 | 24.31 |
| | ATOM | 3232 | C | PHE | 423 | 38.629 | -9.442 | 71.456 | 1.00 | 21.03 |
| | ATOM | 3233 | O | PHE | 423 | 38.989 | -9.680 | 70.308 | 1.00 | 19.38 |
| | ATOM | 3234 | N | HIS | 424 | 39.454 | -8.952 | 72.381 | 1.00 | 20.46 |
| | ATOM | 3235 | CA | HIS | 424 | 40.846 | -8.631 | 72.054 | 1.00 | 23.40 |
| 20 | ATOM | 3236 | CB | HIS | 424 | 41.602 | -8.128 | 73.293 | 1.00 | 24.89 |
| | ATOM | 3237 | CG | HIS | 424 | 41.133 | -6.803 | 73.808 | 1.00 | 25.28 |
| | ATOM | 3238 | CD2 | HIS | 424 | 40.391 | -5.828 | 73.230 | 1.00 | 24.67 |
| | ATOM | 3239 | ND1 | HIS | 424 | 41.419 | -6.361 | 75.083 | 1.00 | 25.18 |
| | ATOM | 3240 | CE1 | HIS | 424 | 40.869 | -5.174 | 75.269 | 1.00 | 22.64 |
| 25 | ATOM | 3241 | NE2 | HIS | 424 | 40.239 | -4.829 | 74.161 | 1.00 | 24.12 |
| | ATOM | 3242 | C | HIS | 424 | 41.604 | -9.834 | 71.486 | 1.00 | 24.51 |
| | ATOM | 3243 | O | HIS | 424 | 42.239 | -9.741 | 70.432 | 1.00 | 23.58 |
| | ATOM | 3244 | N | ALA | 425 | 41.540 | -10.962 | 72.191 | 1.00 | 24.51 |
| | ATOM | 3245 | CA | ALA | 425 | 42.242 | -12.164 | 71.746 | 1.00 | 26.94 |

- 128 -

| | ATOM | 3246 | CB | ALA | 425 | 42.068 | -13.306 | 72.774 | 1.00 | 27.10 |
|---|------|------|-----|-----|-----|--------|---------|--------|------|-------|
| | ATOM | 3247 | C | ALA | 425 | 41.759 | -12.605 | 70.370 | 1.00 | 25.71 |
| | ATOM | 3248 | O | ALA | 425 | 42.559 | -12.937 | 69.505 | 1.00 | 27.02 |
| | ATOM | 3249 | N | SER | 426 | 40.453 | -12.600 | 70.151 | 1.00 | 24.30 |
| 5 | ATOM | 3250 | CA | SER | 426 | 39.967 | -13.003 | 68.850 | 1.00 | 23.93 |
| | ATOM | 3251 | CB | SER | 426 | 38.450 | -13.142 | 68.863 | 1.00 | 20.85 |
| | ATOM | 3252 | OG | SER | 426 | 38.007 | -13.582 | 67.596 | 1.00 | 21.86 |
| | ATOM | 3253 | C | SER | 426 | 40.394 | -12.039 | 67.743 | 1.00 | 25.72 |
| | ATOM | 3254 | O | SER | 426 | 40.760 | -12.483 | 66.660 | 1.00 | 25.40 |
| 10 | ATOM | 3255 | N | VAL | 427 | 40.363 | -10.727 | 68.007 | 1.00 | 27.03 |
| | ATOM | 3256 | CA | VAL | 427 | 40.761 | -9.750 | 66.983 | 1.00 | 27.43 |
| | ATOM | 3257 | CB | VAL | 427 | 40.591 | -8.269 | 67.450 | 1.00 | 28.91 |
| | ATOM | 3258 | CG1 | VAL | 427 | 40.999 | -7.323 | 66.314 | 1.00 | 29.57 |
| | ATOM | 3259 | CG2 | VAL | 427 | 39.150 | -7.990 | 67.852 | 1.00 | 27.73 |
| 15 | ATOM | 3260 | C | VAL | 427 | 42.226 | -9.919 | 66.601 | 1.00 | 28.67 |
| | ATOM | 3261 | O | VAL | 427 | 42.582 | -9.858 | 65.424 | 1.00 | 27.30 |
| | ATOM | 3262 | N | ARG | 428 | 43.076 | -10.119 | 67.603 | 1.00 | 28.43 |
| | ATOM | 3263 | CA | ARG | 428 | 44.498 | -10.281 | 67.350 | 1.00 | 31.91 |
| | ATOM | 3264 | CB | ARG | 428 | 45.273 | -10.231 | 68.670 | 1.00 | 31.80 |
| 20 | ATOM | 3265 | CG | ARG | 428 | 45.449 | -8.793 | 69.130 | 1.00 | 31.90 |
| | ATOM | 3266 | CD | ARG | 428 | 45.662 | -8.639 | 70.617 | 1.00 | 34.40 |
| | ATOM | 3267 | NE | ARG | 428 | 45.867 | -7.231 | 70.971 | 1.00 | 34.78 |
| | ATOM | 3268 | CZ | ARG | 428 | 45.668 | -6.728 | 72.186 | 1.00 | 38.69 |
| | ATOM | 3269 | NH1 | ARG | 428 | 45.251 | -7.516 | 73.172 | 1.00 | 38.56 |
| 25 | ATOM | 3270 | NH2 | ARG | 428 | 45.901 | -5.442 | 72.424 | 1.00 | 39.08 |
| | ATOM | 3271 | C | ARG | 428 | 44.797 | -11.548 | 66.572 | 1.00 | 33.56 |
| | ATOM | 3272 | O | ARG | 428 | 45.694 | -11.558 | 65.731 | 1.00 | 32.81 |
| | ATOM | 3273 | N | ARG | 429 | 44.037 | -12.609 | 66.837 | 1.00 | 34.25 |
| | ATOM | 3274 | CA | ARG | 429 | 44.224 | -13.859 | 66.115 | 1.00 | 33.42 |

- 129 -

| | ATOM | 3275 | CB | ARG | 429 | 43.252 | -14.941 | 66.601 | 1.00 | 36.36 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3276 | CG | ARG | 429 | 43.756 | -15.769 | 67.760 | 1.00 | 43.73 |
| | ATOM | 3277 | CD | ARG | 429 | 42.930 | -17.038 | 67.939 | 1.00 | 47.67 |
| | ATOM | 3278 | NE | ARG | 429 | 41.561 | -16.789 | 68.398 | 1.00 | 51.58 |
| 5 | ATOM | 3279 | CZ | ARG | 429 | 41.222 | -16.467 | 69.646 | 1.00 | 51.70 |
| | ATOM | 3280 | NH1 | ARG | 429 | 42.154 | -16.345 | 70.585 | 1.00 | 50.85 |
| | ATOM | 3281 | NH2 | ARG | 429 | 39.945 | -16.288 | 69.962 | 1.00 | 49.95 |
| | ATOM | 3282 | C | ARG | 429 | 43.960 | -13.618 | 64.639 | 1.00 | 32.81 |
| | ATOM | 3283 | O | ARG | 429 | 44.610 | -14.215 | 63.783 | 1.00 | 32.29 |
| 10 | ATOM | 3284 | N | LEU | 430 | 43.001 | -12.741 | 64.345 | 1.00 | 30.18 |
| | ATOM | 3285 | CA | LEU | 430 | 42.623 | -12.455 | 62.965 | 1.00 | 29.19 |
| | ATOM | 3286 | CB | LEU | 430 | 41.132 | -12.109 | 62.904 | 1.00 | 29.15 |
| | ATOM | 3287 | CG | LEU | 430 | 40.173 | -13.164 | 63.453 | 1.00 | 31.83 |
| | ATOM | 3288 | CD1 | LEU | 430 | 38.746 | -12.629 | 63.437 | 1.00 | 28.32 |
| 15 | ATOM | 3289 | CD2 | LEU | 430 | 40.281 | -14.441 | 62.613 | 1.00 | 32.03 |
| | ATOM | 3290 | C | LEU | 430 | 43.407 | -11.355 | 62.251 | 1.00 | 27.64 |
| | ATOM | 3291 | O | LEU | 430 | 43.244 | -11.151 | 61.048 | 1.00 | 28.08 |
| | ATOM | 3292 | N | THR | 431 | 44.261 | -10.645 | 62.966 | 1.00 | 28.04 |
| | ATOM | 3293 | CA | THR | 431 | 44.988 | -9.567 | 62.326 | 1.00 | 31.15 |
| 20 | ATOM | 3294 | CB | THR | 431 | 44.569 | -8.201 | 62.934 | 1.00 | 30.03 |
| | ATOM | 3295 | OG1 | THR | 431 | 44.666 | -8.254 | 64.363 | 1.00 | 31.84 |
| | ATOM | 3296 | CG2 | THR | 431 | 43.137 | -7.879 | 62.561 | 1.00 | 26.93 |
| | ATOM | 3297 | C | THR | 431 | 46.507 | -9.719 | 62.367 | 1.00 | 34.65 |
| | ATOM | 3298 | O | THR | 431 | 47.190 | -9.015 | 63.101 | 1.00 | 34.08 |
| 25 | ATOM | 3299 | N | PRO | 432 | 47.049 | -10.655 | 61.566 | 1.00 | 37.36 |
| | ATOM | 3300 | CD | PRO | 432 | 46.296 | -11.603 | 60.726 | 1.00 | 37.91 |
| | ATOM | 3301 | CA | PRO | 432 | 48.489 | -10.923 | 61.484 | 1.00 | 38.59 |
| | ATOM | 3302 | CB | PRO | 432 | 48.572 | -12.080 | 60.487 | 1.00 | 38.98 |
| | ATOM | 3303 | CG | PRO | 432 | 47.245 | -12.758 | 60.630 | 1.00 | 40.10 |

- 130 -

|  | ATOM | 3304 | C | PRO | 432 | 49.224 | -9.689 | 60.969 | 1.00 | 39.65 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 3305 | O | PRO | 432 | 48.712 | -8.968 | 60.113 | 1.00 | 39.80 |
|  | ATOM | 3306 | N | SER | 433 | 50.420 | -9.461 | 61.495 | 1.00 | 39.94 |
|  | ATOM | 3307 | CA | SER | 433 | 51.254 | -8.326 | 61.112 | 1.00 | 42.47 |
| 5 | ATOM | 3308 | CB | SER | 433 | 51.467 | -8.280 | 59.586 | 1.00 | 44.12 |
|  | ATOM | 3309 | OG | SER | 433 | 50.363 | -7.707 | 58.898 | 1.00 | 48.10 |
|  | ATOM | 3310 | C | SER | 433 | 50.687 | -6.996 | 61.598 | 1.00 | 42.26 |
|  | ATOM | 3311 | O | SER | 433 | 51.085 | -5.932 | 61.121 | 1.00 | 42.50 |
|  | ATOM | 3312 | N | CYS | 434 | 49.756 | -7.053 | 62.544 | 1.00 | 40.68 |
| 10 | ATOM | 3313 | CA | CYS | 434 | 49.184 | -5.831 | 63.092 | 1.00 | 40.64 |
|  | ATOM | 3314 | CB | CYS | 434 | 47.679 | -5.735 | 62.826 | 1.00 | 39.36 |
|  | ATOM | 3315 | SG | CYS | 434 | 47.196 | -5.674 | 61.111 | 1.00 | 39.36 |
|  | ATOM | 3316 | C | CYS | 434 | 49.398 | -5.789 | 64.590 | 1.00 | 40.17 |
|  | ATOM | 3317 | O | CYS | 434 | 49.258 | -6.801 | 65.281 | 1.00 | 40.51 |
| 15 | ATOM | 3318 | N | GLU | 435 | 49.743 | -4.609 | 65.081 | 1.00 | 38.91 |
|  | ATOM | 3319 | CA | GLU | 435 | 49.945 | -4.388 | 66.504 | 1.00 | 39.30 |
|  | ATOM | 3320 | CB | GLU | 435 | 51.302 | -3.733 | 66.738 | 1.00 | 42.29 |
|  | ATOM | 3321 | CG | GLU | 435 | 51.779 | -3.766 | 68.162 | 1.00 | 49.24 |
|  | ATOM | 3322 | CD | GLU | 435 | 53.072 | -2.993 | 68.340 | 1.00 | 53.77 |
| 20 | ATOM | 3323 | OE1 | GLU | 435 | 54.106 | -3.421 | 67.781 | 1.00 | 56.24 |
|  | ATOM | 3324 | OE2 | GLU | 435 | 53.047 | -1.950 | 69.032 | 1.00 | 54.88 |
|  | ATOM | 3325 | C | GLU | 435 | 48.801 | -3.430 | 66.839 | 1.00 | 37.06 |
|  | ATOM | 3326 | O | GLU | 435 | 48.866 | -2.241 | 66.532 | 1.00 | 34.30 |
|  | ATOM | 3327 | N | ILE | 436 | 47.749 | -3.971 | 67.449 | 1.00 | 36.39 |
| 25 | ATOM | 3328 | CA | ILE | 436 | 46.552 | -3.203 | 67.786 | 1.00 | 34.47 |
|  | ATOM | 3329 | CB | ILE | 436 | 45.280 | -4.040 | 67.508 | 1.00 | 34.15 |
|  | ATOM | 3330 | CG2 | ILE | 436 | 44.024 | -3.166 | 67.639 | 1.00 | 33.64 |
|  | ATOM | 3331 | CG1 | ILE | 436 | 45.357 | -4.633 | 66.100 | 1.00 | 36.06 |
|  | ATOM | 3332 | CD1 | ILE | 436 | 44.166 | -5.487 | 65.719 | 1.00 | 36.35 |

- 131 -

```
   ATOM  3333  C   ILE  436  46.492  -2.717  69.228  1.00  34.50
   ATOM  3334  O   ILE  436  46.612  -3.506  70.164  1.00  35.88
   ATOM  3335  N   THR  437  46.308  -1.411  69.405  1.00  32.66
   ATOM  3336  CA  THR  437  46.196  -0.837  70.741  1.00  30.32
 5 ATOM  3337  CB  THR  437  47.134   0.370  70.930  1.00  29.83
   ATOM  3338  OG1 THR  437  48.496  -0.060  70.833  1.00  33.74
   ATOM  3339  CG2 THR  437  46.925   0.996  72.294  1.00  28.96
   ATOM  3340  C   THR  437  44.759  -0.377  70.949  1.00  29.92
   ATOM  3341  O   THR  437  44.177   0.293  70.090  1.00  28.24
10 ATOM  3342  N   PHE  438  44.179  -0.750  72.083  1.00  29.43
   ATOM  3343  CA  PHE  438  42.807  -0.359  72.390  1.00  29.35
   ATOM  3344  CB  PHE  438  41.991  -1.567  72.853  1.00  27.92
   ATOM  3345  CG  PHE  438  41.794  -2.614  71.789  1.00  27.95
   ATOM  3346  CD1 PHE  438  42.695  -3.661  71.648  1.00  27.90
15 ATOM  3347  CD2 PHE  438  40.703  -2.549  70.930  1.00  24.76
   ATOM  3348  CE1 PHE  438  42.505  -4.634  70.662  1.00  29.21
   ATOM  3349  CE2 PHE  438  40.506  -3.505  69.950  1.00  28.87
   ATOM  3350  CZ  PHE  438  41.408  -4.554  69.814  1.00  28.70
   ATOM  3351  C   PHE  438  42.772   0.712  73.467  1.00  30.41
20 ATOM  3352  O   PHE  438  43.469   0.601  74.474  1.00  30.53
   ATOM  3353  N   ILE  439  41.968   1.752  73.250  1.00  30.35
   ATOM  3354  CA  ILE  439  41.839   2.832  74.220  1.00  31.89
   ATOM  3355  CB  ILE  439  42.544   4.124  73.751  1.00  33.03
   ATOM  3356  CG2 ILE  439  42.233   5.269  74.721  1.00  36.00
25 ATOM  3357  CG1 ILE  439  44.053   3.916  73.704  1.00  33.82
   ATOM  3358  CD1 ILE  439  44.818   5.165  73.296  1.00  36.93
   ATOM  3359  C   ILE  439  40.373   3.158  74.420  1.00  32.85
   ATOM  3360  O   ILE  439  39.603   3.157  73.467  1.00  33.09
   ATOM  3361  N   GLU  440  39.991   3.442  75.659  1.00  35.09
```

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3362 | CA | GLU | 440 | 38. 608 | 3. 789 | 75. 956 | 1. 00 39. 34 |
| | ATOM | 3363 | CB | GLU | 440 | 38. 133 | 3. 041 | 77. 199 | 1. 00 37. 95 |
| | ATOM | 3364 | CG | GLU | 440 | 38. 213 | 1. 526 | 77. 038 | 1. 00 39. 96 |
| | ATOM | 3365 | CD | GLU | 440 | 37. 837 | 0. 773 | 78. 298 | 1. 00 40. 82 |
| 5 | ATOM | 3366 | OE1 | GLU | 440 | 38. 058 | -0. 456 | 78. 340 | 1. 00 41. 23 |
| | ATOM | 3367 | OE2 | GLU | 440 | 37. 318 | 1. 403 | 79. 245 | 1. 00 41. 08 |
| | ATOM | 3368 | C | GLU | 440 | 38. 495 | 5. 298 | 76. 156 | 1. 00 41. 28 |
| | ATOM | 3369 | O | GLU | 440 | 39. 356 | 5. 918 | 76. 769 | 1. 00 42. 10 |
| | ATOM | 3370 | N | SER | 441 | 37. 431 | 5. 886 | 75. 627 | 1. 00 43. 99 |
| 10 | ATOM | 3371 | CA | SER | 441 | 37. 231 | 7. 327 | 75. 738 | 1. 00 48. 53 |
| | ATOM | 3372 | CB | SER | 441 | 36. 390 | 7. 823 | 74. 550 | 1. 00 47. 96 |
| | ATOM | 3373 | OG | SER | 441 | 35. 196 | 7. 066 | 74. 390 | 1. 00 48. 42 |
| | ATOM | 3374 | C | SER | 441 | 36. 577 | 7. 752 | 77. 051 | 1. 00 50. 20 |
| | ATOM | 3375 | O | SER | 441 | 35. 654 | 7. 087 | 77. 531 | 1. 00 51. 01 |
| 15 | ATOM | 3376 | N | GLU | 442 | 37. 060 | 8. 852 | 77. 634 | 1. 00 53. 24 |
| | ATOM | 3377 | CA | GLU | 442 | 36. 490 | 9. 359 | 78. 885 | 1. 00 55. 51 |
| | ATOM | 3378 | CB | GLU | 442 | 37. 362 | 10. 454 | 79. 507 | 1. 00 60. 16 |
| | ATOM | 3379 | CG | GLU | 442 | 36. 822 | 10. 936 | 80. 859 | 1. 00 65. 44 |
| | ATOM | 3380 | CD | GLU | 442 | 37. 596 | 12. 107 | 81. 450 | 1. 00 69. 63 |
| 20 | ATOM | 3381 | OE1 | GLU | 442 | 38. 824 | 11. 984 | 81. 667 | 1. 00 71. 27 |
| | ATOM | 3382 | OE2 | GLU | 442 | 36. 965 | 13. 155 | 81. 709 | 1. 00 72. 91 |
| | ATOM | 3383 | C | GLU | 442 | 35. 118 | 9. 938 | 78. 579 | 1. 00 54. 68 |
| | ATOM | 3384 | O | GLU | 442 | 34. 104 | 9. 495 | 79. 126 | 1. 00 56. 30 |
| | ATOM | 3385 | N | GLU | 443 | 35. 094 | 10. 942 | 77. 714 | 1. 00 51. 73 |
| 25 | ATOM | 3386 | CA | GLU | 443 | 33. 840 | 11. 555 | 77. 307 | 1. 00 51. 12 |
| | ATOM | 3387 | CB | GLU | 443 | 33. 706 | 12. 960 | 77. 888 | 1. 00 51. 77 |
| | ATOM | 3388 | CG | GLU | 443 | 32. 561 | 13. 086 | 78. 869 | 1. 00 49. 05 |
| | ATOM | 3389 | CD | GLU | 443 | 31. 202 | 12. 812 | 78. 239 | 1. 00 48. 41 |
| | ATOM | 3390 | OE1 | GLU | 443 | 30. 245 | 12. 572 | 79. 006 | 1. 00 48. 06 |

- 133 -

| | ATOM | 3391 | OE2 | GLU | 443 | 31.084 | 12.842 | 76.990 | 1.00 | 44.46 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 3392 | C | GLU | 443 | 33.851 | 11.614 | 75.793 | 1.00 | 50.48 |
| | ATOM | 3393 | O | GLU | 443 | 33.624 | 12.662 | 75.191 | 1.00 | 50.61 |
| | ATOM | 3394 | N | GLY | 444 | 34.131 | 10.458 | 75.199 | 1.00 | 49.69 |
| 5 | ATOM | 3395 | CA | GLY | 444 | 34.213 | 10.321 | 73.760 | 1.00 | 46.29 |
| | ATOM | 3396 | C | GLY | 444 | 33.300 | 11.190 | 72.928 | 1.00 | 45.39 |
| | ATOM | 3397 | O | GLY | 444 | 33.786 | 12.031 | 72.181 | 1.00 | 44.10 |
| | ATOM | 3398 | N | SER | 445 | 31.990 | 10.996 | 73.052 | 1.00 | 44.40 |
| | ATOM | 3399 | CA | SER | 445 | 31.035 | 11.765 | 72.263 | 1.00 | 45.82 |
| 10 | ATOM | 3400 | CB | SER | 445 | 29.614 | 11.258 | 72.505 | 1.00 | 43.70 |
| | ATOM | 3401 | OG | SER | 445 | 29.248 | 11.396 | 73.860 | 1.00 | 51.13 |
| | ATOM | 3402 | C | SER | 445 | 31.108 | 13.265 | 72.523 | 1.00 | 45.79 |
| | ATOM | 3403 | O | SER | 445 | 31.381 | 14.043 | 71.607 | 1.00 | 46.62 |
| | ATOM | 3404 | N | GLY | 446 | 30.867 | 13.666 | 73.766 | 1.00 | 45.46 |
| 15 | ATOM | 3405 | CA | GLY | 446 | 30.924 | 15.075 | 74.112 | 1.00 | 44.61 |
| | ATOM | 3406 | C | GLY | 446 | 32.176 | 15.778 | 73.615 | 1.00 | 44.65 |
| | ATOM | 3407 | O | GLY | 446 | 32.085 | 16.754 | 72.872 | 1.00 | 45.17 |
| | ATOM | 3408 | N | ARG | 447 | 33.344 | 15.286 | 74.024 | 1.00 | 44.10 |
| | ATOM | 3409 | CA | ARG | 447 | 34.615 | 15.878 | 73.615 | 1.00 | 44.23 |
| 20 | ATOM | 3410 | CB | ARG | 447 | 35.765 | 15.244 | 74.396 | 1.00 | 44.71 |
| | ATOM | 3411 | CG | ARG | 447 | 36.079 | 15.917 | 75.720 | 1.00 | 46.63 |
| | ATOM | 3412 | CD | ARG | 447 | 36.405 | 14.896 | 76.794 | 1.00 | 48.87 |
| | ATOM | 3413 | NE | ARG | 447 | 37.226 | 13.804 | 76.286 | 1.00 | 53.97 |
| | ATOM | 3414 | CZ | ARG | 447 | 38.507 | 13.915 | 75.956 | 1.00 | 55.65 |
| 25 | ATOM | 3415 | NH1 | ARG | 447 | 39.130 | 15.076 | 76.085 | 1.00 | 56.71 |
| | ATOM | 3416 | NH2 | ARG | 447 | 39.161 | 12.862 | 75.486 | 1.00 | 58.00 |
| | ATOM | 3417 | C | ARG | 447 | 34.891 | 15.739 | 72.122 | 1.00 | 45.53 |
| | ATOM | 3418 | O | ARG | 447 | 35.506 | 16.617 | 71.508 | 1.00 | 45.95 |
| | ATOM | 3419 | N | GLY | 448 | 34.444 | 14.630 | 71.543 | 1.00 | 45.12 |

- 134 -

|   | ATOM | 3420 | CA | GLY | 448 | 34.667 | 14.395 | 70.129 | 1.00 | 43.75 |
|---|------|------|-----|------|-----|--------|--------|--------|------|-------|
|   | ATOM | 3421 | C | GLY | 448 | 33.915 | 15.390 | 69.275 | 1.00 | 44.42 |
|   | ATOM | 3422 | O | GLY | 448 | 34.497 | 16.033 | 68.401 | 1.00 | 43.25 |
|   | ATOM | 3423 | N | ALA | 449 | 32.617 | 15.508 | 69.530 | 1.00 | 44.33 |
| 5 | ATOM | 3424 | CA | ALA | 449 | 31.764 | 16.435 | 68.798 | 1.00 | 46.02 |
|   | ATOM | 3425 | CB | ALA | 449 | 30.349 | 16.393 | 69.362 | 1.00 | 44.02 |
|   | ATOM | 3426 | C | ALA | 449 | 32.334 | 17.852 | 68.901 | 1.00 | 47.27 |
|   | ATOM | 3427 | O | ALA | 449 | 32.388 | 18.585 | 67.910 | 1.00 | 46.99 |
|   | ATOM | 3428 | N | ALA | 450 | 32.771 | 18.226 | 70.100 | 1.00 | 47.32 |
| 10 | ATOM | 3429 | CA | ALA | 450 | 33.337 | 19.549 | 70.320 | 1.00 | 48.93 |
|   | ATOM | 3430 | CB | ALA | 450 | 33.590 | 19.771 | 71.803 | 1.00 | 48.70 |
|   | ATOM | 3431 | C | ALA | 450 | 34.630 | 19.752 | 69.537 | 1.00 | 49.10 |
|   | ATOM | 3432 | O | ALA | 450 | 34.795 | 20.770 | 68.864 | 1.00 | 51.55 |
|   | ATOM | 3433 | N | LEU | 451 | 35.546 | 18.792 | 69.625 | 1.00 | 47.13 |
| 15 | ATOM | 3434 | CA | LEU | 451 | 36.828 | 18.889 | 68.923 | 1.00 | 46.08 |
|   | ATOM | 3435 | CB | LEU | 451 | 37.693 | 17.661 | 69.226 | 1.00 | 43.72 |
|   | ATOM | 3436 | CG | LEU | 451 | 38.376 | 17.636 | 70.598 | 1.00 | 44.07 |
|   | ATOM | 3437 | CD1 | LEU | 451 | 38.798 | 16.218 | 70.955 | 1.00 | 41.74 |
|   | ATOM | 3438 | CD2 | LEU | 451 | 39.577 | 18.574 | 70.574 | 1.00 | 40.23 |
| 20 | ATOM | 3439 | C | LEU | 451 | 36.672 | 19.055 | 67.410 | 1.00 | 45.46 |
|   | ATOM | 3440 | O | LEU | 451 | 37.495 | 19.708 | 66.760 | 1.00 | 46.36 |
|   | ATOM | 3441 | N | VAL | 452 | 35.618 | 18.465 | 66.857 | 1.00 | 43.95 |
|   | ATOM | 3442 | CA | VAL | 452 | 35.348 | 18.552 | 65.428 | 1.00 | 44.38 |
|   | ATOM | 3443 | CB | VAL | 452 | 34.426 | 17.376 | 64.959 | 1.00 | 43.85 |
| 25 | ATOM | 3444 | CG1 | VAL | 452 | 33.998 | 17.576 | 63.513 | 1.00 | 41.59 |
|   | ATOM | 3445 | CG2 | VAL | 452 | 35.169 | 16.040 | 65.087 | 1.00 | 40.86 |
|   | ATOM | 3446 | C | VAL | 452 | 34.687 | 19.905 | 65.125 | 1.00 | 45.31 |
|   | ATOM | 3447 | O | VAL | 452 | 34.881 | 20.482 | 64.056 | 1.00 | 42.97 |
|   | ATOM | 3448 | N | SER | 453 | 33.912 | 20.411 | 66.077 | 1.00 | 46.60 |

- 135 -

| | ATOM | 3449 | CA | SER | 453 | 33.253 | 21.693 | 65.900 | 1.00 | 49.07 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3450 | CB | SER | 453 | 32.204 | 21.902 | 66.986 | 1.00 | 47.21 |
| | ATOM | 3451 | OG | SER | 453 | 31.146 | 20.972 | 66.845 | 1.00 | 44.37 |
| | ATOM | 3452 | C | SER | 453 | 34.293 | 22.806 | 65.951 | 1.00 | 51.53 |
| 5 | ATOM | 3453 | O | SER | 453 | 34.150 | 23.820 | 65.281 | 1.00 | 52.56 |
| | ATOM | 3454 | N | ALA | 454 | 35.352 | 22.593 | 66.728 | 1.00 | 54.40 |
| | ATOM | 3455 | CA | ALA | 454 | 36.430 | 23.567 | 66.881 | 1.00 | 56.39 |
| | ATOM | 3456 | CB | ALA | 454 | 37.336 | 23.158 | 68.031 | 1.00 | 55.74 |
| | ATOM | 3457 | C | ALA | 454 | 37.259 | 23.751 | 65.614 | 1.00 | 58.75 |
| 10 | ATOM | 3458 | O | ALA | 454 | 37.863 | 24.807 | 65.408 | 1.00 | 59.45 |
| | ATOM | 3459 | N | VAL | 455 | 37.310 | 22.719 | 64.779 | 1.00 | 60.29 |
| | ATOM | 3460 | CA | VAL | 455 | 38.063 | 22.796 | 63.535 | 1.00 | 61.78 |
| | ATOM | 3461 | CB | VAL | 455 | 38.603 | 21.416 | 63.112 | 1.00 | 61.44 |
| | ATOM | 3462 | CG1 | VAL | 455 | 39.090 | 21.464 | 61.672 | 1.00 | 60.81 |
| 15 | ATOM | 3463 | CG2 | VAL | 455 | 39.737 | 21.005 | 64.031 | 1.00 | 60.68 |
| | ATOM | 3464 | C | VAL | 455 | 37.152 | 23.330 | 62.442 | 1.00 | 63.56 |
| | ATOM | 3465 | O | VAL | 455 | 37.550 | 24.176 | 61.643 | 1.00 | 63.25 |
| | ATOM | 3466 | N | ALA | 456 | 35.921 | 22.835 | 62.416 | 1.00 | 65.38 |
| | ATOM | 3467 | CA | ALA | 456 | 34.959 | 23.275 | 61.422 | 1.00 | 69.39 |
| 20 | ATOM | 3468 | CB | ALA | 456 | 33.751 | 22.354 | 61.423 | 1.00 | 68.17 |
| | ATOM | 3469 | C | ALA | 456 | 34.522 | 24.709 | 61.710 | 1.00 | 73.10 |
| | ATOM | 3470 | O | ALA | 456 | 33.975 | 25.382 | 60.837 | 1.00 | 73.04 |
| | ATOM | 3471 | N | CYS | 457 | 34.771 | 25.170 | 62.935 | 1.00 | 77.06 |
| | ATOM | 3472 | CA | CYS | 457 | 34.390 | 26.521 | 63.341 | 1.00 | 81.01 |
| 25 | ATOM | 3473 | CB | CYS | 457 | 34.192 | 26.599 | 64.856 | 1.00 | 80.51 |
| | ATOM | 3474 | SG | CYS | 457 | 33.478 | 28.151 | 65.432 | 1.00 | 81.75 |
| | ATOM | 3475 | C | CYS | 457 | 35.420 | 27.554 | 62.916 | 1.00 | 83.65 |
| | ATOM | 3476 | O | CYS | 457 | 35.312 | 28.726 | 63.275 | 1.00 | 85.11 |
| | ATOM | 3477 | N | LYS | 458 | 36.430 | 27.118 | 62.172 | 1.00 | 86.29 |

|   | ATOM | 3478 | CA  | LYS | 458 | 37.441 | 28.041 | 61.683 | 1.00 | 89.14 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 3479 | CB  | LYS | 458 | 38.843 | 27.441 | 61.803 | 1.00 | 88.60 |
|   | ATOM | 3480 | CG  | LYS | 458 | 39.932 | 28.486 | 61.632 | 1.00 | 89.51 |
|   | ATOM | 3481 | CD  | LYS | 458 | 41.276 | 27.992 | 62.130 | 1.00 | 89.70 |
| 5 | ATOM | 3482 | CE  | LYS | 458 | 42.257 | 29.146 | 62.269 | 1.00 | 89.22 |
|   | ATOM | 3483 | NZ  | LYS | 458 | 41.718 | 30.194 | 63.180 | 1.00 | 88.81 |
|   | ATOM | 3484 | C   | LYS | 458 | 37.096 | 28.310 | 60.232 | 1.00 | 91.26 |
|   | ATOM | 3485 | O   | LYS | 458 | 37.936 | 28.733 | 59.438 | 1.00 | 91.56 |
|   | ATOM | 3486 | N   | LYS | 459 | 35.834 | 28.043 | 59.901 | 1.00 | 93.94 |
| 10 | ATOM | 3487 | CA  | LYS | 459 | 35.302 | 28.240 | 58.548 | 1.00 | 96.28 |
|   | ATOM | 3488 | CB  | LYS | 459 | 35.323 | 26.923 | 57.765 | 1.00 | 96.25 |
|   | ATOM | 3489 | CG  | LYS | 459 | 36.719 | 26.409 | 57.421 | 1.00 | 96.30 |
|   | ATOM | 3490 | CD  | LYS | 459 | 37.458 | 27.348 | 56.475 | 1.00 | 96.73 |
|   | ATOM | 3491 | CE  | LYS | 459 | 38.833 | 26.801 | 56.111 | 1.00 | 97.12 |
| 15 | ATOM | 3492 | NZ  | LYS | 459 | 39.577 | 27.717 | 55.197 | 1.00 | 97.75 |
|   | ATOM | 3493 | C   | LYS | 459 | 33.863 | 28.759 | 58.624 | 1.00 | 97.78 |
|   | ATOM | 3494 | O   | LYS | 459 | 33.417 | 29.516 | 57.758 | 1.00 | 98.11 |
|   | ATOM | 3495 | N   | ALA | 460 | 33.153 | 28.327 | 59.666 | 1.00 | 99.29 |
|   | ATOM | 3496 | CA  | ALA | 460 | 31.778 | 28.738 | 59.916 | 1.00 | 100.54 |
| 20 | ATOM | 3497 | CB  | ALA | 460 | 31.028 | 27.644 | 60.681 | 1.00 | 100.58 |
|   | ATOM | 3498 | C   | ALA | 460 | 31.765 | 30.042 | 60.719 | 1.00 | 101.56 |
|   | ATOM | 3499 | O   | ALA | 460 | 30.755 | 30.750 | 60.777 | 1.00 | 101.79 |
|   | ATOM | 3500 | N   | CYS | 461 | 32.899 | 30.360 | 61.338 | 1.00 | 102.59 |
|   | ATOM | 3501 | CA  | CYS | 461 | 33.033 | 31.572 | 62.156 | 1.00 | 103.00 |
| 25 | ATOM | 3502 | CB  | CYS | 461 | 33.145 | 31.169 | 63.624 | 1.00 | 103.05 |
|   | ATOM | 3503 | SG  | CYS | 461 | 33.354 | 32.536 | 64.774 | 1.00 | 103.32 |
|   | ATOM | 3504 | C   | CYS | 461 | 34.265 | 32.367 | 61.753 | 1.00 | 103.21 |
|   | ATOM | 3505 | O   | CYS | 461 | 34.788 | 33.098 | 62.620 | 1.00 | 103.54 |
|   | ATOM | 3506 | OXT | CYS | 461 | 34.665 | 32.248 | 60.578 | 1.00 | 103.24 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | TER | 3507 | CYS | 461 | | | | | |
| | ATOM | 3508 | C1 | GLC | 500 | 23.469 | 1.767 | 65.521 | 1.00 30.82 |
| | ATOM | 3509 | C2 | GLC | 500 | 23.418 | 3.122 | 64.706 | 1.00 29.40 |
| | ATOM | 3510 | C3 | GLC | 500 | 24.837 | 3.619 | 64.445 | 1.00 29.78 |
| 5 | ATOM | 3511 | C4 | GLC | 500 | 25.496 | 3.860 | 65.778 | 1.00 28.77 |
| | ATOM | 3512 | C5 | GLC | 500 | 25.529 | 2.514 | 66.593 | 1.00 27.72 |
| | ATOM | 3513 | C6 | GLC | 500 | 26.162 | 2.717 | 67.936 | 1.00 26.98 |
| | ATOM | 3514 | O1 | GLC | 500 | 24.127 | 0.765 | 64.857 | 1.00 36.62 |
| | ATOM | 3515 | O2 | GLC | 500 | 22.756 | 2.872 | 63.483 | 1.00 32.75 |
| 10 | ATOM | 3516 | O3 | GLC | 500 | 24.786 | 4.837 | 63.698 | 1.00 29.31 |
| | ATOM | 3517 | O4 | GLC | 500 | 26.853 | 4.253 | 65.639 | 1.00 29.10 |
| | ATOM | 3518 | O5 | GLC | 500 | 24.152 | 2.040 | 66.770 | 1.00 29.59 |
| | ATOM | 3519 | O6 | GLC | 500 | 25.517 | 3.687 | 68.814 | 1.00 30.98 |
| | TER | 3520 | GLC | 500 | | | | | |
| 15 | ATOM | 3521 | S1 | CP1 | 501 | 36.312 | 19.051 | 60.824 | 1.00 50.83 |
| | ATOM | 3522 | C2 | CP1 | 501 | 35.720 | 19.405 | 59.240 | 1.00 49.96 |
| | ATOM | 3523 | C3 | CP1 | 501 | 36.398 | 18.662 | 58.318 | 1.00 49.96 |
| | ATOM | 3524 | N4 | CP1 | 501 | 37.363 | 17.829 | 58.827 | 1.00 49.99 |
| | ATOM | 3525 | C5 | CP1 | 501 | 37.429 | 17.932 | 60.162 | 1.00 49.39 |
| 20 | ATOM | 3526 | N6 | CP1 | 501 | 38.317 | 17.183 | 60.878 | 1.00 48.07 |
| | ATOM | 3527 | C7 | CP1 | 501 | 38.575 | 17.220 | 62.294 | 1.00 46.71 |
| | ATOM | 3528 | O8 | CP1 | 501 | 37.968 | 18.001 | 63.039 | 1.00 47.48 |
| | ATOM | 3529 | C9 | CP1 | 501 | 40.386 | 16.405 | 64.107 | 1.00 46.71 |
| | ATOM | 3530 | C10 | CP1 | 501 | 39.620 | 16.253 | 62.884 | 1.00 47.34 |
| 25 | ATOM | 3531 | C11 | CP1 | 501 | 39.831 | 15.053 | 62.110 | 1.00 46.39 |
| | ATOM | 3532 | C12 | CP1 | 501 | 40.749 | 14.066 | 62.520 | 1.00 46.34 |
| | ATOM | 3533 | C13 | CP1 | 501 | 41.496 | 14.237 | 63.722 | 1.00 47.57 |
| | ATOM | 3534 | F | CP1 | 501 | 42.392 | 13.310 | 64.155 | 1.00 48.24 |
| | ATOM | 3535 | C15 | CP1 | 501 | 41.306 | 15.404 | 64.502 | 1.00 46.98 |

- 138 -

| | ATOM | 3536 | S16 | CP1 | 501 | 40.907 | 12.638 | 61.485 | 1.00 | 44.61 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3537 | N17 | CP1 | 501 | 42.782 | 10.864 | 62.327 | 1.00 | 40.11 |
| | ATOM | 3538 | C18 | CP1 | 501 | 42.525 | 11.942 | 61.488 | 1.00 | 41.49 |
| | ATOM | 3539 | N19 | CP1 | 501 | 43.528 | 12.436 | 60.686 | 1.00 | 42.95 |
| 5 | ATOM | 3540 | C20 | CP1 | 501 | 44.549 | 11.571 | 61.054 | 1.00 | 43.00 |
| | ATOM | 3541 | C21 | CP1 | 501 | 44.116 | 10.651 | 62.014 | 1.00 | 39.24 |
| | ATOM | 3542 | C22 | CP1 | 501 | 41.894 | 10.152 | 63.276 | 1.00 | 32.83 |
| | ATOM | 3543 | N23 | CP1 | 501 | 40.279 | 17.465 | 64.913 | 1.00 | 46.10 |
| | TER | 3544 | | CP1 | 501 | JJJJ | | | | |
| 10 | ATOM | 3545 | NA+1 | NA1 | 600 | 36.903 | 10.609 | 46.484 | 1.00 | 48.71 |
| | ATOM | 3546 | O | HOH | 601 | 20.332 | -23.624 | 70.208 | 1.00 | 45.57 |
| | ATOM | 3547 | O | HOH | 602 | 18.766 | -22.456 | 65.630 | 1.00 | 41.87 |
| | ATOM | 3548 | O | HOH | 603 | 13.471 | -20.599 | 70.297 | 1.00 | 45.83 |
| | ATOM | 3549 | O | HOH | 604 | 11.104 | -30.408 | 72.307 | 1.00 | 48.61 |
| 15 | ATOM | 3550 | O | HOH | 605 | 6.606 | -26.352 | 79.319 | 1.00 | 59.47 |
| | ATOM | 3551 | O | HOH | 606 | 15.315 | -28.400 | 85.522 | 1.00 | 48.85 |
| | ATOM | 3552 | O | HOH | 607 | 18.765 | -29.705 | 82.807 | 1.00 | 55.60 |
| | ATOM | 3553 | O | HOH | 608 | 27.649 | -22.465 | 84.914 | 1.00 | 39.29 |
| | ATOM | 3554 | O | HOH | 609 | 28.890 | -18.936 | 88.942 | 1.00 | 38.24 |
| 20 | ATOM | 3555 | O | HOH | 610 | 31.397 | -19.437 | 88.300 | 1.00 | 44.33 |
| | ATOM | 3556 | O | HOH | 611 | 33.495 | -12.487 | 88.943 | 1.00 | 40.63 |
| | ATOM | 3557 | O | HOH | 612 | 28.110 | -14.193 | 93.119 | 1.00 | 37.41 |
| | ATOM | 3558 | O | HOH | 613 | 22.501 | -9.921 | 93.883 | 1.00 | 55.62 |
| | ATOM | 3559 | O | HOH | 614 | 18.084 | -9.259 | 91.966 | 1.00 | 48.69 |
| 25 | ATOM | 3560 | O | HOH | 615 | 19.985 | -7.585 | 89.518 | 1.00 | 54.30 |
| | ATOM | 3561 | O | HOH | 616 | 18.162 | -4.982 | 77.583 | 1.00 | 42.44 |
| | ATOM | 3562 | O | HOH | 617 | 15.728 | -5.792 | 77.752 | 1.00 | 49.61 |
| | ATOM | 3563 | O | HOH | 618 | 17.869 | -7.338 | 75.263 | 1.00 | 52.43 |
| | ATOM | 3564 | O | HOH | 619 | 14.631 | -9.827 | 77.339 | 1.00 | 27.38 |

- 139 -

| | ATOM | 3565 | O | HOH | 620 | 14.305 | -5.926 | 69.446 | 1.00 | 38.14 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3566 | O | HOH | 621 | 13.616 | -3.087 | 68.452 | 1.00 | 51.29 |
| | ATOM | 3567 | O | HOH | 622 | 15.537 | -2.602 | 66.865 | 1.00 | 35.42 |
| | ATOM | 3568 | O | HOH | 623 | 18.821 | -1.831 | 65.405 | 1.00 | 31.67 |
| 5 | ATOM | 3569 | O | HOH | 624 | 17.261 | 0.174 | 60.996 | 1.00 | 34.87 |
| | ATOM | 3570 | O | HOH | 625 | 18.895 | -0.653 | 58.995 | 1.00 | 41.82 |
| | ATOM | 3571 | O | HOH | 626 | 20.053 | -2.478 | 55.373 | 1.00 | 35.91 |
| | ATOM | 3572 | O | HOH | 627 | 22.217 | -1.019 | 55.062 | 1.00 | 36.64 |
| | ATOM | 3573 | O | HOH | 628 | 25.137 | -0.153 | 56.470 | 1.00 | 24.69 |
| 10 | ATOM | 3574 | O | HOH | 629 | 22.562 | 1.498 | 59.774 | 1.00 | 31.68 |
| | ATOM | 3575 | O | HOH | 630 | 24.912 | 0.122 | 62.135 | 1.00 | 25.12 |
| | ATOM | 3576 | O | HOH | 631 | 25.071 | 2.179 | 71.129 | 1.00 | 26.49 |
| | ATOM | 3577 | O | HOH | 632 | 27.157 | 5.888 | 71.903 | 1.00 | 41.05 |
| | ATOM | 3578 | O | HOH | 633 | 29.481 | 7.227 | 73.290 | 1.00 | 47.52 |
| 15 | ATOM | 3579 | O | HOH | 634 | 31.223 | 8.383 | 71.417 | 1.00 | 44.33 |
| | ATOM | 3580 | O | HOH | 635 | 32.517 | 7.788 | 77.983 | 1.00 | 44.30 |
| | ATOM | 3581 | O | HOH | 636 | 35.945 | 15.748 | 80.298 | 1.00 | 32.85 |
| | ATOM | 3582 | O | HOH | 637 | 41.395 | 13.522 | 74.250 | 1.00 | 52.40 |
| | ATOM | 3583 | O | HOH | 638 | 41.454 | 16.603 | 73.492 | 1.00 | 35.38 |
| 20 | ATOM | 3584 | O | HOH | 639 | 44.238 | 18.657 | 64.621 | 1.00 | 57.41 |
| | ATOM | 3585 | O | HOH | 640 | 48.524 | 12.679 | 62.857 | 1.00 | 55.80 |
| | ATOM | 3586 | O | HOH | 641 | 50.088 | 10.035 | 69.707 | 1.00 | 37.86 |
| | ATOM | 3587 | O | HOH | 642 | 47.834 | 4.897 | 73.654 | 1.00 | 43.91 |
| | ATOM | 3588 | O | HOH | 643 | 47.658 | 2.456 | 75.515 | 1.00 | 46.89 |
| 25 | ATOM | 3589 | O | HOH | 644 | 45.862 | 0.872 | 75.793 | 1.00 | 36.22 |
| | ATOM | 3590 | O | HOH | 645 | 42.167 | -0.401 | 77.407 | 1.00 | 46.09 |
| | ATOM | 3591 | O | HOH | 646 | 39.939 | -1.664 | 76.818 | 1.00 | 28.80 |
| | ATOM | 3592 | O | HOH | 647 | 41.804 | 2.590 | 77.672 | 1.00 | 30.06 |
| | ATOM | 3593 | O | HOH | 648 | 35.946 | -0.230 | 81.704 | 1.00 | 44.47 |

– 140 –

| | ATOM | 3594 | O | HOH | 649 | 35.692 | −3.832 | 84.533 | 1.00 | 48.68 |
| | ATOM | 3595 | O | HOH | 650 | 35.503 | −5.648 | 82.602 | 1.00 | 39.36 |
| | ATOM | 3596 | O | HOH | 651 | 34.249 | −6.282 | 78.743 | 1.00 | 28.80 |
| | ATOM | 3597 | O | HOH | 652 | 41.570 | −6.014 | 79.114 | 1.00 | 41.31 |
| 5 | ATOM | 3598 | O | HOH | 653 | 42.725 | −8.259 | 76.851 | 1.00 | 34.12 |
| | ATOM | 3599 | O | HOH | 654 | 42.400 | −10.619 | 75.649 | 1.00 | 32.12 |
| | ATOM | 3600 | O | HOH | 655 | 44.745 | −10.112 | 73.414 | 1.00 | 30.95 |
| | ATOM | 3601 | O | HOH | 656 | 44.977 | −6.287 | 75.709 | 1.00 | 54.82 |
| | ATOM | 3602 | O | HOH | 657 | 49.536 | −3.896 | 71.639 | 1.00 | 46.68 |
| 10 | ATOM | 3603 | O | HOH | 658 | 47.500 | −6.424 | 68.659 | 1.00 | 37.00 |
| | ATOM | 3604 | O | HOH | 659 | 46.887 | −8.289 | 65.948 | 1.00 | 35.73 |
| | ATOM | 3605 | O | HOH | 660 | 45.007 | −14.004 | 70.403 | 1.00 | 31.53 |
| | ATOM | 3606 | O | HOH | 661 | 44.785 | −16.666 | 70.958 | 1.00 | 39.67 |
| | ATOM | 3607 | O | HOH | 662 | 39.546 | −15.899 | 74.666 | 1.00 | 38.86 |
| 15 | ATOM | 3608 | O | HOH | 663 | 38.539 | −14.985 | 72.232 | 1.00 | 34.80 |
| | ATOM | 3609 | O | HOH | 664 | 38.252 | −17.032 | 68.208 | 1.00 | 47.76 |
| | ATOM | 3610 | O | HOH | 665 | 39.836 | −15.454 | 66.437 | 1.00 | 38.55 |
| | ATOM | 3611 | O | HOH | 666 | 36.975 | −19.549 | 67.636 | 1.00 | 43.12 |
| | ATOM | 3612 | O | HOH | 667 | 37.200 | −20.262 | 70.388 | 1.00 | 51.64 |
| 20 | ATOM | 3613 | O | HOH | 668 | 33.328 | −20.695 | 70.543 | 1.00 | 49.91 |
| | ATOM | 3614 | O | HOH | 669 | 32.877 | −18.716 | 69.209 | 1.00 | 30.69 |
| | ATOM | 3615 | O | HOH | 670 | 30.463 | −18.228 | 69.770 | 1.00 | 29.35 |
| | ATOM | 3616 | O | HOH | 671 | 29.403 | −18.862 | 72.028 | 1.00 | 29.94 |
| | ATOM | 3617 | O | HOH | 672 | 31.677 | −19.876 | 75.929 | 1.00 | 57.83 |
| 25 | ATOM | 3618 | O | HOH | 673 | 32.105 | −15.120 | 81.811 | 1.00 | 56.36 |
| | ATOM | 3619 | O | HOH | 674 | 25.408 | −13.262 | 70.399 | 1.00 | 19.73 |
| | ATOM | 3620 | O | HOH | 675 | 20.199 | −11.770 | 66.567 | 1.00 | 31.95 |
| | ATOM | 3621 | O | HOH | 676 | 20.589 | −11.169 | 63.684 | 1.00 | 28.18 |
| | ATOM | 3622 | O | HOH | 677 | 18.416 | −12.169 | 62.695 | 1.00 | 34.73 |

- 141 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3623 | O | HOH | 678 | 18.037 | -12.657 | 56.097 | 1.00 | 62.31 |
| ATOM | 3624 | O | HOH | 679 | 15.700 | -10.616 | 55.942 | 1.00 | 49.61 |
| ATOM | 3625 | O | HOH | 680 | 17.485 | -8.240 | 55.372 | 1.00 | 37.91 |
| ATOM | 3626 | O | HOH | 681 | 22.370 | -12.555 | 56.733 | 1.00 | 27.53 |
| ATOM | 3627 | O | HOH | 682 | 21.048 | -16.039 | 51.265 | 1.00 | 53.09 |
| ATOM | 3628 | O | HOH | 683 | 25.649 | -8.890 | 49.620 | 1.00 | 43.30 |
| ATOM | 3629 | O | HOH | 684 | 25.472 | -5.908 | 50.031 | 1.00 | 43.23 |
| ATOM | 3630 | O | HOH | 685 | 27.841 | -3.633 | 51.119 | 1.00 | 34.64 |
| ATOM | 3631 | O | HOH | 686 | 23.209 | 1.359 | 50.792 | 1.00 | 44.06 |
| ATOM | 3632 | O | HOH | 687 | 26.198 | 3.711 | 50.151 | 1.00 | 38.65 |
| ATOM | 3633 | O | HOH | 688 | 27.728 | 6.416 | 50.494 | 1.00 | 39.66 |
| ATOM | 3634 | O | HOH | 689 | 30.171 | 5.238 | 50.152 | 1.00 | 36.90 |
| ATOM | 3635 | O | HOH | 690 | 32.248 | 6.334 | 48.750 | 1.00 | 33.36 |
| ATOM | 3636 | O | HOH | 691 | 36.665 | 2.495 | 46.196 | 1.00 | 32.68 |
| ATOM | 3637 | O | HOH | 692 | 37.821 | 0.573 | 47.634 | 1.00 | 47.42 |
| ATOM | 3638 | O | HOH | 693 | 42.794 | 0.201 | 52.097 | 1.00 | 44.65 |
| ATOM | 3639 | O | HOH | 694 | 41.559 | 1.725 | 53.810 | 1.00 | 38.52 |
| ATOM | 3640 | O | HOH | 695 | 43.105 | 3.662 | 55.242 | 1.00 | 34.89 |
| ATOM | 3641 | O | HOH | 696 | 45.510 | 2.836 | 56.086 | 1.00 | 40.92 |
| ATOM | 3642 | O | HOH | 697 | 50.206 | 2.510 | 60.598 | 1.00 | 45.86 |
| ATOM | 3643 | O | HOH | 698 | 52.258 | 1.308 | 61.720 | 1.00 | 45.43 |
| ATOM | 3644 | O | HOH | 699 | 48.954 | 1.961 | 67.618 | 1.00 | 35.43 |
| ATOM | 3645 | O | HOH | 700 | 49.694 | -0.399 | 68.442 | 1.00 | 39.38 |
| ATOM | 3646 | O | HOH | 701 | 40.015 | -5.106 | 51.960 | 1.00 | 36.49 |
| ATOM | 3647 | O | HOH | 702 | 34.048 | -12.903 | 50.839 | 1.00 | 37.87 |
| ATOM | 3648 | O | HOH | 703 | 33.190 | -14.541 | 52.882 | 1.00 | 51.09 |
| ATOM | 3649 | O | HOH | 704 | 34.961 | -16.254 | 52.067 | 1.00 | 35.42 |
| ATOM | 3650 | O | HOH | 705 | 30.397 | -15.105 | 52.902 | 1.00 | 39.69 |
| ATOM | 3651 | O | HOH | 706 | 31.770 | -20.985 | 57.467 | 1.00 | 48.16 |

- 142 -

| ATOM | 3652 | O | HOH | 707 | 37.192 | -19.637 | 55.866 | 1.00 | 46.43 |
|------|------|---|-----|-----|--------|---------|--------|------|-------|
| ATOM | 3653 | O | HOH | 708 | 38.187 | -23.567 | 61.924 | 1.00 | 40.92 |
| ATOM | 3654 | O | HOH | 709 | 38.470 | -23.126 | 65.456 | 1.00 | 45.43 |
| ATOM | 3655 | O | HOH | 710 | 30.533 | -23.844 | 62.578 | 1.00 | 37.90 |
| ATOM | 3656 | O | HOH | 711 | 26.515 | -21.678 | 62.544 | 1.00 | 39.08 |
| ATOM | 3657 | O | HOH | 712 | 27.242 | -20.400 | 65.671 | 1.00 | 33.60 |
| ATOM | 3658 | O | HOH | 713 | 25.907 | -18.116 | 65.171 | 1.00 | 24.64 |
| ATOM | 3659 | O | HOH | 714 | 28.226 | -26.567 | 74.622 | 1.00 | 44.93 |
| ATOM | 3660 | O | HOH | 715 | 31.091 | -28.151 | 73.632 | 1.00 | 39.43 |
| ATOM | 3661 | O | HOH | 716 | 28.020 | -32.685 | 74.512 | 1.00 | 48.35 |
| ATOM | 3662 | O | HOH | 717 | 28.401 | -36.363 | 77.956 | 1.00 | 47.24 |
| ATOM | 3663 | O | HOH | 718 | 26.796 | -22.733 | 95.375 | 1.00 | 34.50 |
| ATOM | 3664 | O | HOH | 719 | 23.506 | -18.729 | 96.532 | 1.00 | 46.50 |
| ATOM | 3665 | O | HOH | 720 | 7.193 | -13.392 | 87.134 | 1.00 | 48.33 |
| ATOM | 3666 | O | HOH | 721 | 23.769 | -2.393 | 77.130 | 1.00 | 39.79 |
| ATOM | 3667 | O | HOH | 722 | 21.538 | 6.141 | 76.432 | 1.00 | 52.58 |
| ATOM | 3668 | O | HOH | 723 | 26.038 | 13.552 | 80.579 | 1.00 | 47.60 |
| ATOM | 3669 | O | HOH | 724 | 25.460 | 9.823 | 62.329 | 1.00 | 33.10 |
| ATOM | 3670 | O | HOH | 725 | 27.321 | 10.443 | 60.403 | 1.00 | 39.23 |
| ATOM | 3671 | O | HOH | 726 | 26.658 | 8.602 | 58.871 | 1.00 | 32.16 |
| ATOM | 3672 | O | HOH | 727 | 29.670 | 11.059 | 61.417 | 1.00 | 24.95 |
| ATOM | 3673 | O | HOH | 728 | 30.585 | 13.937 | 60.932 | 1.00 | 41.90 |
| ATOM | 3674 | O | HOH | 729 | 34.591 | 18.790 | 55.094 | 1.00 | 40.47 |
| ATOM | 3675 | O | HOH | 730 | 34.117 | 19.353 | 52.182 | 1.00 | 54.62 |
| ATOM | 3676 | O | HOH | 731 | 31.428 | 16.535 | 48.224 | 1.00 | 37.06 |
| ATOM | 3677 | O | HOH | 732 | 31.432 | 15.488 | 46.047 | 1.00 | 33.85 |
| ATOM | 3678 | O | HOH | 733 | 27.660 | 11.291 | 51.289 | 1.00 | 40.74 |
| ATOM | 3679 | O | HOH | 734 | 27.629 | 10.029 | 53.857 | 1.00 | 30.56 |
| ATOM | 3680 | O | HOH | 735 | 22.996 | 7.311 | 45.724 | 1.00 | 57.65 |

| | ATOM | 3681 | O | HOH | 736 | 25. 532 | 2. 038 | 43. 263 | 1. 00 | 34. 43 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3682 | O | HOH | 737 | 33. 508 | 3. 221 | 40. 211 | 1. 00 | 45. 05 |
| | ATOM | 3683 | O | HOH | 738 | 35. 525 | 1. 426 | 41. 242 | 1. 00 | 44. 71 |
| | ATOM | 3684 | O | HOH | 739 | 37. 227 | 9. 576 | 44. 352 | 1. 00 | 31. 96 |
| 5 | ATOM | 3685 | O | HOH | 740 | 39. 858 | 15. 804 | 52. 237 | 1. 00 | 43. 41 |
| | ATOM | 3686 | O | HOH | 741 | 42. 053 | 15. 415 | 53. 940 | 1. 00 | 47. 39 |
| | ATOM | 3687 | O | HOH | 742 | 32. 200 | 24. 148 | 58. 683 | 1. 00 | 45. 42 |
| | ATOM | 3688 | O | HOH | 743 | 28. 016 | 21. 804 | 51. 201 | 1. 00 | 44. 12 |
| | ATOM | 3689 | O | HOH | 744 | 22. 797 | 26. 498 | 63. 763 | 1. 00 | 53. 69 |
| 10 | ATOM | 3690 | O | HOH | 745 | 10. 552 | 26. 073 | 62. 119 | 1. 00 | 43. 13 |
| | ATOM | 3691 | O | HOH | 746 | 11. 190 | 7. 673 | 68. 338 | 1. 00 | 57. 06 |
| | ATOM | 3692 | O | HOH | 747 | 20. 818 | -3. 881 | 51. 225 | 1. 00 | 56. 55 |
| | ATOM | 3693 | O | HOH | 748 | 29. 885 | -6. 633 | 43. 981 | 1. 00 | 46. 17 |
| | ATOM | 3694 | O | HOH | 749 | 40. 811 | 30. 945 | 68. 309 | 1. 00 | 45. 88 |
| 15 | TER | 3695 | | HOH | | | | | | |

　　なお、表1は、当業者によって慣用されているプロテイン・データ・バンクの表記方法に準拠して作成されている。表1中、ＧＬＣはグルコース分子を表

20　し、ＣＰ１は式ＩＩＩａで表される化合物を表し、ＨＯＨは水分子を表す。

　　また、本発明においては、配列番号8に示すＧＫタンパク質の結晶を調製することに成功している（後述の実施例参照）。そしてこのようにして得られたＧＫタンパク質の結晶は、格子定数が、下記式（5）〜（8）：

25　　　　a=b=103.2±5 オングストローム　　…（5）

　　　　c=281.0±7 オングストローム　　　…（6）

　　　　$\alpha = \beta = 90°$　　　　　　　　　　…（7）

　　　　$\gamma = 120°$　　　　　　　　　…（8）

を満たすものであった。また、この結晶は、空間群が$P6_522$であることが

- 144 -

解明された。ここで、前記 a=b は 103.2±3 オングストロームであることが好ましく、103.2±2 オングストロームであることがより好ましく、103.2±1 オングストロームであることがさらに好ましい。また、前記 c は 281.0±6 オングストロームであることが好ましく、281.0±4 オングストロームであることがより好ましく、281.0±2 オングストロームであることがさらに好ましい。このようにして得られたGKタンパク質結晶の3次元構造座標を表2に示す。

表2

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1 | CB | MET | 15 | 54.150 | 5.972 | 67.103 | 1.00 | 55.10 |
| ATOM | 2 | CG | MET | 15 | 55.594 | 5.943 | 67.591 | 1.00 | 55.46 |
| ATOM | 3 | SD | MET | 15 | 56.013 | 4.505 | 68.603 | 1.00 | 52.92 |
| ATOM | 4 | CE | MET | 15 | 56.517 | 5.326 | 70.108 | 1.00 | 51.73 |
| ATOM | 5 | C | MET | 15 | 52.357 | 4.955 | 65.669 | 1.00 | 56.87 |
| ATOM | 6 | O | MET | 15 | 52.057 | 4.609 | 64.524 | 1.00 | 57.60 |
| ATOM | 7 | N | MET | 15 | 54.770 | 4.766 | 65.028 | 1.00 | 55.00 |
| ATOM | 8 | CA | MET | 15 | 53.800 | 4.813 | 66.167 | 1.00 | 56.04 |
| ATOM | 9 | N | VAL | 16 | 51.468 | 5.456 | 66.525 | 1.00 | 55.58 |
| ATOM | 10 | CA | VAL | 16 | 50.065 | 5.625 | 66.154 | 1.00 | 52.87 |
| ATOM | 11 | CB | VAL | 16 | 49.141 | 4.862 | 67.129 | 1.00 | 49.32 |
| ATOM | 12 | CG1 | VAL | 16 | 47.696 | 5.016 | 66.716 | 1.00 | 48.26 |
| ATOM | 13 | CG2 | VAL | 16 | 49.508 | 3.394 | 67.126 | 1.00 | 47.28 |
| ATOM | 14 | C | VAL | 16 | 49.666 | 7.097 | 66.085 | 1.00 | 53.26 |
| ATOM | 15 | O | VAL | 16 | 49.218 | 7.563 | 65.040 | 1.00 | 52.32 |
| ATOM | 16 | N | GLU | 17 | 49.845 | 7.828 | 67.182 | 1.00 | 56.12 |
| ATOM | 17 | CA | GLU | 17 | 49.511 | 9.253 | 67.210 | 1.00 | 59.41 |
| ATOM | 18 | CB | GLU | 17 | 50.102 | 9.921 | 68.456 | 1.00 | 63.35 |
| ATOM | 19 | CG | GLU | 17 | 49.063 | 10.373 | 69.484 | 1.00 | 68.69 |
| ATOM | 20 | CD | GLU | 17 | 48.174 | 11.525 | 69.004 | 1.00 | 72.00 |
| ATOM | 21 | OE1 | GLU | 17 | 47.314 | 11.964 | 69.805 | 1.00 | 74.22 |

|   | ATOM | 22 | OE2 | GLU | 17 | 48.328 | 11.992 | 67.847 | 1.00 | 72.36 |
|---|------|----|-----|-----|----|--------|--------|--------|------|-------|
|   | ATOM | 23 | C | GLU | 17 | 50.035 | 9.963 | 65.967 | 1.00 | 59.05 |
|   | ATOM | 24 | O | GLU | 17 | 49.521 | 11.011 | 65.566 | 1.00 | 57.70 |
|   | ATOM | 25 | N | GLN | 18 | 51.070 | 9.389 | 65.367 | 1.00 | 60.75 |
| 5 | ATOM | 26 | CA | GLN | 18 | 51.661 | 9.960 | 64.170 | 1.00 | 61.70 |
|   | ATOM | 27 | CB | GLN | 18 | 53.038 | 9.329 | 63.895 | 1.00 | 66.55 |
|   | ATOM | 28 | CG | GLN | 18 | 54.001 | 9.219 | 65.110 | 1.00 | 72.22 |
|   | ATOM | 29 | CD | GLN | 18 | 54.509 | 10.566 | 65.654 | 1.00 | 75.87 |
|   | ATOM | 30 | OE1 | GLN | 18 | 55.317 | 10.605 | 66.595 | 1.00 | 75.55 |
| 10 | ATOM | 31 | NE2 | GLN | 18 | 54.037 | 11.669 | 65.067 | 1.00 | 77.63 |
|   | ATOM | 32 | C | GLN | 18 | 50.709 | 9.682 | 63.004 | 1.00 | 59.33 |
|   | ATOM | 33 | O | GLN | 18 | 50.322 | 10.601 | 62.287 | 1.00 | 59.09 |
|   | ATOM | 34 | N | ILE | 19 | 50.321 | 8.418 | 62.832 | 1.00 | 55.64 |
|   | ATOM | 35 | CA | ILE | 19 | 49.416 | 8.029 | 61.747 | 1.00 | 53.41 |
| 15 | ATOM | 36 | CB | ILE | 19 | 49.113 | 6.529 | 61.778 | 1.00 | 52.34 |
|   | ATOM | 37 | CG2 | ILE | 19 | 47.964 | 6.211 | 60.832 | 1.00 | 50.69 |
|   | ATOM | 38 | CG1 | ILE | 19 | 50.374 | 5.754 | 61.389 | 1.00 | 52.73 |
|   | ATOM | 39 | CD1 | ILE | 19 | 50.186 | 4.256 | 61.274 | 1.00 | 53.73 |
|   | ATOM | 40 | C | ILE | 19 | 48.088 | 8.774 | 61.741 | 1.00 | 53.03 |
| 20 | ATOM | 41 | O | ILE | 19 | 47.791 | 9.528 | 60.812 | 1.00 | 52.86 |
|   | ATOM | 42 | N | LEU | 20 | 47.279 | 8.548 | 62.766 | 1.00 | 52.38 |
|   | ATOM | 43 | CA | LEU | 20 | 45.997 | 9.228 | 62.861 | 1.00 | 51.95 |
|   | ATOM | 44 | CB | LEU | 20 | 45.336 | 8.937 | 64.195 | 1.00 | 50.70 |
|   | ATOM | 45 | CG | LEU | 20 | 44.563 | 7.632 | 64.212 | 1.00 | 51.65 |
| 25 | ATOM | 46 | CD1 | LEU | 20 | 45.450 | 6.454 | 63.803 | 1.00 | 51.77 |
|   | ATOM | 47 | CD2 | LEU | 20 | 44.010 | 7.463 | 65.599 | 1.00 | 51.02 |
|   | ATOM | 48 | C | LEU | 20 | 46.158 | 10.723 | 62.727 | 1.00 | 52.33 |
|   | ATOM | 49 | O | LEU | 20 | 45.204 | 11.427 | 62.401 | 1.00 | 54.11 |
|   | ATOM | 50 | N | ALA | 21 | 47.366 | 11.207 | 62.990 | 1.00 | 51.49 |

| | ATOM | 51 | CA | ALA | 21 | 47.643 | 12.628 | 62.907 | 1.00 | 49.87 |
|---|------|----|----|-----|----|--------|--------|--------|------|-------|
| | ATOM | 52 | CB | ALA | 21 | 49.066 | 12.899 | 63.342 | 1.00 | 50.58 |
| | ATOM | 53 | C | ALA | 21 | 47.414 | 13.133 | 61.491 | 1.00 | 48.63 |
| | ATOM | 54 | O | ALA | 21 | 47.090 | 14.301 | 61.286 | 1.00 | 47.74 |
| 5 | ATOM | 55 | N | GLU | 22 | 47.571 | 12.243 | 60.517 | 1.00 | 47.60 |
| | ATOM | 56 | CA | GLU | 22 | 47.383 | 12.605 | 59.121 | 1.00 | 48.69 |
| | ATOM | 57 | CB | GLU | 22 | 47.818 | 11.457 | 58.215 | 1.00 | 51.49 |
| | ATOM | 58 | CG | GLU | 22 | 49.282 | 11.520 | 57.838 | 1.00 | 59.47 |
| | ATOM | 59 | CD | GLU | 22 | 49.738 | 10.335 | 57.003 | 1.00 | 64.78 |
| 10 | ATOM | 60 | OE1 | GLU | 22 | 50.896 | 10.369 | 56.519 | 1.00 | 66.47 |
| | ATOM | 61 | OE2 | GLU | 22 | 48.948 | 9.373 | 56.839 | 1.00 | 68.05 |
| | ATOM | 62 | C | GLU | 22 | 45.954 | 12.999 | 58.794 | 1.00 | 48.26 |
| | ATOM | 63 | O | GLU | 22 | 45.683 | 13.538 | 57.721 | 1.00 | 48.86 |
| | ATOM | 64 | N | PHE | 23 | 45.036 | 12.733 | 59.715 | 1.00 | 47.14 |
| 15 | ATOM | 65 | CA | PHE | 23 | 43.641 | 13.076 | 59.490 | 1.00 | 45.51 |
| | ATOM | 66 | CB | PHE | 23 | 42.722 | 12.045 | 60.147 | 1.00 | 41.36 |
| | ATOM | 67 | CG | PHE | 23 | 42.544 | 10.783 | 59.347 | 1.00 | 37.96 |
| | ATOM | 68 | CD1 | PHE | 23 | 43.208 | 9.613 | 59.697 | 1.00 | 35.23 |
| | ATOM | 69 | CD2 | PHE | 23 | 41.687 | 10.758 | 58.255 | 1.00 | 37.67 |
| 20 | ATOM | 70 | CE1 | PHE | 23 | 43.016 | 8.435 | 58.968 | 1.00 | 32.67 |
| | ATOM | 71 | CE2 | PHE | 23 | 41.492 | 9.583 | 57.523 | 1.00 | 37.15 |
| | ATOM | 72 | CZ | PHE | 23 | 42.158 | 8.423 | 57.883 | 1.00 | 33.48 |
| | ATOM | 73 | C | PHE | 23 | 43.310 | 14.468 | 60.013 | 1.00 | 47.24 |
| | ATOM | 74 | O | PHE | 23 | 42.227 | 14.993 | 59.767 | 1.00 | 46.34 |
| 25 | ATOM | 75 | N | GLN | 24 | 44.245 | 15.068 | 60.735 | 1.00 | 50.44 |
| | ATOM | 76 | CA | GLN | 24 | 44.028 | 16.400 | 61.279 | 1.00 | 55.06 |
| | ATOM | 77 | CB | GLN | 24 | 45.306 | 16.882 | 61.979 | 1.00 | 59.10 |
| | ATOM | 78 | CG | GLN | 24 | 45.715 | 16.023 | 63.168 | 1.00 | 62.03 |
| | ATOM | 79 | CD | GLN | 24 | 44.686 | 16.075 | 64.277 | 1.00 | 65.56 |

| ATOM | 80 | OE1 | GLN | 24 | 44. 653 | 15. 207 | 65. 156 | 1. 00 | 66. 95 |
|------|-----|-----|-----|-----|---------|---------|---------|-------|--------|
| ATOM | 81 | NE2 | GLN | 24 | 43. 834 | 17. 103 | 64. 245 | 1. 00 | 65. 89 |
| ATOM | 82 | C | GLN | 24 | 43. 644 | 17. 359 | 60. 149 | 1. 00 | 56. 09 |
| ATOM | 83 | 0 | GLN | 24 | 43. 892 | 17. 073 | 58. 979 | 1. 00 | 57. 63 |
| ATOM | 84 | N | LEU | 25 | 43. 016 | 18. 476 | 60. 504 | 1. 00 | 55. 99 |
| ATOM | 85 | CA | LEU | 25 | 42. 616 | 19. 501 | 59. 540 | 1. 00 | 55. 27 |
| ATOM | 86 | CB | LEU | 25 | 41. 303 | 19. 128 | 58. 841 | 1. 00 | 54. 71 |
| ATOM | 87 | CG | LEU | 25 | 41. 325 | 17. 896 | 57. 922 | 1. 00 | 53. 30 |
| ATOM | 88 | CD1 | LEU | 25 | 39. 928 | 17. 618 | 57. 419 | 1. 00 | 53. 18 |
| ATOM | 89 | CD2 | LEU | 25 | 42. 264 | 18. 113 | 56. 755 | 1. 00 | 51. 55 |
| ATOM | 90 | C | LEU | 25 | 42. 444 | 20. 786 | 60. 336 | 1. 00 | 56. 31 |
| ATOM | 91 | 0 | LEU | 25 | 41. 377 | 21. 061 | 60. 889 | 1. 00 | 55. 85 |
| ATOM | 92 | N | GLN | 26 | 43. 519 | 21. 563 | 60. 399 | 1. 00 | 58. 22 |
| ATOM | 93 | CA | GLN | 26 | 43. 527 | 22. 807 | 61. 153 | 1. 00 | 58. 31 |
| ATOM | 94 | CB | GLN | 26 | 44. 980 | 23. 280 | 61. 361 | 1. 00 | 63. 03 |
| ATOM | 95 | CG | GLN | 26 | 45. 118 | 24. 480 | 62. 313 | 1. 00 | 69. 87 |
| ATOM | 96 | CD | GLN | 26 | 46. 490 | 25. 161 | 62. 245 | 1. 00 | 73. 70 |
| ATOM | 97 | OE1 | GLN | 26 | 47. 009 | 25. 446 | 61. 158 | 1. 00 | 74. 68 |
| ATOM | 98 | NE2 | GLN | 26 | 47. 067 | 25. 446 | 63. 411 | 1. 00 | 74. 99 |
| ATOM | 99 | C | GLN | 26 | 42. 702 | 23. 903 | 60. 485 | 1. 00 | 55. 29 |
| ATOM | 100 | 0 | GLN | 26 | 42. 358 | 23. 811 | 59. 308 | 1. 00 | 51. 30 |
| ATOM | 101 | N | GLU | 27 | 42. 389 | 24. 931 | 61. 267 | 1. 00 | 55. 08 |
| ATOM | 102 | CA | GLU | 27 | 41. 617 | 26. 083 | 60. 824 | 1. 00 | 55. 66 |
| ATOM | 103 | CB | GLU | 27 | 41. 940 | 27. 280 | 61. 709 | 1. 00 | 57. 13 |
| ATOM | 104 | CG | GLU | 27 | 41. 029 | 28. 469 | 61. 523 | 1. 00 | 59. 64 |
| ATOM | 105 | CD | GLU | 27 | 39. 694 | 28. 272 | 62. 208 | 1. 00 | 62. 00 |
| ATOM | 106 | OE1 | GLU | 27 | 39. 685 | 27. 840 | 63. 382 | 1. 00 | 62. 44 |
| ATOM | 107 | OE2 | GLU | 27 | 38. 653 | 28. 559 | 61. 581 | 1. 00 | 64. 27 |
| ATOM | 108 | C | GLU | 27 | 41. 905 | 26. 454 | 59. 380 | 1. 00 | 55. 70 |

- 148 -

|    | ATOM | 109 | O   | GLU | 27 | 41.025 | 26.416 | 58.531 | 1.00 | 56.30 |
|----|------|-----|-----|-----|----|--------|--------|--------|------|-------|
|    | ATOM | 110 | N   | GLU | 28 | 43.147 | 26.828 | 59.113 | 1.00 | 56.74 |
|    | ATOM | 111 | CA  | GLU | 28 | 43.571 | 27.208 | 57.770 | 1.00 | 58.34 |
|    | ATOM | 112 | CB  | GLU | 28 | 45.102 | 27.226 | 57.714 | 1.00 | 63.94 |
| 5  | ATOM | 113 | CG  | GLU | 28 | 45.704 | 28.026 | 56.573 | 1.00 | 70.36 |
|    | ATOM | 114 | CD  | GLU | 28 | 45.615 | 29.524 | 56.806 | 1.00 | 74.74 |
|    | ATOM | 115 | OE1 | GLU | 28 | 46.245 | 30.289 | 56.040 | 1.00 | 77.18 |
|    | ATOM | 116 | OE2 | GLU | 28 | 44.912 | 29.938 | 57.755 | 1.00 | 77.44 |
|    | ATOM | 117 | C   | GLU | 28 | 43.032 | 26.231 | 56.721 | 1.00 | 56.56 |
| 10 | ATOM | 118 | O   | GLU | 28 | 42.375 | 26.641 | 55.764 | 1.00 | 54.38 |
|    | ATOM | 119 | N   | ASP | 29 | 43.316 | 24.942 | 56.921 | 1.00 | 55.20 |
|    | ATOM | 120 | CA  | ASP | 29 | 42.893 | 23.869 | 56.015 | 1.00 | 53.13 |
|    | ATOM | 121 | CB  | ASP | 29 | 43.106 | 22.499 | 56.667 | 1.00 | 56.36 |
|    | ATOM | 122 | CG  | ASP | 29 | 44.570 | 22.116 | 56.758 | 1.00 | 59.69 |
| 15 | ATOM | 123 | OD1 | ASP | 29 | 45.263 | 22.198 | 55.717 | 1.00 | 61.07 |
|    | ATOM | 124 | OD2 | ASP | 29 | 45.021 | 21.727 | 57.863 | 1.00 | 60.92 |
|    | ATOM | 125 | C   | ASP | 29 | 41.439 | 23.995 | 55.607 | 1.00 | 49.74 |
|    | ATOM | 126 | O   | ASP | 29 | 41.100 | 23.924 | 54.424 | 1.00 | 47.81 |
|    | ATOM | 127 | N   | LEU | 30 | 40.579 | 24.156 | 56.603 | 1.00 | 46.04 |
| 20 | ATOM | 128 | CA  | LEU | 30 | 39.167 | 24.309 | 56.344 | 1.00 | 43.06 |
|    | ATOM | 129 | CB  | LEU | 30 | 38.393 | 24.491 | 57.649 | 1.00 | 39.08 |
|    | ATOM | 130 | CG  | LEU | 30 | 38.026 | 23.218 | 58.404 | 1.00 | 36.61 |
|    | ATOM | 131 | CD1 | LEU | 30 | 39.280 | 22.441 | 58.756 | 1.00 | 37.28 |
|    | ATOM | 132 | CD2 | LEU | 30 | 37.233 | 23.576 | 59.642 | 1.00 | 35.29 |
| 25 | ATOM | 133 | C   | LEU | 30 | 38.948 | 25.516 | 55.452 | 1.00 | 44.18 |
|    | ATOM | 134 | O   | LEU | 30 | 38.410 | 25.388 | 54.354 | 1.00 | 45.60 |
|    | ATOM | 135 | N   | LYS | 31 | 39.381 | 26.685 | 55.920 | 1.00 | 44.63 |
|    | ATOM | 136 | CA  | LYS | 31 | 39.206 | 27.927 | 55.170 | 1.00 | 43.67 |
|    | ATOM | 137 | CB  | LYS | 31 | 40.136 | 29.020 | 55.695 | 1.00 | 45.23 |

- 149 -

|  | ATOM | 138 | CG | LYS 31 | 39.968 | 29.361 | 57.165 | 1.00 | 46.98 |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 139 | CD | LYS 31 | 38.743 | 30.221 | 57.440 | 1.00 | 45.54 |
|  | ATOM | 140 | CE | LYS 31 | 38.695 | 30.675 | 58.915 | 1.00 | 45.82 |
|  | ATOM | 141 | NZ | LYS 31 | 39.836 | 31.545 | 59.387 | 1.00 | 42.73 |
| 5 | ATOM | 142 | C | LYS 31 | 39.483 | 27.725 | 53.697 | 1.00 | 42.23 |
|  | ATOM | 143 | O | LYS 31 | 38.759 | 28.241 | 52.855 | 1.00 | 41.29 |
|  | ATOM | 144 | N | LYS 32 | 40.535 | 26.976 | 53.385 | 1.00 | 41.79 |
|  | ATOM | 145 | CA | LYS 32 | 40.877 | 26.737 | 51.994 | 1.00 | 43.47 |
|  | ATOM | 146 | CB | LYS 32 | 42.171 | 25.928 | 51.888 | 1.00 | 45.16 |
| 10 | ATOM | 147 | CG | LYS 32 | 42.811 | 25.974 | 50.499 | 1.00 | 50.49 |
|  | ATOM | 148 | CD | LYS 32 | 44.302 | 25.565 | 50.510 | 1.00 | 54.48 |
|  | ATOM | 149 | CE | LYS 32 | 44.505 | 24.086 | 50.900 | 1.00 | 57.45 |
|  | ATOM | 150 | NZ | LYS 32 | 45.934 | 23.610 | 51.002 | 1.00 | 56.65 |
|  | ATOM | 151 | C | LYS 32 | 39.740 | 25.995 | 51.308 | 1.00 | 43.99 |
| 15 | ATOM | 152 | O | LYS 32 | 39.260 | 26.407 | 50.246 | 1.00 | 43.34 |
|  | ATOM | 153 | N | VAL 33 | 39.306 | 24.901 | 51.925 | 1.00 | 43.47 |
|  | ATOM | 154 | CA | VAL 33 | 38.218 | 24.100 | 51.382 | 1.00 | 40.87 |
|  | ATOM | 155 | CB | VAL 33 | 37.895 | 22.927 | 52.310 | 1.00 | 40.53 |
|  | ATOM | 156 | CG1 | VAL 33 | 36.977 | 21.939 | 51.604 | 1.00 | 40.20 |
| 20 | ATOM | 157 | CG2 | VAL 33 | 39.183 | 22.248 | 52.729 | 1.00 | 40.29 |
|  | ATOM | 158 | C | VAL 33 | 36.994 | 24.981 | 51.226 | 1.00 | 39.39 |
|  | ATOM | 159 | O | VAL 33 | 36.370 | 25.011 | 50.165 | 1.00 | 37.22 |
|  | ATOM | 160 | N | MET 34 | 36.675 | 25.707 | 52.290 | 1.00 | 39.46 |
|  | ATOM | 161 | CA | MET 34 | 35.539 | 26.609 | 52.288 | 1.00 | 42.17 |
| 25 | ATOM | 162 | CB | MET 34 | 35.515 | 27.460 | 53.555 | 1.00 | 43.81 |
|  | ATOM | 163 | CG | MET 34 | 34.259 | 28.305 | 53.656 | 1.00 | 48.81 |
|  | ATOM | 164 | SD | MET 34 | 34.302 | 29.606 | 54.908 | 1.00 | 56.60 |
|  | ATOM | 165 | CE | MET 34 | 34.576 | 31.074 | 53.859 | 1.00 | 55.54 |
|  | ATOM | 166 | C | MET 34 | 35.612 | 27.535 | 51.086 | 1.00 | 43.35 |

- 150 -

| | ATOM | 167 | O | MET | 34 | 34. 626 | 27. 735 | 50. 383 | 1. 00 | 43. 86 |
|---|------|-----|-----|-----|----|---------|---------|---------|-------|--------|
| | ATOM | 168 | N | ARG | 35 | 36. 785 | 28. 104 | 50. 847 | 1. 00 | 44. 90 |
| | ATOM | 169 | CA | ARG | 35 | 36. 938 | 29. 015 | 49. 729 | 1. 00 | 45. 60 |
| | ATOM | 170 | CB | ARG | 35 | 38. 286 | 29. 727 | 49. 815 | 1. 00 | 49. 40 |
| 5 | ATOM | 171 | CG | ARG | 35 | 38. 459 | 30. 563 | 51. 075 | 1. 00 | 53. 81 |
| | ATOM | 172 | CD | ARG | 35 | 38. 231 | 32. 052 | 50. 851 | 1. 00 | 57. 78 |
| | ATOM | 173 | NE | ARG | 35 | 38. 483 | 32. 807 | 52. 077 | 1. 00 | 63. 20 |
| | ATOM | 174 | CZ | ARG | 35 | 39. 587 | 32. 696 | 52. 820 | 1. 00 | 65. 30 |
| | ATOM | 175 | NH1 | ARG | 35 | 40. 557 | 31. 854 | 52. 466 | 1. 00 | 64. 80 |
| 10 | ATOM | 176 | NH2 | ARG | 35 | 39. 720 | 33. 425 | 53. 925 | 1. 00 | 66. 89 |
| | ATOM | 177 | C | ARG | 35 | 36. 814 | 28. 262 | 48. 418 | 1. 00 | 44. 08 |
| | ATOM | 178 | O | ARG | 35 | 35. 977 | 28. 605 | 47. 586 | 1. 00 | 43. 75 |
| | ATOM | 179 | N | ARG | 36 | 37. 633 | 27. 227 | 48. 245 | 1. 00 | 43. 43 |
| | ATOM | 180 | CA | ARG | 36 | 37. 612 | 26. 418 | 47. 026 | 1. 00 | 43. 94 |
| 15 | ATOM | 181 | CB | ARG | 36 | 38. 547 | 25. 212 | 47. 174 | 1. 00 | 44. 76 |
| | ATOM | 182 | CG | ARG | 36 | 40. 020 | 25. 580 | 47. 244 | 1. 00 | 44. 66 |
| | ATOM | 183 | CD | ARG | 36 | 40. 898 | 24. 392 | 47. 617 | 1. 00 | 44. 20 |
| | ATOM | 184 | NE | ARG | 36 | 41. 728 | 23. 919 | 46. 512 | 1. 00 | 44. 66 |
| | ATOM | 185 | CZ | ARG | 36 | 42. 890 | 23. 292 | 46. 678 | 1. 00 | 45. 10 |
| 20 | ATOM | 186 | NH1 | ARG | 36 | 43. 350 | 23. 075 | 47. 900 | 1. 00 | 44. 34 |
| | ATOM | 187 | NH2 | ARG | 36 | 43. 590 | 22. 870 | 45. 631 | 1. 00 | 45. 47 |
| | ATOM | 188 | C | ARG | 36 | 36. 202 | 25. 941 | 46. 660 | 1. 00 | 43. 73 |
| | ATOM | 189 | O | ARG | 36 | 35. 921 | 25. 645 | 45. 497 | 1. 00 | 43. 31 |
| | ATOM | 190 | N | MET | 37 | 35. 324 | 25. 851 | 47. 656 | 1. 00 | 42. 87 |
| 25 | ATOM | 191 | CA | MET | 37 | 33. 946 | 25. 440 | 47. 413 | 1. 00 | 41. 30 |
| | ATOM | 192 | CB | MET | 37 | 33. 222 | 25. 136 | 48. 726 | 1. 00 | 43. 30 |
| | ATOM | 193 | CG | MET | 37 | 31. 782 | 24. 636 | 48. 556 | 1. 00 | 45. 16 |
| | ATOM | 194 | SD | MET | 37 | 31. 646 | 22. 826 | 48. 280 | 1. 00 | 52. 61 |
| | ATOM | 195 | CE | MET | 37 | 31. 892 | 22. 708 | 46. 492 | 1. 00 | 46. 47 |

- 151 -

| ATOM | 196 | C | MET | 37 | 33. 249 | 26. 603 | 46. 723 | 1. 00 | 39. 52 |
|------|-----|------|-----|----|---------|---------|---------|-------|--------|
| ATOM | 197 | 0 | MET | 37 | 32. 702 | 26. 458 | 45. 635 | 1. 00 | 39. 06 |
| ATOM | 198 | N | GLN | 38 | 33. 275 | 27. 767 | 47. 359 | 1. 00 | 37. 22 |
| ATOM | 199 | CA | GLN | 38 | 32. 637 | 28. 927 | 46. 776 | 1. 00 | 35. 67 |
| ATOM | 200 | CB | GLN | 38 | 32. 874 | 30. 155 | 47. 643 | 1. 00 | 36. 29 |
| ATOM | 201 | CG | GLN | 38 | 32. 128 | 30. 122 | 48. 950 | 1. 00 | 37. 44 |
| ATOM | 202 | CD | GLN | 38 | 32. 689 | 31. 108 | 49. 950 | 1. 00 | 41. 99 |
| ATOM | 203 | OE1 | GLN | 38 | 33. 841 | 30. 992 | 50. 376 | 1. 00 | 44. 33 |
| ATOM | 204 | NE2 | GLN | 38 | 31. 880 | 32. 091 | 50. 331 | 1. 00 | 44. 58 |
| ATOM | 205 | C | GLN | 38 | 33. 184 | 29. 155 | 45. 382 | 1. 00 | 35. 21 |
| ATOM | 206 | 0 | GLN | 38 | 32. 454 | 29. 557 | 44. 486 | 1. 00 | 34. 82 |
| ATOM | 207 | N | LYS | 39 | 34. 467 | 28. 884 | 45. 188 | 1. 00 | 36. 41 |
| ATOM | 208 | CA | LYS | 39 | 35. 069 | 29. 081 | 43. 875 | 1. 00 | 38. 60 |
| ATOM | 209 | CB | LYS | 39 | 36. 560 | 28. 708 | 43. 888 | 1. 00 | 42. 47 |
| ATOM | 210 | CG | LYS | 39 | 37. 395 | 29. 263 | 42. 714 | 1. 00 | 45. 02 |
| ATOM | 211 | CD | LYS | 39 | 37. 638 | 30. 775 | 42. 861 | 1. 00 | 49. 54 |
| ATOM | 212 | CE | LYS | 39 | 38. 523 | 31. 365 | 41. 752 | 1. 00 | 51. 65 |
| ATOM | 213 | NZ | LYS | 39 | 38. 621 | 32. 865 | 41. 821 | 1. 00 | 53. 58 |
| ATOM | 214 | C | LYS | 39 | 34. 339 | 28. 196 | 42. 884 | 1. 00 | 38. 31 |
| ATOM | 215 | 0 | LYS | 39 | 34. 229 | 28. 534 | 41. 710 | 1. 00 | 40. 28 |
| ATOM | 216 | N | GLU | 40 | 33. 827 | 27. 066 | 43. 369 | 1. 00 | 37. 21 |
| ATOM | 217 | CA | GLU | 40 | 33. 117 | 26. 107 | 42. 525 | 1. 00 | 34. 69 |
| ATOM | 218 | CB | GLU | 40 | 33. 329 | 24. 705 | 43. 072 | 1. 00 | 32. 80 |
| ATOM | 219 | CG | GLU | 40 | 34. 742 | 24. 245 | 42. 900 | 1. 00 | 33. 53 |
| ATOM | 220 | CD | GLU | 40 | 35. 164 | 24. 348 | 41. 459 | 1. 00 | 36. 48 |
| ATOM | 221 | OE1 | GLU | 40 | 34. 318 | 24. 044 | 40. 589 | 1. 00 | 39. 36 |
| ATOM | 222 | OE2 | GLU | 40 | 36. 326 | 24. 720 | 41. 187 | 1. 00 | 37. 18 |
| ATOM | 223 | C | GLU | 40 | 31. 632 | 26. 387 | 42. 375 | 1. 00 | 34. 48 |
| ATOM | 224 | 0 | GLU | 40 | 31. 040 | 26. 110 | 41. 332 | 1. 00 | 32. 30 |

- 152 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 225 | N | MET | 41 | 31.030 | 26.928 | 43.425 | 1.00 | 35.61 |
| ATOM | 226 | CA | MET | 41 | 29.621 | 27.256 | 43.373 | 1.00 | 39.30 |
| ATOM | 227 | CB | MET | 41 | 29.155 | 27.852 | 44.692 | 1.00 | 39.16 |
| ATOM | 228 | CG | MET | 41 | 29.146 | 26.910 | 45.867 | 1.00 | 40.71 |
| ATOM | 229 | SD | MET | 41 | 27.930 | 27.569 | 47.040 | 1.00 | 46.34 |
| ATOM | 230 | CE | MET | 41 | 28.978 | 28.338 | 48.243 | 1.00 | 46.54 |
| ATOM | 231 | C | MET | 41 | 29.336 | 28.258 | 42.251 | 1.00 | 42.24 |
| ATOM | 232 | O | MET | 41 | 28.358 | 28.113 | 41.517 | 1.00 | 44.97 |
| ATOM | 233 | N | ASP | 42 | 30.173 | 29.284 | 42.118 | 1.00 | 43.47 |
| ATOM | 234 | CA | ASP | 42 | 29.952 | 30.274 | 41.069 | 1.00 | 42.69 |
| ATOM | 235 | CB | ASP | 42 | 30.848 | 31.497 | 41.249 | 1.00 | 44.70 |
| ATOM | 236 | CG | ASP | 42 | 30.548 | 32.254 | 42.523 | 1.00 | 49.63 |
| ATOM | 237 | OD1 | ASP | 42 | 31.352 | 32.128 | 43.477 | 1.00 | 52.14 |
| ATOM | 238 | OD2 | ASP | 42 | 29.510 | 32.968 | 42.572 | 1.00 | 49.66 |
| ATOM | 239 | C | ASP | 42 | 30.248 | 29.641 | 39.739 | 1.00 | 41.40 |
| ATOM | 240 | O | ASP | 42 | 29.550 | 29.880 | 38.759 | 1.00 | 41.06 |
| ATOM | 241 | N | ARG | 43 | 31.289 | 28.826 | 39.707 | 1.00 | 39.70 |
| ATOM | 242 | CA | ARG | 43 | 31.668 | 28.171 | 38.477 | 1.00 | 39.99 |
| ATOM | 243 | CB | ARG | 43 | 32.835 | 27.227 | 38.739 | 1.00 | 43.98 |
| ATOM | 244 | CG | ARG | 43 | 33.329 | 26.482 | 37.516 | 1.00 | 49.72 |
| ATOM | 245 | CD | ARG | 43 | 34.636 | 25.777 | 37.831 | 1.00 | 55.67 |
| ATOM | 246 | NE | ARG | 43 | 34.962 | 24.746 | 36.854 | 1.00 | 62.98 |
| ATOM | 247 | CZ | ARG | 43 | 36.062 | 24.002 | 36.899 | 1.00 | 67.95 |
| ATOM | 248 | NH1 | ARG | 43 | 36.950 | 24.178 | 37.877 | 1.00 | 69.41 |
| ATOM | 249 | NH2 | ARG | 43 | 36.269 | 23.075 | 35.969 | 1.00 | 70.32 |
| ATOM | 250 | C | ARG | 43 | 30.488 | 27.417 | 37.881 | 1.00 | 38.35 |
| ATOM | 251 | O | ARG | 43 | 30.253 | 27.493 | 36.677 | 1.00 | 38.07 |
| ATOM | 252 | N | GLY | 44 | 29.739 | 26.709 | 38.728 | 1.00 | 36.44 |
| ATOM | 253 | CA | GLY | 44 | 28.592 | 25.938 | 38.262 | 1.00 | 32.80 |

- 153 -

|       | ATOM | 254 | C   | GLY 44 | 27.344 | 26.772 | 38.062 | 1.00 | 31.71 |
|-------|------|-----|-----|--------|--------|--------|--------|------|-------|
|       | ATOM | 255 | O   | GLY 44 | 26.483 | 26.448 | 37.251 | 1.00 | 30.43 |
|       | ATOM | 256 | N   | LEU 45 | 27.258 | 27.854 | 38.820 | 1.00 | 31.23 |
|       | ATOM | 257 | CA  | LEU 45 | 26.144 | 28.774 | 38.761 | 1.00 | 31.72 |
| 5     | ATOM | 258 | CB  | LEU 45 | 26.168 | 29.638 | 40.010 | 1.00 | 30.96 |
|       | ATOM | 259 | CG  | LEU 45 | 25.063 | 29.363 | 41.013 | 1.00 | 34.38 |
|       | ATOM | 260 | CD1 | LEU 45 | 25.346 | 30.066 | 42.334 | 1.00 | 34.74 |
|       | ATOM | 261 | CD2 | LEU 45 | 23.750 | 29.849 | 40.413 | 1.00 | 37.12 |
|       | ATOM | 262 | C   | LEU 45 | 26.204 | 29.666 | 37.517 | 1.00 | 33.39 |
| 10    | ATOM | 263 | O   | LEU 45 | 25.184 | 30.211 | 37.086 | 1.00 | 34.01 |
|       | ATOM | 264 | N   | ARG 46 | 27.402 | 29.813 | 36.955 | 1.00 | 34.39 |
|       | ATOM | 265 | CA  | ARG 46 | 27.628 | 30.651 | 35.774 | 1.00 | 37.39 |
|       | ATOM | 266 | CB  | ARG 46 | 29.092 | 31.140 | 35.744 | 1.00 | 42.80 |
|       | ATOM | 267 | CG  | ARG 46 | 29.463 | 32.067 | 34.562 | 1.00 | 48.17 |
| 15    | ATOM | 268 | CD  | ARG 46 | 30.951 | 32.487 | 34.546 | 1.00 | 49.35 |
|       | ATOM | 269 | NE  | ARG 46 | 31.250 | 33.400 | 33.441 | 1.00 | 54.04 |
|       | ATOM | 270 | CZ  | ARG 46 | 30.599 | 34.542 | 33.216 | 1.00 | 57.98 |
|       | ATOM | 271 | NH1 | ARG 46 | 29.608 | 34.915 | 34.019 | 1.00 | 56.34 |
|       | ATOM | 272 | NH2 | ARG 46 | 30.936 | 35.316 | 32.187 | 1.00 | 59.91 |
| 20    | ATOM | 273 | C   | ARG 46 | 27.301 | 29.920 | 34.477 | 1.00 | 37.53 |
|       | ATOM | 274 | O   | ARG 46 | 27.773 | 28.804 | 34.243 | 1.00 | 38.11 |
|       | ATOM | 275 | N   | LEU 47 | 26.515 | 30.573 | 33.623 | 1.00 | 36.42 |
|       | ATOM | 276 | CA  | LEU 47 | 26.089 | 29.993 | 32.350 | 1.00 | 35.82 |
|       | ATOM | 277 | CB  | LEU 47 | 25.151 | 30.957 | 31.617 | 1.00 | 31.45 |
| 25    | ATOM | 278 | CG  | LEU 47 | 24.771 | 30.548 | 30.196 | 1.00 | 29.68 |
|       | ATOM | 279 | CD1 | LEU 47 | 24.031 | 29.240 | 30.230 | 1.00 | 28.93 |
|       | ATOM | 280 | CD2 | LEU 47 | 23.929 | 31.622 | 29.559 | 1.00 | 28.83 |
|       | ATOM | 281 | C   | LEU 47 | 27.223 | 29.578 | 31.418 | 1.00 | 37.14 |
|       | ATOM | 282 | O   | LEU 47 | 27.152 | 28.534 | 30.764 | 1.00 | 36.41 |

- 154 -

| | ATOM | 283 | N | GLU | 48 | 28.272 | 30.383 | 31.347 | 1.00 | 39.28 |
|---|------|-----|------|-----|----|--------|--------|--------|------|-------|
| | ATOM | 284 | CA | GLU | 48 | 29.371 | 30.034 | 30.462 | 1.00 | 42.38 |
| | ATOM | 285 | CB | GLU | 48 | 30.448 | 31.126 | 30.473 | 1.00 | 43.91 |
| | ATOM | 286 | CG | GLU | 48 | 30.126 | 32.354 | 29.631 | 1.00 | 46.02 |
| 5 | ATOM | 287 | CD | GLU | 48 | 29.022 | 33.215 | 30.221 | 1.00 | 48.71 |
| | ATOM | 288 | OE1 | GLU | 48 | 28.581 | 34.157 | 29.524 | 1.00 | 48.10 |
| | ATOM | 289 | OE2 | GLU | 48 | 28.600 | 32.959 | 31.375 | 1.00 | 49.31 |
| | ATOM | 290 | C | GLU | 48 | 30.005 | 28.691 | 30.809 | 1.00 | 43.42 |
| | ATOM | 291 | O | GLU | 48 | 30.593 | 28.045 | 29.939 | 1.00 | 43.61 |
| 10 | ATOM | 292 | N | THR | 49 | 29.873 | 28.262 | 32.066 | 1.00 | 44.28 |
| | ATOM | 293 | CA | THR | 49 | 30.484 | 26.999 | 32.508 | 1.00 | 46.81 |
| | ATOM | 294 | CB | THR | 49 | 31.761 | 27.267 | 33.366 | 1.00 | 47.70 |
| | ATOM | 295 | OG1 | THR | 49 | 31.477 | 28.265 | 34.356 | 1.00 | 45.18 |
| | ATOM | 296 | CG2 | THR | 49 | 32.921 | 27.739 | 32.486 | 1.00 | 48.17 |
| 15 | ATOM | 297 | C | THR | 49 | 29.595 | 26.024 | 33.293 | 1.00 | 46.50 |
| | ATOM | 298 | O | THR | 49 | 30.043 | 24.932 | 33.683 | 1.00 | 45.72 |
| | ATOM | 299 | N | HIS | 50 | 28.340 | 26.405 | 33.508 | 1.00 | 44.18 |
| | ATOM | 300 | CA | HIS | 50 | 27.416 | 25.565 | 34.262 | 1.00 | 41.93 |
| | ATOM | 301 | CB | HIS | 50 | 25.980 | 26.129 | 34.190 | 1.00 | 38.83 |
| 20 | ATOM | 302 | CG | HIS | 50 | 25.217 | 25.754 | 32.953 | 1.00 | 35.50 |
| | ATOM | 303 | CD2 | HIS | 50 | 23.950 | 25.304 | 32.795 | 1.00 | 33.70 |
| | ATOM | 304 | ND1 | HIS | 50 | 25.730 | 25.894 | 31.682 | 1.00 | 36.24 |
| | ATOM | 305 | CE1 | HIS | 50 | 24.812 | 25.550 | 30.796 | 1.00 | 33.56 |
| | ATOM | 306 | NE2 | HIS | 50 | 23.722 | 25.189 | 31.446 | 1.00 | 32.06 |
| 25 | ATOM | 307 | C | HIS | 50 | 27.447 | 24.117 | 33.804 | 1.00 | 41.73 |
| | ATOM | 308 | O | HIS | 50 | 27.144 | 23.212 | 34.572 | 1.00 | 41.14 |
| | ATOM | 309 | N | GLU | 51 | 27.848 | 23.883 | 32.566 | 1.00 | 42.00 |
| | ATOM | 310 | CA | GLU | 51 | 27.863 | 22.519 | 32.103 | 1.00 | 45.79 |
| | ATOM | 311 | CB | GLU | 51 | 27.573 | 22.463 | 30.617 | 1.00 | 46.76 |

- 155 -

|   | ATOM | 312 | CG  | GLU 51 | 27.523 | 21.048 | 30.100 | 1.00 | 50.98 |
|---|------|-----|-----|--------|--------|--------|--------|------|-------|
|   | ATOM | 313 | CD  | GLU 51 | 26.521 | 20.885 | 28.989 | 1.00 | 53.94 |
|   | ATOM | 314 | OE1 | GLU 51 | 25.313 | 21.082 | 29.253 | 1.00 | 55.61 |
|   | ATOM | 315 | OE2 | GLU 51 | 26.940 | 20.560 | 27.857 | 1.00 | 55.48 |
| 5 | ATOM | 316 | C   | GLU 51 | 29.139 | 21.757 | 32.402 | 1.00 | 48.17 |
|   | ATOM | 317 | O   | GLU 51 | 29.094 | 20.657 | 32.953 | 1.00 | 49.35 |
|   | ATOM | 318 | N   | GLU 52 | 30.276 | 22.331 | 32.034 | 1.00 | 50.75 |
|   | ATOM | 319 | CA  | GLU 52 | 31.565 | 21.681 | 32.264 | 1.00 | 52.07 |
|   | ATOM | 320 | CB  | GLU 52 | 32.633 | 22.321 | 31.352 | 1.00 | 56.66 |
| 10 | ATOM | 321 | CG  | GLU 52 | 32.768 | 23.854 | 31.476 | 1.00 | 63.81 |
|   | ATOM | 322 | CD  | GLU 52 | 33.420 | 24.528 | 30.253 | 1.00 | 67.84 |
|   | ATOM | 323 | OE1 | GLU 52 | 33.601 | 25.770 | 30.278 | 1.00 | 68.83 |
|   | ATOM | 324 | OE2 | GLU 52 | 33.742 | 23.826 | 29.266 | 1.00 | 70.00 |
|   | ATOM | 325 | C   | GLU 52 | 31.982 | 21.760 | 33.738 | 1.00 | 49.95 |
| 15 | ATOM | 326 | O   | GLU 52 | 33.013 | 21.215 | 34.132 | 1.00 | 47.47 |
|   | ATOM | 327 | N   | ALA 53 | 31.162 | 22.429 | 34.548 | 1.00 | 48.46 |
|   | ATOM | 328 | CA  | ALA 53 | 31.449 | 22.594 | 35.972 | 1.00 | 47.88 |
|   | ATOM | 329 | CB  | ALA 53 | 30.418 | 23.510 | 36.615 | 1.00 | 47.30 |
|   | ATOM | 330 | C   | ALA 53 | 31.510 | 21.278 | 36.731 | 1.00 | 46.84 |
| 20 | ATOM | 331 | O   | ALA 53 | 31.287 | 20.206 | 36.172 | 1.00 | 48.51 |
|   | ATOM | 332 | N   | SER 54 | 31.816 | 21.353 | 38.016 | 1.00 | 44.67 |
|   | ATOM | 333 | CA  | SER 54 | 31.895 | 20.133 | 38.792 | 1.00 | 42.38 |
|   | ATOM | 334 | CB  | SER 54 | 33.201 | 20.090 | 39.581 | 1.00 | 44.26 |
|   | ATOM | 335 | OG  | SER 54 | 33.290 | 18.883 | 40.316 | 1.00 | 45.49 |
| 25 | ATOM | 336 | C   | SER 54 | 30.712 | 20.059 | 39.734 | 1.00 | 39.72 |
|   | ATOM | 337 | O   | SER 54 | 30.058 | 19.028 | 39.841 | 1.00 | 41.09 |
|   | ATOM | 338 | N   | VAL 55 | 30.440 | 21.165 | 40.411 | 1.00 | 34.77 |
|   | ATOM | 339 | CA  | VAL 55 | 29.326 | 21.239 | 41.343 | 1.00 | 30.58 |
|   | ATOM | 340 | CB  | VAL 55 | 29.682 | 22.186 | 42.498 | 1.00 | 28.73 |

| | ATOM | 341 | CG1 | VAL | 55 | 28.480 | 22.433 | 43.383 | 1.00 | 30.75 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 342 | CG2 | VAL | 55 | 30.814 | 21.596 | 43.297 | 1.00 | 25.80 |
| | ATOM | 343 | C | VAL | 55 | 28.094 | 21.760 | 40.597 | 1.00 | 30.28 |
| | ATOM | 344 | O | VAL | 55 | 27.704 | 22.920 | 40.745 | 1.00 | 32.16 |
| 5 | ATOM | 345 | N | LYS | 56 | 27.482 | 20.887 | 39.803 | 1.00 | 26.82 |
| | ATOM | 346 | CA | LYS | 56 | 26.323 | 21.235 | 38.986 | 1.00 | 21.66 |
| | ATOM | 347 | CB | LYS | 56 | 25.362 | 20.046 | 38.891 | 1.00 | 26.53 |
| | ATOM | 348 | CG | LYS | 56 | 25.936 | 18.737 | 38.337 | 1.00 | 29.32 |
| | ATOM | 349 | CD | LYS | 56 | 26.311 | 18.836 | 36.875 | 1.00 | 29.86 |
| 10 | ATOM | 350 | CE | LYS | 56 | 27.609 | 19.592 | 36.698 | 1.00 | 29.73 |
| | ATOM | 351 | NZ | LYS | 56 | 27.932 | 19.759 | 35.259 | 1.00 | 32.80 |
| | ATOM | 352 | C | LYS | 56 | 25.520 | 22.470 | 39.374 | 1.00 | 17.56 |
| | ATOM | 353 | O | LYS | 56 | 25.133 | 23.236 | 38.498 | 1.00 | 15.95 |
| | ATOM | 354 | N | MET | 57 | 25.257 | 22.660 | 40.665 | 1.00 | 14.30 |
| 15 | ATOM | 355 | CA | MET | 57 | 24.462 | 23.803 | 41.128 | 1.00 | 12.73 |
| | ATOM | 356 | CB | MET | 57 | 25.277 | 25.089 | 41.059 | 1.00 | 9.92 |
| | ATOM | 357 | CG | MET | 57 | 26.515 | 25.090 | 41.930 | 1.00 | 6.47 |
| | ATOM | 358 | SD | MET | 57 | 26.219 | 25.164 | 43.694 | 1.00 | 8.00 |
| | ATOM | 359 | CE | MET | 57 | 25.523 | 26.842 | 43.905 | 1.00 | 1.00 |
| 20 | ATOM | 360 | C | MET | 57 | 23.207 | 23.953 | 40.270 | 1.00 | 14.05 |
| | ATOM | 361 | O | MET | 57 | 23.000 | 24.972 | 39.610 | 1.00 | 12.36 |
| | ATOM | 362 | N | LEU | 58 | 22.371 | 22.923 | 40.290 | 1.00 | 17.80 |
| | ATOM | 363 | CA | LEU | 58 | 21.154 | 22.914 | 39.498 | 1.00 | 19.02 |
| | ATOM | 364 | CB | LEU | 58 | 20.710 | 21.466 | 39.245 | 1.00 | 18.03 |
| 25 | ATOM | 365 | CG | LEU | 58 | 21.726 | 20.444 | 38.720 | 1.00 | 16.28 |
| | ATOM | 366 | CD1 | LEU | 58 | 21.193 | 19.068 | 39.021 | 1.00 | 20.44 |
| | ATOM | 367 | CD2 | LEU | 58 | 21.999 | 20.608 | 37.233 | 1.00 | 15.03 |
| | ATOM | 368 | C | LEU | 58 | 20.005 | 23.696 | 40.134 | 1.00 | 20.20 |
| | ATOM | 369 | O | LEU | 58 | 19.752 | 23.602 | 41.340 | 1.00 | 19.91 |

- 157 -

| ATOM | 370 | N | PRO 59 | 19.316 | 24.507 | 39.320 | 1.00 | 20.57 |
|------|-----|-----|--------|--------|--------|--------|------|-------|
| ATOM | 371 | CD | PRO 59 | 19.856 | 24.939 | 38.022 | 1.00 | 20.39 |
| ATOM | 372 | CA | PRO 59 | 18.171 | 25.342 | 39.694 | 1.00 | 22.50 |
| ATOM | 373 | CB | PRO 59 | 17.939 | 26.168 | 38.437 | 1.00 | 22.07 |
| ATOM | 374 | CG | PRO 59 | 19.306 | 26.329 | 37.906 | 1.00 | 21.92 |
| ATOM | 375 | C | PRO 59 | 16.975 | 24.437 | 40.010 | 1.00 | 23.49 |
| ATOM | 376 | O | PRO 59 | 16.698 | 23.504 | 39.264 | 1.00 | 25.36 |
| ATOM | 377 | N | THR 60 | 16.258 | 24.714 | 41.092 | 1.00 | 22.35 |
| ATOM | 378 | CA | THR 60 | 15.133 | 23.871 | 41.469 | 1.00 | 20.99 |
| ATOM | 379 | CB | THR 60 | 15.097 | 23.607 | 42.964 | 1.00 | 22.35 |
| ATOM | 380 | OG1 | THR 60 | 14.823 | 24.837 | 43.647 | 1.00 | 24.53 |
| ATOM | 381 | CG2 | THR 60 | 16.408 | 23.049 | 43.441 | 1.00 | 24.88 |
| ATOM | 382 | C | THR 60 | 13.815 | 24.516 | 41.160 | 1.00 | 20.21 |
| ATOM | 383 | O | THR 60 | 12.793 | 23.848 | 41.119 | 1.00 | 24.18 |
| ATOM | 384 | N | TYR 61 | 13.839 | 25.822 | 40.973 | 1.00 | 19.09 |
| ATOM | 385 | CA | TYR 61 | 12.628 | 26.595 | 40.715 | 1.00 | 20.03 |
| ATOM | 386 | CB | TYR 61 | 11.955 | 26.172 | 39.427 | 1.00 | 13.50 |
| ATOM | 387 | CG | TYR 61 | 12.581 | 26.830 | 38.234 | 1.00 | 13.18 |
| ATOM | 388 | CD1 | TYR 61 | 12.028 | 27.983 | 37.666 | 1.00 | 8.00 |
| ATOM | 389 | CE1 | TYR 61 | 12.596 | 28.551 | 36.536 | 1.00 | 4.24 |
| ATOM | 390 | CD2 | TYR 61 | 13.725 | 26.281 | 37.647 | 1.00 | 14.04 |
| ATOM | 391 | CE2 | TYR 61 | 14.296 | 26.843 | 36.529 | 1.00 | 10.05 |
| ATOM | 392 | CZ | TYR 61 | 13.730 | 27.963 | 35.976 | 1.00 | 5.80 |
| ATOM | 393 | OH | TYR 61 | 14.307 | 28.423 | 34.828 | 1.00 | 4.54 |
| ATOM | 394 | C | TYR 61 | 11.620 | 26.572 | 41.833 | 1.00 | 21.95 |
| ATOM | 395 | O | TYR 61 | 10.437 | 26.816 | 41.609 | 1.00 | 22.47 |
| ATOM | 396 | N | VAL 62 | 12.102 | 26.293 | 43.037 | 1.00 | 24.47 |
| ATOM | 397 | CA | VAL 62 | 11.265 | 26.288 | 44.218 | 1.00 | 29.86 |
| ATOM | 398 | CB | VAL 62 | 11.750 | 25.231 | 45.207 | 1.00 | 28.92 |

- 158 -

|   | ATOM | 399 | CG1 | VAL | 62 | 10.780 | 25.091 | 46.370 | 1.00 | 28.30 |
|---|------|-----|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 400 | CG2 | VAL | 62 | 11.909 | 23.926 | 44.480 | 1.00 | 28.58 |
|   | ATOM | 401 | C   | VAL | 62 | 11.494 | 27.680 | 44.786 | 1.00 | 34.67 |
|   | ATOM | 402 | O   | VAL | 62 | 11.584 | 27.879 | 45.993 | 1.00 | 39.01 |
| 5 | ATOM | 403 | N   | ARG | 63 | 11.589 | 28.638 | 43.874 | 1.00 | 38.40 |
|   | ATOM | 404 | CA  | ARG | 63 | 11.847 | 30.038 | 44.182 | 1.00 | 41.10 |
|   | ATOM | 405 | CB  | ARG | 63 | 12.041 | 30.804 | 42.874 | 1.00 | 42.02 |
|   | ATOM | 406 | CG  | ARG | 63 | 10.794 | 30.798 | 41.996 | 1.00 | 44.76 |
|   | ATOM | 407 | CD  | ARG | 63 | 11.072 | 31.197 | 40.550 | 1.00 | 46.61 |
| 10| ATOM | 408 | NE  | ARG | 63 | 9.827  | 31.366 | 39.804 | 1.00 | 48.56 |
|   | ATOM | 409 | CZ  | ARG | 63 | 8.972  | 30.381 | 39.541 | 1.00 | 50.39 |
|   | ATOM | 410 | NH1 | ARG | 63 | 9.225  | 29.145 | 39.955 | 1.00 | 50.83 |
|   | ATOM | 411 | NH2 | ARG | 63 | 7.854  | 30.635 | 38.875 | 1.00 | 51.11 |
|   | ATOM | 412 | C   | ARG | 63 | 10.788 | 30.751 | 45.004 | 1.00 | 42.71 |
| 15| ATOM | 413 | O   | ARG | 63 | 9.790  | 30.167 | 45.424 | 1.00 | 41.58 |
|   | ATOM | 414 | N   | SER | 64 | 11.047 | 32.036 | 45.224 | 1.00 | 46.12 |
|   | ATOM | 415 | CA  | SER | 64 | 10.155 | 32.922 | 45.954 | 1.00 | 49.96 |
|   | ATOM | 416 | CB  | SER | 64 | 10.400 | 32.826 | 47.454 | 1.00 | 50.57 |
|   | ATOM | 417 | OG  | SER | 64 | 9.374  | 33.507 | 48.157 | 1.00 | 53.70 |
| 20| ATOM | 418 | C   | SER | 64 | 10.435 | 34.340 | 45.458 | 1.00 | 51.04 |
|   | ATOM | 419 | O   | SER | 64 | 11.300 | 35.047 | 45.985 | 1.00 | 50.38 |
|   | ATOM | 420 | N   | THR | 65 | 9.690  | 34.728 | 44.425 | 1.00 | 53.23 |
|   | ATOM | 421 | CA  | THR | 65 | 9.827  | 36.031 | 43.791 | 1.00 | 54.89 |
|   | ATOM | 422 | CB  | THR | 65 | 10.151 | 35.871 | 42.281 | 1.00 | 56.21 |
| 25| ATOM | 423 | OG1 | THR | 65 | 9.094  | 35.158 | 41.622 | 1.00 | 55.23 |
|   | ATOM | 424 | CG2 | THR | 65 | 11.461 | 35.112 | 42.103 | 1.00 | 56.71 |
|   | ATOM | 425 | C   | THR | 65 | 8.582  | 36.911 | 43.939 | 1.00 | 56.01 |
|   | ATOM | 426 | O   | THR | 65 | 7.503  | 36.430 | 44.291 | 1.00 | 56.26 |
|   | ATOM | 427 | N   | PRO | 66 | 8.728  | 38.222 | 43.676 | 1.00 | 56.49 |

- 159 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 428 | CD | PRO | 66 | 10. 019 | 38. 866 | 43. 377 | 1. 00 56. 96 |
| | ATOM | 429 | CA | PRO | 66 | 7. 666 | 39. 228 | 43. 758 | 1. 00 56. 28 |
| | ATOM | 430 | CB | PRO | 66 | 8. 369 | 40. 502 | 43. 313 | 1. 00 57. 08 |
| | ATOM | 431 | CG | PRO | 66 | 9. 759 | 40. 287 | 43. 786 | 1. 00 58. 08 |
| 5 | ATOM | 432 | C | PRO | 66 | 6. 487 | 38. 901 | 42. 864 | 1. 00 56. 75 |
| | ATOM | 433 | 0 | PRO | 66 | 5. 477 | 39. 604 | 42. 874 | 1. 00 57. 23 |
| | ATOM | 434 | N | GLU | 67 | 6. 631 | 37. 849 | 42. 072 | 1. 00 56. 42 |
| | ATOM | 435 | CA | GLU | 67 | 5. 540 | 37. 445 | 41. 193 | 1. 00 56. 82 |
| | ATOM | 436 | CB | GLU | 67 | 6. 048 | 36. 487 | 40. 115 | 1. 00 61. 19 |
| 10 | ATOM | 437 | CG | GLU | 67 | 6. 421 | 35. 108 | 40. 637 | 1. 00 66. 99 |
| | ATOM | 438 | CD | GLU | 67 | 7. 123 | 34. 261 | 39. 594 | 1. 00 69. 61 |
| | ATOM | 439 | OE1 | GLU | 67 | 8. 253 | 34. 618 | 39. 201 | 1. 00 70. 19 |
| | ATOM | 440 | OE2 | GLU | 67 | 6. 541 | 33. 241 | 39. 168 | 1. 00 70. 18 |
| | ATOM | 441 | C | GLU | 67 | 4. 406 | 36. 803 | 41. 984 | 1. 00 54. 30 |
| 15 | ATOM | 442 | 0 | GLU | 67 | 3. 241 | 36. 940 | 41. 633 | 1. 00 54. 25 |
| | ATOM | 443 | N | GLY | 68 | 4. 753 | 36. 116 | 43. 076 | 1. 00 50. 50 |
| | ATOM | 444 | CA | GLY | 68 | 3. 741 | 35. 478 | 43. 901 | 1. 00 45. 77 |
| | ATOM | 445 | C | GLY | 68 | 4. 166 | 34. 087 | 44. 316 | 1. 00 43. 04 |
| | ATOM | 446 | 0 | GLY | 68 | 3. 626 | 33. 503 | 45. 259 | 1. 00 40. 69 |
| 20 | ATOM | 447 | N | SER | 69 | 5. 154 | 33. 564 | 43. 599 | 1. 00 42. 30 |
| | ATOM | 448 | CA | SER | 69 | 5. 690 | 32. 230 | 43. 845 | 1. 00 41. 02 |
| | ATOM | 449 | CB | SER | 69 | 6. 769 | 31. 902 | 42. 804 | 1. 00 41. 03 |
| | ATOM | 450 | OG | SER | 69 | 6. 438 | 32. 404 | 41. 517 | 1. 00 42. 34 |
| | ATOM | 451 | C | SER | 69 | 6. 301 | 32. 126 | 45. 240 | 1. 00 39. 68 |
| 25 | ATOM | 452 | 0 | SER | 69 | 7. 163 | 32. 920 | 45. 607 | 1. 00 38. 89 |
| | ATOM | 453 | N | GLU | 70 | 5. 857 | 31. 143 | 46. 014 | 1. 00 39. 96 |
| | ATOM | 454 | CA | GLU | 70 | 6. 388 | 30. 942 | 47. 355 | 1. 00 40. 53 |
| | ATOM | 455 | CB | GLU | 70 | 5. 265 | 31. 074 | 48. 391 | 1. 00 44. 80 |
| | ATOM | 456 | CG | GLU | 70 | 4. 675 | 32. 483 | 48. 492 | 1. 00 52. 74 |

- 160 -

|  | ATOM | 457 | CD | GLU | 70 | 5.705 | 33.554 | 48.900 | 1.00 | 58.55 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 458 | OE1 | GLU | 70 | 5.362 | 34.763 | 48.866 | 1.00 | 59.55 |
|  | ATOM | 459 | OE2 | GLU | 70 | 6.852 | 33.192 | 49.258 | 1.00 | 60.30 |
|  | ATOM | 460 | C | GLU | 70 | 7.075 | 29.583 | 47.483 | 1.00 | 38.65 |
| 5 | ATOM | 461 | O | GLU | 70 | 6.807 | 28.660 | 46.704 | 1.00 | 37.89 |
|  | ATOM | 462 | N | VAL | 71 | 7.962 | 29.459 | 48.466 | 1.00 | 35.96 |
|  | ATOM | 463 | CA | VAL | 71 | 8.670 | 28.207 | 48.653 | 1.00 | 34.46 |
|  | ATOM | 464 | CB | VAL | 71 | 9.723 | 28.319 | 49.755 | 1.00 | 33.00 |
|  | ATOM | 465 | CG1 | VAL | 71 | 10.236 | 26.949 | 50.120 | 1.00 | 33.91 |
| 10 | ATOM | 466 | CG2 | VAL | 71 | 10.885 | 29.152 | 49.249 | 1.00 | 32.56 |
|  | ATOM | 467 | C | VAL | 71 | 7.730 | 27.042 | 48.931 | 1.00 | 34.75 |
|  | ATOM | 468 | O | VAL | 71 | 7.851 | 25.985 | 48.310 | 1.00 | 37.23 |
|  | ATOM | 469 | N | GLY | 72 | 6.783 | 27.219 | 49.841 | 1.00 | 33.37 |
|  | ATOM | 470 | CA | GLY | 72 | 5.842 | 26.139 | 50.105 | 1.00 | 32.39 |
| 15 | ATOM | 471 | C | GLY | 72 | 5.066 | 25.644 | 48.879 | 1.00 | 31.10 |
|  | ATOM | 472 | O | GLY | 72 | 4.631 | 24.493 | 48.859 | 1.00 | 28.98 |
|  | ATOM | 473 | N | ASP | 73 | 4.878 | 26.503 | 47.870 | 1.00 | 31.05 |
|  | ATOM | 474 | CA | ASP | 73 | 4.156 | 26.129 | 46.650 | 1.00 | 31.14 |
|  | ATOM | 475 | CB | ASP | 73 | 4.389 | 27.147 | 45.532 | 1.00 | 34.00 |
| 20 | ATOM | 476 | CG | ASP | 73 | 3.759 | 28.491 | 45.817 | 1.00 | 38.43 |
|  | ATOM | 477 | OD1 | ASP | 73 | 3.758 | 29.355 | 44.907 | 1.00 | 41.88 |
|  | ATOM | 478 | OD2 | ASP | 73 | 3.262 | 28.690 | 46.945 | 1.00 | 41.23 |
|  | ATOM | 479 | C | ASP | 73 | 4.675 | 24.785 | 46.189 | 1.00 | 30.89 |
|  | ATOM | 480 | O | ASP | 73 | 5.875 | 24.544 | 46.256 | 1.00 | 32.81 |
| 25 | ATOM | 481 | N | PHE | 74 | 3.796 | 23.921 | 45.694 | 1.00 | 28.84 |
|  | ATOM | 482 | CA | PHE | 74 | 4.233 | 22.595 | 45.271 | 1.00 | 27.21 |
|  | ATOM | 483 | CB | PHE | 74 | 4.728 | 21.834 | 46.502 | 1.00 | 26.13 |
|  | ATOM | 484 | CG | PHE | 74 | 5.407 | 20.551 | 46.185 | 1.00 | 25.61 |
|  | ATOM | 485 | CD1 | PHE | 74 | 6.641 | 20.546 | 45.547 | 1.00 | 29.29 |

- 161 -

|  | ATOM | 486 | CD2 | PHE | 74 | 4.805 | 19.344 | 46.496 | 1.00 | 24.94 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 487 | CE1 | PHE | 74 | 7.259 | 19.354 | 45.213 | 1.00 | 31.36 |
|  | ATOM | 488 | CE2 | PHE | 74 | 5.408 | 18.149 | 46.168 | 1.00 | 27.38 |
|  | ATOM | 489 | CZ | PHE | 74 | 6.640 | 18.149 | 45.527 | 1.00 | 30.18 |
| 5 | ATOM | 490 | C | PHE | 74 | 3.080 | 21.837 | 44.604 | 1.00 | 27.31 |
|  | ATOM | 491 | O | PHE | 74 | 1.912 | 22.034 | 44.951 | 1.00 | 28.04 |
|  | ATOM | 492 | N | LEU | 75 | 3.402 | 20.965 | 43.654 | 1.00 | 23.99 |
|  | ATOM | 493 | CA | LEU | 75 | 2.370 | 20.214 | 42.958 | 1.00 | 20.00 |
|  | ATOM | 494 | CB | LEU | 75 | 2.222 | 20.725 | 41.534 | 1.00 | 19.88 |
| 10 | ATOM | 495 | CG | LEU | 75 | 0.868 | 20.487 | 40.865 | 1.00 | 21.27 |
|  | ATOM | 496 | CD1 | LEU | 75 | 1.083 | 20.282 | 39.354 | 1.00 | 19.58 |
|  | ATOM | 497 | CD2 | LEU | 75 | 0.190 | 19.279 | 41.474 | 1.00 | 18.85 |
|  | ATOM | 498 | C | LEU | 75 | 2.755 | 18.758 | 42.911 | 1.00 | 18.82 |
|  | ATOM | 499 | O | LEU | 75 | 3.587 | 18.369 | 42.102 | 1.00 | 19.49 |
| 15 | ATOM | 500 | N | SER | 76 | 2.143 | 17.957 | 43.774 | 1.00 | 21.08 |
|  | ATOM | 501 | CA | SER | 76 | 2.434 | 16.530 | 43.834 | 1.00 | 22.49 |
|  | ATOM | 502 | CB | SER | 76 | 2.333 | 16.001 | 45.261 | 1.00 | 22.74 |
|  | ATOM | 503 | OG | SER | 76 | 2.591 | 14.612 | 45.292 | 1.00 | 20.37 |
|  | ATOM | 504 | C | SER | 76 | 1.507 | 15.720 | 42.967 | 1.00 | 23.58 |
| 20 | ATOM | 505 | O | SER | 76 | 0.309 | 15.980 | 42.866 | 1.00 | 23.06 |
|  | ATOM | 506 | N | LEU | 77 | 2.064 | 14.686 | 42.378 | 1.00 | 25.35 |
|  | ATOM | 507 | CA | LEU | 77 | 1.280 | 13.862 | 41.509 | 1.00 | 27.55 |
|  | ATOM | 508 | CB | LEU | 77 | 1.758 | 14.122 | 40.089 | 1.00 | 29.38 |
|  | ATOM | 509 | CG | LEU | 77 | 1.176 | 13.275 | 38.980 | 1.00 | 32.75 |
| 25 | ATOM | 510 | CD1 | LEU | 77 | -0.334 | 13.434 | 38.974 | 1.00 | 34.55 |
|  | ATOM | 511 | CD2 | LEU | 77 | 1.796 | 13.695 | 37.661 | 1.00 | 32.83 |
|  | ATOM | 512 | C | LEU | 77 | 1.445 | 12.402 | 41.913 | 1.00 | 28.86 |
|  | ATOM | 513 | O | LEU | 77 | 2.527 | 11.826 | 41.760 | 1.00 | 26.84 |
|  | ATOM | 514 | N | ASP | 78 | 0.386 | 11.811 | 42.465 | 1.00 | 29.41 |

- 162 -

| | ATOM | 515 | CA | ASP | 78 | 0.457 | 10.407 | 42.865 | 1.00 | 30.41 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 516 | CB | ASP | 78 | -0.150 | 10.186 | 44.255 | 1.00 | 31.87 |
| | ATOM | 517 | CG | ASP | 78 | -0.286 | 8.702 | 44.606 | 1.00 | 33.99 |
| | ATOM | 518 | OD1 | ASP | 78 | -1.025 | 7.993 | 43.894 | 1.00 | 35.38 |
| 5 | ATOM | 519 | OD2 | ASP | 78 | 0.338 | 8.241 | 45.586 | 1.00 | 33.31 |
| | ATOM | 520 | C | ASP | 78 | -0.270 | 9.530 | 41.860 | 1.00 | 29.41 |
| | ATOM | 521 | O | ASP | 78 | -1.484 | 9.587 | 41.732 | 1.00 | 29.74 |
| | ATOM | 522 | N | LEU | 79 | 0.472 | 8.710 | 41.143 | 1.00 | 27.93 |
| | ATOM | 523 | CA | LEU | 79 | -0.169 | 7.858 | 40.184 | 1.00 | 28.08 |
| 10 | ATOM | 524 | CB | LEU | 79 | 0.323 | 8.173 | 38.781 | 1.00 | 25.78 |
| | ATOM | 525 | CG | LEU | 79 | 1.676 | 7.627 | 38.371 | 1.00 | 24.57 |
| | ATOM | 526 | CD1 | LEU | 79 | 1.845 | 7.871 | 36.904 | 1.00 | 25.82 |
| | ATOM | 527 | CD2 | LEU | 79 | 2.779 | 8.274 | 39.166 | 1.00 | 26.37 |
| | ATOM | 528 | C | LEU | 79 | 0.114 | 6.420 | 40.548 | 1.00 | 31.25 |
| 15 | ATOM | 529 | O | LEU | 79 | 1.265 | 6.017 | 40.712 | 1.00 | 32.14 |
| | ATOM | 530 | N | GLY | 80 | -0.955 | 5.652 | 40.699 | 1.00 | 34.99 |
| | ATOM | 531 | CA | GLY | 80 | -0.812 | 4.259 | 41.056 | 1.00 | 38.29 |
| | ATOM | 532 | C | GLY | 80 | -2.088 | 3.499 | 40.776 | 1.00 | 40.81 |
| | ATOM | 533 | O | GLY | 80 | -3.100 | 3.686 | 41.452 | 1.00 | 40.77 |
| 20 | ATOM | 534 | N | GLY | 81 | -2.038 | 2.642 | 39.765 | 1.00 | 43.19 |
| | ATOM | 535 | CA | GLY | 81 | -3.197 | 1.850 | 39.422 | 1.00 | 45.84 |
| | ATOM | 536 | C | GLY | 81 | -3.936 | 2.428 | 38.244 | 1.00 | 49.22 |
| | ATOM | 537 | O | GLY | 81 | -3.328 | 2.825 | 37.241 | 1.00 | 49.20 |
| | ATOM | 538 | N | THR | 82 | -5.260 | 2.465 | 38.365 | 1.00 | 51.93 |
| 25 | ATOM | 539 | CA | THR | 82 | -6.117 | 3.003 | 37.312 | 1.00 | 54.41 |
| | ATOM | 540 | CB | THR | 82 | -7.344 | 2.090 | 37.060 | 1.00 | 56.74 |
| | ATOM | 541 | OG1 | THR | 82 | -6.908 | 0.727 | 36.952 | 1.00 | 60.43 |
| | ATOM | 542 | CG2 | THR | 82 | -8.043 | 2.473 | 35.752 | 1.00 | 58.23 |
| | ATOM | 543 | C | THR | 82 | -6.584 | 4.382 | 37.759 | 1.00 | 52.48 |

- 163 -

| ATOM | 544 | O | THR 82 | -7.308 | 5.077 | 37.046 | 1.00 | 52.21 |
|------|-----|-----|--------|--------|-------|--------|------|-------|
| ATOM | 545 | N | ASN 83 | -6.148 | 4.778 | 38.946 | 1.00 | 50.63 |
| ATOM | 546 | CA | ASN 83 | -6.523 | 6.071 | 39.466 | 1.00 | 50.52 |
| ATOM | 547 | CB | ASN 83 | -7.574 | 5.911 | 40.568 | 1.00 | 53.97 |
| ATOM | 548 | CG | ASN 83 | -8.955 | 5.560 | 40.020 | 1.00 | 58.88 |
| ATOM | 549 | OD1 | ASN 83 | -9.508 | 6.290 | 39.190 | 1.00 | 60.51 |
| ATOM | 550 | ND2 | ASN 83 | -9.521 | 4.444 | 40.489 | 1.00 | 60.30 |
| ATOM | 551 | C | ASN 83 | -5.338 | 6.861 | 39.997 | 1.00 | 48.79 |
| ATOM | 552 | O | ASN 83 | -4.682 | 6.442 | 40.956 | 1.00 | 48.09 |
| ATOM | 553 | N | PHE 84 | -5.068 | 8.003 | 39.356 | 1.00 | 45.51 |
| ATOM | 554 | CA | PHE 84 | -3.995 | 8.907 | 39.772 | 1.00 | 40.32 |
| ATOM | 555 | CB | PHE 84 | -2.998 | 9.145 | 38.644 | 1.00 | 39.20 |
| ATOM | 556 | CG | PHE 84 | -3.436 | 10.175 | 37.652 | 1.00 | 39.52 |
| ATOM | 557 | CD1 | PHE 84 | -4.096 | 9.802 | 36.494 | 1.00 | 40.87 |
| ATOM | 558 | CD2 | PHE 84 | -3.159 | 11.524 | 37.860 | 1.00 | 39.69 |
| ATOM | 559 | CE1 | PHE 84 | -4.479 | 10.758 | 35.549 | 1.00 | 41.79 |
| ATOM | 560 | CE2 | PHE 84 | -3.540 | 12.490 | 36.922 | 1.00 | 40.16 |
| ATOM | 561 | CZ | PHE 84 | -4.198 | 12.105 | 35.762 | 1.00 | 40.38 |
| ATOM | 562 | C | PHE 84 | -4.604 | 10.246 | 40.176 | 1.00 | 37.84 |
| ATOM | 563 | O | PHE 84 | -5.405 | 10.806 | 39.439 | 1.00 | 37.11 |
| ATOM | 564 | N | ARG 85 | -4.216 | 10.762 | 41.338 | 1.00 | 36.37 |
| ATOM | 565 | CA | ARG 85 | -4.738 | 12.032 | 41.840 | 1.00 | 35.14 |
| ATOM | 566 | CB | ARG 85 | -5.496 | 11.779 | 43.136 | 1.00 | 39.80 |
| ATOM | 567 | CG | ARG 85 | -4.888 | 10.677 | 43.970 | 1.00 | 47.71 |
| ATOM | 568 | CD | ARG 85 | -5.948 | 9.964 | 44.805 | 1.00 | 55.73 |
| ATOM | 569 | NE | ARG 85 | -5.391 | 8.801 | 45.493 | 1.00 | 62.76 |
| ATOM | 570 | CZ | ARG 85 | -4.799 | 7.772 | 44.883 | 1.00 | 65.65 |
| ATOM | 571 | NH1 | ARG 85 | -4.684 | 7.749 | 43.557 | 1.00 | 63.79 |
| ATOM | 572 | NH2 | ARG 85 | -4.314 | 6.765 | 45.605 | 1.00 | 66.67 |

- 164 -

| | ATOM | 573 | C | ARG | 85 | -3.664 | 13.088 | 42.075 | 1.00 | 32.14 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 574 | O | ARG | 85 | -2.561 | 12.772 | 42.522 | 1.00 | 32.77 |
| | ATOM | 575 | N | VAL | 86 | -3.977 | 14.345 | 41.778 | 1.00 | 27.45 |
| | ATOM | 576 | CA | VAL | 86 | -2.997 | 15.405 | 41.983 | 1.00 | 26.49 |
| 5 | ATOM | 577 | CB | VAL | 86 | -2.975 | 16.400 | 40.821 | 1.00 | 24.77 |
| | ATOM | 578 | CG1 | VAL | 86 | -3.033 | 15.655 | 39.510 | 1.00 | 26.70 |
| | ATOM | 579 | CG2 | VAL | 86 | -4.109 | 17.373 | 40.948 | 1.00 | 24.73 |
| | ATOM | 580 | C | VAL | 86 | -3.292 | 16.177 | 43.257 | 1.00 | 26.66 |
| | ATOM | 581 | O | VAL | 86 | -4.401 | 16.121 | 43.779 | 1.00 | 28.06 |
| 10 | ATOM | 582 | N | MET | 87 | -2.289 | 16.888 | 43.757 | 1.00 | 26.93 |
| | ATOM | 583 | CA | MET | 87 | -2.427 | 17.677 | 44.973 | 1.00 | 25.08 |
| | ATOM | 584 | CB | MET | 87 | -1.748 | 16.979 | 46.138 | 1.00 | 25.05 |
| | ATOM | 585 | CG | MET | 87 | -1.674 | 17.833 | 47.375 | 1.00 | 24.83 |
| | ATOM | 586 | SD | MET | 87 | -0.509 | 17.090 | 48.503 | 1.00 | 30.68 |
| 15 | ATOM | 587 | CE | MET | 87 | -1.544 | 16.749 | 49.894 | 1.00 | 29.41 |
| | ATOM | 588 | C | MET | 87 | -1.768 | 19.021 | 44.774 | 1.00 | 24.52 |
| | ATOM | 589 | O | MET | 87 | -0.638 | 19.097 | 44.298 | 1.00 | 27.12 |
| | ATOM | 590 | N | LEU | 88 | -2.455 | 20.087 | 45.146 | 1.00 | 22.16 |
| | ATOM | 591 | CA | LEU | 88 | -1.872 | 21.398 | 44.975 | 1.00 | 20.70 |
| 20 | ATOM | 592 | CB | LEU | 88 | -2.825 | 22.309 | 44.230 | 1.00 | 20.34 |
| | ATOM | 593 | CG | LEU | 88 | -2.178 | 23.663 | 43.991 | 1.00 | 23.49 |
| | ATOM | 594 | CD1 | LEU | 88 | -0.806 | 23.470 | 43.354 | 1.00 | 24.39 |
| | ATOM | 595 | CD2 | LEU | 88 | -3.078 | 24.493 | 43.094 | 1.00 | 25.91 |
| | ATOM | 596 | C | LEU | 88 | -1.535 | 22.021 | 46.301 | 1.00 | 19.94 |
| 25 | ATOM | 597 | O | LEU | 88 | -2.225 | 21.794 | 47.282 | 1.00 | 21.18 |
| | ATOM | 598 | N | VAL | 89 | -0.463 | 22.799 | 46.343 | 1.00 | 20.16 |
| | ATOM | 599 | CA | VAL | 89 | -0.082 | 23.462 | 47.580 | 1.00 | 21.15 |
| | ATOM | 600 | CB | VAL | 89 | 0.984 | 22.676 | 48.357 | 1.00 | 14.95 |
| | ATOM | 601 | CG1 | VAL | 89 | 1.292 | 23.385 | 49.657 | 1.00 | 7.73 |

- 165 -

| ATOM | 602 | CG2 | VAL | 89 | 0.515 | 21.268 | 48.609 | 1.00 | 10.59 |
|------|-----|-----|-----|----|-------|--------|--------|------|-------|
| ATOM | 603 | C | VAL | 89 | 0.491 | 24.829 | 47.254 | 1.00 | 27.10 |
| ATOM | 604 | O | VAL | 89 | 1.410 | 24.939 | 46.442 | 1.00 | 27.22 |
| ATOM | 605 | N | LYS | 90 | -0.066 | 25.866 | 47.875 | 1.00 | 33.21 |
| ATOM | 606 | CA | LYS | 90 | 0.401 | 27.235 | 47.671 | 1.00 | 40.01 |
| ATOM | 607 | CB | LYS | 90 | -0.443 | 27.962 | 46.604 | 1.00 | 41.03 |
| ATOM | 608 | CG | LYS | 90 | -1.941 | 27.979 | 46.850 | 1.00 | 47.19 |
| ATOM | 609 | CD | LYS | 90 | -2.749 | 28.454 | 45.622 | 1.00 | 52.33 |
| ATOM | 610 | CE | LYS | 90 | -4.274 | 28.393 | 45.899 | 1.00 | 55.73 |
| ATOM | 611 | NZ | LYS | 90 | -5.161 | 28.724 | 44.731 | 1.00 | 56.02 |
| ATOM | 612 | C | LYS | 90 | 0.384 | 28.009 | 48.981 | 1.00 | 43.61 |
| ATOM | 613 | O | LYS | 90 | -0.577 | 27.943 | 49.747 | 1.00 | 44.04 |
| ATOM | 614 | N | VAL | 91 | 1.469 | 28.728 | 49.241 | 1.00 | 47.88 |
| ATOM | 615 | CA | VAL | 91 | 1.587 | 29.513 | 50.458 | 1.00 | 51.82 |
| ATOM | 616 | CB | VAL | 91 | 3.059 | 29.780 | 50.788 | 1.00 | 51.29 |
| ATOM | 617 | CG1 | VAL | 91 | 3.160 | 30.748 | 51.947 | 1.00 | 54.88 |
| ATOM | 618 | CG2 | VAL | 91 | 3.749 | 28.479 | 51.137 | 1.00 | 48.18 |
| ATOM | 619 | C | VAL | 91 | 0.849 | 30.846 | 50.355 | 1.00 | 55.01 |
| ATOM | 620 | O | VAL | 91 | 0.994 | 31.569 | 49.369 | 1.00 | 54.57 |
| ATOM | 621 | N | GLY | 92 | 0.060 | 31.157 | 51.382 | 1.00 | 59.16 |
| ATOM | 622 | CA | GLY | 92 | -0.696 | 32.396 | 51.401 | 1.00 | 64.58 |
| ATOM | 623 | C | GLY | 92 | -0.305 | 33.297 | 52.558 | 1.00 | 68.39 |
| ATOM | 624 | O | GLY | 92 | 0.637 | 32.992 | 53.295 | 1.00 | 66.92 |
| ATOM | 625 | N | GLU | 93 | -1.025 | 34.410 | 52.712 | 1.00 | 73.13 |
| ATOM | 626 | CA | GLU | 93 | -0.751 | 35.351 | 53.792 | 1.00 | 78.27 |
| ATOM | 627 | CB | GLU | 93 | -0.623 | 36.780 | 53.248 | 1.00 | 79.11 |
| ATOM | 628 | CG | GLU | 93 | 0.334 | 37.635 | 54.077 | 1.00 | 82.44 |
| ATOM | 629 | CD | GLU | 93 | 0.218 | 39.120 | 53.795 | 1.00 | 84.34 |
| ATOM | 630 | OE1 | GLU | 93 | -0.877 | 39.688 | 54.018 | 1.00 | 84.71 |

- 166 -

|  | ATOM | 631 | OE2 | GLU 93 | 1.228 | 39.718 | 53.359 | 1.00 | 85.45 |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 632 | C | GLU 93 | -1.813 | 35.309 | 54.904 | 1.00 | 80.72 |
|  | ATOM | 633 | O | GLU 93 | -1.469 | 35.340 | 56.086 | 1.00 | 81.42 |
|  | ATOM | 634 | N | GLY 94 | -3.093 | 35.240 | 54.536 | 1.00 | 83.03 |
| 5 | ATOM | 635 | CA | GLY 94 | -4.153 | 35.182 | 55.538 | 1.00 | 85.37 |
|  | ATOM | 636 | C | GLY 94 | -4.867 | 36.502 | 55.792 | 1.00 | 87.51 |
|  | ATOM | 637 | O | GLY 94 | -4.356 | 37.562 | 55.430 | 1.00 | 88.65 |
|  | ATOM | 638 | N | GLU 95 | -6.041 | 36.447 | 56.427 | 1.00 | 88.43 |
|  | ATOM | 639 | CA | GLU 95 | -6.831 | 37.653 | 56.716 | 1.00 | 88.66 |
| 10 | ATOM | 640 | CB | GLU 95 | -8.192 | 37.281 | 57.328 | 1.00 | 89.61 |
|  | ATOM | 641 | CG | GLU 95 | -9.077 | 36.406 | 56.448 | 1.00 | 90.41 |
|  | ATOM | 642 | CD | GLU 95 | -8.620 | 34.958 | 56.408 | 1.00 | 91.01 |
|  | ATOM | 643 | OE1 | GLU 95 | -9.089 | 34.211 | 55.523 | 1.00 | 90.26 |
|  | ATOM | 644 | OE2 | GLU 95 | -7.800 | 34.565 | 57.266 | 1.00 | 91.81 |
| 15 | ATOM | 645 | C | GLU 95 | -6.115 | 38.625 | 57.652 | 1.00 | 88.62 |
|  | ATOM | 646 | O | GLU 95 | -6.576 | 39.748 | 57.868 | 1.00 | 88.29 |
|  | ATOM | 647 | N | GLU 96 | -4.991 | 38.182 | 58.208 | 1.00 | 89.03 |
|  | ATOM | 648 | CA | GLU 96 | -4.200 | 38.995 | 59.124 | 1.00 | 88.80 |
|  | ATOM | 649 | CB | GLU 96 | -4.065 | 38.282 | 60.476 | 1.00 | 88.55 |
| 20 | ATOM | 650 | CG | GLU 96 | -5.368 | 38.155 | 61.268 | 1.00 | 89.59 |
|  | ATOM | 651 | CD | GLU 96 | -6.400 | 37.262 | 60.593 | 1.00 | 90.56 |
|  | ATOM | 652 | OE1 | GLU 96 | -6.163 | 36.040 | 60.481 | 1.00 | 90.53 |
|  | ATOM | 653 | OE2 | GLU 96 | -7.452 | 37.785 | 60.172 | 1.00 | 90.67 |
|  | ATOM | 654 | C | GLU 96 | -2.810 | 39.327 | 58.519 | 1.00 | 88.40 |
| 25 | ATOM | 655 | O | GLU 96 | -2.097 | 40.166 | 59.052 | 1.00 | 89.12 |
|  | ATOM | 656 | N | GLY 97 | -2.431 | 38.700 | 57.404 | 1.00 | 86.87 |
|  | ATOM | 657 | CA | GLY 97 | -1.133 | 38.917 | 56.789 | 1.00 | 85.05 |
|  | ATOM | 658 | C | GLY 97 | -0.161 | 37.976 | 57.494 | 1.00 | 84.17 |
|  | ATOM | 659 | O | GLY 97 | 1.044 | 38.179 | 57.605 | 1.00 | 83.49 |

- 167 -

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 660 | N | GLN | 98 | -0.820 | 36.901 | 57.977 | 1.00 | 83.07 |
| | ATOM | 661 | CA | GLN | 98 | -0.253 | 35.810 | 58.769 | 1.00 | 82.28 |
| | ATOM | 662 | CB | GLN | 98 | -1.346 | 34.825 | 59.250 | 1.00 | 82.41 |
| | ATOM | 663 | CG | GLN | 98 | -2.647 | 35.462 | 59.699 | 1.00 | 83.61 |
| 5 | ATOM | 664 | CD | GLN | 98 | -3.740 | 34.427 | 60.007 | 1.00 | 84.16 |
| | ATOM | 665 | OE1 | GLN | 98 | -3.606 | 33.239 | 59.714 | 1.00 | 84.01 |
| | ATOM | 666 | NE2 | GLN | 98 | -4.905 | 34.685 | 60.592 | 1.00 | 84.46 |
| | ATOM | 667 | C | GLN | 98 | 0.735 | 34.981 | 58.011 | 1.00 | 81.85 |
| | ATOM | 668 | O | GLN | 98 | 1.955 | 35.200 | 57.956 | 1.00 | 83.51 |
| 10 | ATOM | 669 | N | TRP | 99 | 0.118 | 33.962 | 57.470 | 1.00 | 79.05 |
| | ATOM | 670 | CA | TRP | 99 | 0.703 | 32.914 | 56.706 | 1.00 | 75.85 |
| | ATOM | 671 | CB | TRP | 99 | 1.993 | 32.398 | 57.308 | 1.00 | 73.88 |
| | ATOM | 672 | CG | TRP | 99 | 2.968 | 31.780 | 56.325 | 1.00 | 71.82 |
| | ATOM | 673 | CD2 | TRP | 99 | 3.211 | 30.386 | 56.075 | 1.00 | 70.49 |
| 15 | ATOM | 674 | CE2 | TRP | 99 | 4.222 | 30.308 | 55.123 | 1.00 | 69.72 |
| | ATOM | 675 | CE3 | TRP | 99 | 2.671 | 29.200 | 56.550 | 1.00 | 69.52 |
| | ATOM | 676 | CD1 | TRP | 99 | 3.832 | 32.464 | 55.525 | 1.00 | 71.99 |
| | ATOM | 677 | NE1 | TRP | 99 | 4.598 | 31.589 | 54.790 | 1.00 | 71.07 |
| | ATOM | 678 | CZ2 | TRP | 99 | 4.692 | 29.089 | 54.624 | 1.00 | 67.81 |
| 20 | ATOM | 679 | CZ3 | TRP | 99 | 3.136 | 27.984 | 56.080 | 1.00 | 67.31 |
| | ATOM | 680 | CH2 | TRP | 99 | 4.151 | 27.945 | 55.111 | 1.00 | 67.77 |
| | ATOM | 681 | C | TRP | 99 | -0.247 | 31.793 | 56.673 | 1.00 | 74.58 |
| | ATOM | 682 | O | TRP | 99 | -1.060 | 31.567 | 57.556 | 1.00 | 75.00 |
| | ATOM | 683 | N | SER | 100 | -0.090 | 31.087 | 55.647 | 1.00 | 72.11 |
| 25 | ATOM | 684 | CA | SER | 100 | -0.948 | 29.999 | 55.517 | 1.00 | 68.48 |
| | ATOM | 685 | CB | SER | 100 | -2.376 | 30.466 | 55.232 | 1.00 | 68.40 |
| | ATOM | 686 | OG | SER | 100 | -2.467 | 31.128 | 53.985 | 1.00 | 68.76 |
| | ATOM | 687 | C | SER | 100 | -0.522 | 29.152 | 54.382 | 1.00 | 66.28 |
| | ATOM | 688 | O | SER | 100 | 0.405 | 29.473 | 53.632 | 1.00 | 65.13 |

- 168 -

| | ATOM | 689 | N | VAL | 101 | -1.225 | 28.028 | 54.291 | 1.00 | 64.27 |
|---|------|-----|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 690 | CA | VAL | 101 | -0.982 | 27.030 | 53.262 | 1.00 | 62.66 |
| | ATOM | 691 | CB | VAL | 101 | 0.090 | 26.023 | 53.715 | 1.00 | 62.98 |
| | ATOM | 692 | CG1 | VAL | 101 | 1.493 | 26.554 | 53.459 | 1.00 | 66.77 |
| 5 | ATOM | 693 | CG2 | VAL | 101 | -0.075 | 25.688 | 55.198 | 1.00 | 63.17 |
| | ATOM | 694 | C | VAL | 101 | -2.219 | 26.243 | 52.878 | 1.00 | 60.88 |
| | ATOM | 695 | 0 | VAL | 101 | -2.561 | 25.258 | 53.530 | 1.00 | 60.62 |
| | ATOM | 696 | N | LYS | 102 | -2.880 | 26.671 | 51.810 | 1.00 | 58.24 |
| | ATOM | 697 | CA | LYS | 102 | -4.066 | 25.981 | 51.337 | 1.00 | 56.12 |
| 10 | ATOM | 698 | CB | LYS | 102 | -4.887 | 26.880 | 50.410 | 1.00 | 57.06 |
| | ATOM | 699 | CG | LYS | 102 | -5.884 | 27.806 | 51.111 | 1.00 | 60.55 |
| | ATOM | 700 | CD | LYS | 102 | -7.056 | 27.038 | 51.748 | 1.00 | 63.17 |
| | ATOM | 701 | CE | LYS | 102 | -8.282 | 27.944 | 52.036 | 1.00 | 64.70 |
| | ATOM | 702 | NZ | LYS | 102 | -8.021 | 29.150 | 52.899 | 1.00 | 63.52 |
| 15 | ATOM | 703 | C | LYS | 102 | -3.677 | 24.710 | 50.596 | 1.00 | 54.04 |
| | ATOM | 704 | 0 | LYS | 102 | -2.599 | 24.609 | 50.007 | 1.00 | 52.35 |
| | ATOM | 705 | N | THR | 103 | -4.576 | 23.738 | 50.631 | 1.00 | 52.24 |
| | ATOM | 706 | CA | THR | 103 | -4.345 | 22.474 | 49.972 | 1.00 | 49.72 |
| | ATOM | 707 | CB | THR | 103 | -4.139 | 21.385 | 51.010 | 1.00 | 49.49 |
| 20 | ATOM | 708 | OG1 | THR | 103 | -3.399 | 20.316 | 50.422 | 1.00 | 53.11 |
| | ATOM | 709 | CG2 | THR | 103 | -5.475 | 20.861 | 51.517 | 1.00 | 48.32 |
| | ATOM | 710 | C | THR | 103 | -5.563 | 22.158 | 49.106 | 1.00 | 49.61 |
| | ATOM | 711 | 0 | THR | 103 | -6.693 | 22.435 | 49.507 | 1.00 | 50.24 |
| | ATOM | 712 | N | LYS | 104 | -5.330 | 21.587 | 47.924 | 1.00 | 48.56 |
| 25 | ATOM | 713 | CA | LYS | 104 | -6.404 | 21.251 | 46.983 | 1.00 | 48.50 |
| | ATOM | 714 | CB | LYS | 104 | -6.469 | 22.298 | 45.864 | 1.00 | 49.98 |
| | ATOM | 715 | CG | LYS | 104 | -6.753 | 23.737 | 46.313 | 1.00 | 56.05 |
| | ATOM | 716 | CD | LYS | 104 | -8.195 | 23.932 | 46.814 | 1.00 | 60.38 |
| | ATOM | 717 | CE | LYS | 104 | -8.456 | 25.383 | 47.254 | 1.00 | 62.32 |

- 169 -

| | ATOM | 718 | NZ | LYS | 104 | -9.845 | 25.649 | 47.761 | 1.00 | 61.31 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 719 | C | LYS | 104 | -6.224 | 19.878 | 46.332 | 1.00 | 48.13 |
| | ATOM | 720 | O | LYS | 104 | -5.286 | 19.685 | 45.563 | 1.00 | 49.60 |
| | ATOM | 721 | N | HIS | 105 | -7.127 | 18.936 | 46.606 | 1.00 | 47.57 |
| 5 | ATOM | 722 | CA | HIS | 105 | -7.023 | 17.601 | 46.010 | 1.00 | 47.23 |
| | ATOM | 723 | CB | HIS | 105 | -7.165 | 16.529 | 47.074 | 1.00 | 47.40 |
| | ATOM | 724 | CG | HIS | 105 | -6.241 | 16.709 | 48.228 | 1.00 | 49.37 |
| | ATOM | 725 | CD2 | HIS | 105 | -5.098 | 16.066 | 48.563 | 1.00 | 49.55 |
| | ATOM | 726 | ND1 | HIS | 105 | -6.459 | 17.648 | 49.212 | 1.00 | 50.43 |
| 10 | ATOM | 727 | CE1 | HIS | 105 | -5.493 | 17.571 | 50.110 | 1.00 | 51.38 |
| | ATOM | 728 | NE2 | HIS | 105 | -4.655 | 16.619 | 49.740 | 1.00 | 50.58 |
| | ATOM | 729 | C | HIS | 105 | -8.030 | 17.304 | 44.907 | 1.00 | 46.39 |
| | ATOM | 730 | O | HIS | 105 | -9.195 | 17.692 | 44.985 | 1.00 | 49.62 |
| | ATOM | 731 | N | GLN | 106 | -7.575 | 16.580 | 43.894 | 1.00 | 42.98 |
| 15 | ATOM | 732 | CA | GLN | 106 | -8.419 | 16.226 | 42.771 | 1.00 | 40.44 |
| | ATOM | 733 | CB | GLN | 106 | -8.284 | 17.285 | 41.685 | 1.00 | 40.41 |
| | ATOM | 734 | CG | GLN | 106 | -9.546 | 17.548 | 40.908 | 1.00 | 40.59 |
| | ATOM | 735 | CD | GLN | 106 | -10.428 | 16.324 | 40.813 | 1.00 | 40.54 |
| | ATOM | 736 | OE1 | GLN | 106 | -11.061 | 15.927 | 41.795 | 1.00 | 39.16 |
| 20 | ATOM | 737 | NE2 | GLN | 106 | -10.475 | 15.712 | 39.631 | 1.00 | 40.06 |
| | ATOM | 738 | C | GLN | 106 | -7.940 | 14.878 | 42.249 | 1.00 | 40.70 |
| | ATOM | 739 | O | GLN | 106 | -6.745 | 14.699 | 42.012 | 1.00 | 41.69 |
| | ATOM | 740 | N | MET | 107 | -8.867 | 13.937 | 42.066 | 1.00 | 41.01 |
| | ATOM | 741 | CA | MET | 107 | -8.532 | 12.588 | 41.599 | 1.00 | 40.17 |
| 25 | ATOM | 742 | CB | MET | 107 | -9.083 | 11.551 | 42.588 | 1.00 | 42.07 |
| | ATOM | 743 | CG | MET | 107 | -8.772 | 10.094 | 42.249 | 1.00 | 44.67 |
| | ATOM | 744 | SD | MET | 107 | -10.185 | 9.202 | 41.551 | 1.00 | 50.71 |
| | ATOM | 745 | CE | MET | 107 | -10.688 | 8.056 | 42.927 | 1.00 | 43.37 |
| | ATOM | 746 | C | MET | 107 | -9.059 | 12.294 | 40.204 | 1.00 | 38.93 |

- 170 -

| ATOM | 747 | O | MET | 107 | -10.264 | 12.285 | 39.979 | 1.00 | 41.30 |
|------|-----|-----|-----|-----|---------|--------|--------|------|-------|
| ATOM | 748 | N | TYR | 108 | -8.161 | 12.044 | 39.264 | 1.00 | 37.96 |
| ATOM | 749 | CA | TYR | 108 | -8.588 | 11.750 | 37.907 | 1.00 | 38.48 |
| ATOM | 750 | CB | TYR | 108 | -7.670 | 12.454 | 36.900 | 1.00 | 35.63 |
| ATOM | 751 | CG | TYR | 108 | -7.732 | 13.972 | 36.977 | 1.00 | 35.18 |
| ATOM | 752 | CD1 | TYR | 108 | -7.492 | 14.645 | 38.180 | 1.00 | 37.21 |
| ATOM | 753 | CE1 | TYR | 108 | -7.550 | 16.047 | 38.268 | 1.00 | 34.81 |
| ATOM | 754 | CD2 | TYR | 108 | -8.031 | 14.735 | 35.857 | 1.00 | 34.14 |
| ATOM | 755 | CE2 | TYR | 108 | -8.092 | 16.134 | 35.931 | 1.00 | 35.09 |
| ATOM | 756 | CZ | TYR | 108 | -7.852 | 16.783 | 37.139 | 1.00 | 35.25 |
| ATOM | 757 | OH | TYR | 108 | -7.937 | 18.158 | 37.211 | 1.00 | 33.27 |
| ATOM | 758 | C | TYR | 108 | -8.583 | 10.241 | 37.689 | 1.00 | 40.17 |
| ATOM | 759 | O | TYR | 108 | -7.817 | 9.514 | 38.325 | 1.00 | 38.04 |
| ATOM | 760 | N | SER | 109 | -9.469 | 9.765 | 36.818 | 1.00 | 42.63 |
| ATOM | 761 | CA | SER | 109 | -9.524 | 8.341 | 36.530 | 1.00 | 44.60 |
| ATOM | 762 | CB | SER | 109 | -10.929 | 7.787 | 36.736 | 1.00 | 43.05 |
| ATOM | 763 | OG | SER | 109 | -10.926 | 6.385 | 36.522 | 1.00 | 41.66 |
| ATOM | 764 | C | SER | 109 | -9.090 | 8.106 | 35.097 | 1.00 | 46.74 |
| ATOM | 765 | O | SER | 109 | -9.531 | 8.799 | 34.182 | 1.00 | 44.65 |
| ATOM | 766 | N | ILE | 110 | -8.217 | 7.120 | 34.918 | 1.00 | 50.31 |
| ATOM | 767 | CA | ILE | 110 | -7.686 | 6.782 | 33.608 | 1.00 | 55.29 |
| ATOM | 768 | CB | ILE | 110 | -6.326 | 6.060 | 33.731 | 1.00 | 54.32 |
| ATOM | 769 | CG2 | ILE | 110 | -5.690 | 5.932 | 32.364 | 1.00 | 56.16 |
| ATOM | 770 | CG1 | ILE | 110 | -5.373 | 6.844 | 34.626 | 1.00 | 53.30 |
| ATOM | 771 | CD1 | ILE | 110 | -4.067 | 6.117 | 34.869 | 1.00 | 51.57 |
| ATOM | 772 | C | ILE | 110 | -8.621 | 5.882 | 32.799 | 1.00 | 59.70 |
| ATOM | 773 | O | ILE | 110 | -8.906 | 4.749 | 33.199 | 1.00 | 58.82 |
| ATOM | 774 | N | PRO | 111 | -9.114 | 6.381 | 31.650 | 1.00 | 64.10 |
| ATOM | 775 | CD | PRO | 111 | -8.972 | 7.759 | 31.142 | 1.00 | 64.05 |

- 171 -

|   | ATOM | 776 | CA | PRO | 111 | -10.012 | 5.608 | 30.788 | 1.00 | 68.40 |
|---|------|-----|----|-----|-----|---------|-------|--------|------|-------|
|   | ATOM | 777 | CB | PRO | 111 | -10.118 | 6.484 | 29.547 | 1.00 | 67.29 |
|   | ATOM | 778 | CG | PRO | 111 | -10.105 | 7.860 | 30.144 | 1.00 | 63.88 |
|   | ATOM | 779 | C  | PRO | 111 | -9.416  | 4.231 | 30.494 | 1.00 | 72.88 |
| 5 | ATOM | 780 | O  | PRO | 111 | -8.195  | 4.065 | 30.506 | 1.00 | 73.72 |
|   | ATOM | 781 | N  | GLU | 112 | -10.280 | 3.250 | 30.239 | 1.00 | 77.60 |
|   | ATOM | 782 | CA | GLU | 112 | -9.845  | 1.879 | 29.958 | 1.00 | 80.79 |
|   | ATOM | 783 | CB | GLU | 112 | -11.072 | 0.968 | 29.798 | 1.00 | 82.29 |
|   | ATOM | 784 | CG | GLU | 112 | -10.748 | -0.498 | 29.524 | 1.00 | 83.62 |
| 10 | ATOM | 785 | CD | GLU | 112 | -11.896 | -1.247 | 28.851 | 1.00 | 85.04 |
|   | ATOM | 786 | OE1 | GLU | 112 | -11.697 | -2.423 | 28.470 | 1.00 | 85.60 |
|   | ATOM | 787 | OE2 | GLU | 112 | -12.995 | -0.665 | 28.700 | 1.00 | 85.42 |
|   | ATOM | 788 | C  | GLU | 112 | -8.971  | 1.806 | 28.702 | 1.00 | 82.21 |
|   | ATOM | 789 | O  | GLU | 112 | -7.936  | 1.137 | 28.693 | 1.00 | 82.17 |
| 15 | ATOM | 790 | N  | ASP | 113 | -9.394  | 2.501 | 27.649 | 1.00 | 83.97 |
|   | ATOM | 791 | CA | ASP | 113 | -8.660  | 2.522 | 26.385 | 1.00 | 85.79 |
|   | ATOM | 792 | CB | ASP | 113 | -9.506  | 3.221 | 25.302 | 1.00 | 86.45 |
|   | ATOM | 793 | CG | ASP | 113 | -9.961  | 4.624 | 25.712 | 1.00 | 87.32 |
|   | ATOM | 794 | OD1 | ASP | 113 | -10.655 | 4.756 | 26.748 | 1.00 | 86.75 |
| 20 | ATOM | 795 | OD2 | ASP | 113 | -9.629  | 5.595 | 24.991 | 1.00 | 87.18 |
|   | ATOM | 796 | C  | ASP | 113 | -7.297  | 3.215 | 26.533 | 1.00 | 86.44 |
|   | ATOM | 797 | O  | ASP | 113 | -6.467  | 3.195 | 25.617 | 1.00 | 86.35 |
|   | ATOM | 798 | N  | ALA | 114 | -7.075  | 3.813 | 27.701 | 1.00 | 86.34 |
|   | ATOM | 799 | CA | ALA | 114 | -5.837  | 4.533 | 28.000 | 1.00 | 85.22 |
| 25 | ATOM | 800 | CB | ALA | 114 | -6.174  | 5.904 | 28.585 | 1.00 | 84.46 |
|   | ATOM | 801 | C  | ALA | 114 | -4.928  | 3.768 | 28.963 | 1.00 | 83.67 |
|   | ATOM | 802 | O  | ALA | 114 | -3.716  | 3.692 | 28.762 | 1.00 | 83.48 |
|   | ATOM | 803 | N  | MET | 115 | -5.528  | 3.212 | 30.012 | 1.00 | 81.79 |
|   | ATOM | 804 | CA | MET | 115 | -4.802  | 2.457 | 31.023 | 1.00 | 78.70 |

- 172 -

| | ATOM | 805 | CB | MET | 115 | -5.776 | 2.050 | 32.135 | 1.00 | 81.16 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 806 | CG | MET | 115 | -5.148 | 1.863 | 33.503 | 1.00 | 84.52 |
| | ATOM | 807 | SD | MET | 115 | -3.978 | 0.492 | 33.553 | 1.00 | 90.44 |
| | ATOM | 808 | CE | MET | 115 | -5.060 | -0.891 | 34.119 | 1.00 | 88.49 |
| 5 | ATOM | 809 | C | MET | 115 | -4.145 | 1.224 | 30.391 | 1.00 | 76.27 |
| | ATOM | 810 | O | MET | 115 | -3.066 | 0.809 | 30.813 | 1.00 | 74.47 |
| | ATOM | 811 | N | THR | 116 | -4.796 | 0.658 | 29.372 | 1.00 | 74.50 |
| | ATOM | 812 | CA | THR | 116 | -4.282 | -0.518 | 28.666 | 1.00 | 72.46 |
| | ATOM | 813 | CB | THR | 116 | -5.399 | -1.524 | 28.309 | 1.00 | 72.22 |
| 10 | ATOM | 814 | OG1 | THR | 116 | -6.200 | -0.993 | 27.244 | 1.00 | 71.17 |
| | ATOM | 815 | CG2 | THR | 116 | -6.275 | -1.805 | 29.516 | 1.00 | 71.94 |
| | ATOM | 816 | C | THR | 116 | -3.621 | -0.110 | 27.356 | 1.00 | 71.75 |
| | ATOM | 817 | O | THR | 116 | -3.562 | -0.899 | 26.412 | 1.00 | 71.39 |
| | ATOM | 818 | N | GLY | 117 | -3.142 | 1.131 | 27.301 | 1.00 | 71.09 |
| 15 | ATOM | 819 | CA | GLY | 117 | -2.477 | 1.639 | 26.110 | 1.00 | 68.62 |
| | ATOM | 820 | C | GLY | 117 | -0.961 | 1.651 | 26.260 | 1.00 | 66.70 |
| | ATOM | 821 | O | GLY | 117 | -0.384 | 0.702 | 26.798 | 1.00 | 67.20 |
| | ATOM | 822 | N | THR | 118 | -0.313 | 2.716 | 25.783 | 1.00 | 63.05 |
| | ATOM | 823 | CA | THR | 118 | 1.142 | 2.844 | 25.876 | 1.00 | 59.92 |
| 20 | ATOM | 824 | CB | THR | 118 | 1.796 | 3.020 | 24.502 | 1.00 | 59.06 |
| | ATOM | 825 | OG1 | THR | 118 | 1.013 | 3.926 | 23.718 | 1.00 | 57.88 |
| | ATOM | 826 | CG2 | THR | 118 | 1.917 | 1.688 | 23.794 | 1.00 | 59.21 |
| | ATOM | 827 | C | THR | 118 | 1.548 | 4.038 | 26.721 | 1.00 | 58.97 |
| | ATOM | 828 | O | THR | 118 | 0.764 | 4.971 | 26.912 | 1.00 | 58.11 |
| 25 | ATOM | 829 | N | ALA | 119 | 2.782 | 4.001 | 27.218 | 1.00 | 56.72 |
| | ATOM | 830 | CA | ALA | 119 | 3.313 | 5.071 | 28.052 | 1.00 | 52.86 |
| | ATOM | 831 | CB | ALA | 119 | 4.807 | 4.938 | 28.177 | 1.00 | 51.30 |
| | ATOM | 832 | C | ALA | 119 | 2.972 | 6.399 | 27.421 | 1.00 | 51.58 |
| | ATOM | 833 | O | ALA | 119 | 2.456 | 7.301 | 28.080 | 1.00 | 52.70 |

- 173 -

| | ATOM | 834 | N | GLU | 120 | 3. 260 | 6. 502 | 26. 131 | 1. 00 | 48. 02 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 835 | CA | GLU | 120 | 2. 994 | 7. 716 | 25. 386 | 1. 00 | 46. 07 |
| | ATOM | 836 | CB | GLU | 120 | 3. 194 | 7. 471 | 23. 894 | 1. 00 | 49. 10 |
| | ATOM | 837 | CG | GLU | 120 | 4. 210 | 6. 381 | 23. 550 | 1. 00 | 52. 89 |
| 5 | ATOM | 838 | CD | GLU | 120 | 5. 630 | 6. 736 | 23. 945 | 1. 00 | 53. 64 |
| | ATOM | 839 | OE1 | GLU | 120 | 5. 962 | 6. 621 | 25. 141 | 1. 00 | 55. 30 |
| | ATOM | 840 | OE2 | GLU | 120 | 6. 411 | 7. 139 | 23. 057 | 1. 00 | 52. 83 |
| | ATOM | 841 | C | GLU | 120 | 1. 557 | 8. 140 | 25. 630 | 1. 00 | 44. 27 |
| | ATOM | 842 | O | GLU | 120 | 1. 295 | 9. 257 | 26. 070 | 1. 00 | 44. 84 |
| 10 | ATOM | 843 | N | MET | 121 | 0. 627 | 7. 235 | 25. 351 | 1. 00 | 41. 37 |
| | ATOM | 844 | CA | MET | 121 | -0. 791 | 7. 525 | 25. 513 | 1. 00 | 38. 57 |
| | ATOM | 845 | CB | MET | 121 | -1. 626 | 6. 358 | 24. 990 | 1. 00 | 41. 30 |
| | ATOM | 846 | CG | MET | 121 | -1. 721 | 6. 328 | 23. 479 | 1. 00 | 46. 24 |
| | ATOM | 847 | SD | MET | 121 | -2. 483 | 4. 835 | 22. 838 | 1. 00 | 50. 88 |
| 15 | ATOM | 848 | CE | MET | 121 | -3. 908 | 4. 669 | 23. 961 | 1. 00 | 50. 02 |
| | ATOM | 849 | C | MET | 121 | -1. 190 | 7. 820 | 26. 937 | 1. 00 | 34. 60 |
| | ATOM | 850 | O | MET | 121 | -1. 910 | 8. 780 | 27. 204 | 1. 00 | 31. 69 |
| | ATOM | 851 | N | LEU | 122 | -0. 719 | 6. 985 | 27. 852 | 1. 00 | 32. 63 |
| | ATOM | 852 | CA | LEU | 122 | -1. 051 | 7. 141 | 29. 263 | 1. 00 | 30. 24 |
| 20 | ATOM | 853 | CB | LEU | 122 | -0. 256 | 6. 140 | 30. 108 | 1. 00 | 27. 33 |
| | ATOM | 854 | CG | LEU | 122 | -0. 778 | 5. 923 | 31. 533 | 1. 00 | 21. 99 |
| | ATOM | 855 | CD1 | LEU | 122 | -0. 279 | 4. 601 | 32. 031 | 1. 00 | 22. 53 |
| | ATOM | 856 | CD2 | LEU | 122 | -0. 366 | 7. 034 | 32. 456 | 1. 00 | 17. 78 |
| | ATOM | 857 | C | LEU | 122 | -0. 759 | 8. 551 | 29. 746 | 1. 00 | 28. 67 |
| 25 | ATOM | 858 | O | LEU | 122 | -1. 619 | 9. 228 | 30. 326 | 1. 00 | 25. 21 |
| | ATOM | 859 | N | PHE | 123 | 0. 469 | 8. 987 | 29. 502 | 1. 00 | 26. 83 |
| | ATOM | 860 | CA | PHE | 123 | 0. 871 | 10. 306 | 29. 929 | 1. 00 | 25. 29 |
| | ATOM | 861 | CB | PHE | 123 | 2. 387 | 10. 398 | 29. 908 | 1. 00 | 20. 22 |
| | ATOM | 862 | CG | PHE | 123 | 3. 015 | 9. 772 | 31. 112 | 1. 00 | 15. 51 |

- 174 -

|      | ATOM | 863 | CD1 | PHE | 123 | 3.538  | 8.494  | 31.064 | 1.00 | 12.96 |
|------|------|-----|-----|-----|-----|--------|--------|--------|------|-------|
|      | ATOM | 864 | CD2 | PHE | 123 | 3.028  | 10.457 | 32.328 | 1.00 | 13.35 |
|      | ATOM | 865 | CE1 | PHE | 123 | 4.067  | 7.910  | 32.217 | 1.00 | 12.87 |
|      | ATOM | 866 | CE2 | PHE | 123 | 3.552  | 9.879  | 33.484 | 1.00 | 9.69  |
| 5    | ATOM | 867 | CZ  | PHE | 123 | 4.072  | 8.609  | 33.432 | 1.00 | 9.56  |
|      | ATOM | 868 | C   | PHE | 123 | 0.202  | 11.432 | 29.157 | 1.00 | 26.20 |
|      | ATOM | 869 | O   | PHE | 123 | -0.102 | 12.489 | 29.722 | 1.00 | 26.61 |
|      | ATOM | 870 | N   | ASP | 124 | -0.053 | 11.207 | 27.875 | 1.00 | 24.47 |
|      | ATOM | 871 | CA  | ASP | 124 | -0.750 | 12.210 | 27.090 | 1.00 | 23.14 |
| 10   | ATOM | 872 | CB  | ASP | 124 | -1.228 | 11.614 | 25.785 | 1.00 | 24.52 |
|      | ATOM | 873 | CG  | ASP | 124 | -0.178 | 11.628 | 24.747 | 1.00 | 27.01 |
|      | ATOM | 874 | OD1 | ASP | 124 | -0.376 | 10.955 | 23.715 | 1.00 | 26.39 |
|      | ATOM | 875 | OD2 | ASP | 124 | 0.839  | 12.325 | 24.968 | 1.00 | 29.23 |
|      | ATOM | 876 | C   | ASP | 124 | -1.967 | 12.650 | 27.875 | 1.00 | 21.89 |
| 15   | ATOM | 877 | O   | ASP | 124 | -2.361 | 13.815 | 27.841 | 1.00 | 20.01 |
|      | ATOM | 878 | N   | TYR | 125 | -2.562 | 11.688 | 28.574 | 1.00 | 20.84 |
|      | ATOM | 879 | CA  | TYR | 125 | -3.749 | 11.943 | 29.371 | 1.00 | 20.51 |
|      | ATOM | 880 | CB  | TYR | 125 | -4.414 | 10.619 | 29.792 | 1.00 | 20.43 |
|      | ATOM | 881 | CG  | TYR | 125 | -5.796 | 10.794 | 30.394 | 1.00 | 22.84 |
| 20   | ATOM | 882 | CD1 | TYR | 125 | -6.083 | 10.358 | 31.692 | 1.00 | 23.51 |
|      | ATOM | 883 | CE1 | TYR | 125 | -7.345 | 10.584 | 32.268 | 1.00 | 31.08 |
|      | ATOM | 884 | CD2 | TYR | 125 | -6.803 | 11.451 | 29.678 | 1.00 | 26.43 |
|      | ATOM | 885 | CE2 | TYR | 125 | -8.064 | 11.685 | 30.232 | 1.00 | 31.61 |
|      | ATOM | 886 | CZ  | TYR | 125 | -8.336 | 11.255 | 31.528 | 1.00 | 34.64 |
| 25   | ATOM | 887 | OH  | TYR | 125 | -9.585 | 11.520 | 32.073 | 1.00 | 38.10 |
|      | ATOM | 888 | C   | TYR | 125 | -3.382 | 12.752 | 30.605 | 1.00 | 19.11 |
|      | ATOM | 889 | O   | TYR | 125 | -3.904 | 13.848 | 30.824 | 1.00 | 16.08 |
|      | ATOM | 890 | N   | ILE | 126 | -2.465 | 12.212 | 31.399 | 1.00 | 17.91 |
|      | ATOM | 891 | CA  | ILE | 126 | -2.049 | 12.879 | 32.615 | 1.00 | 17.82 |

- 175 -

| | ATOM | 892 | CB | ILE | 126 | -0.819 | 12.236 | 33.203 | 1.00 | 19.82 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 893 | CG2 | ILE | 126 | -0.489 | 12.905 | 34.538 | 1.00 | 18.77 |
| | ATOM | 894 | CG1 | ILE | 126 | -1.055 | 10.732 | 33.331 | 1.00 | 21.27 |
| | ATOM | 895 | CD1 | ILE | 126 | 0.045 | 9.984 | 34.062 | 1.00 | 23.92 |
| 5 | ATOM | 896 | C | ILE | 126 | -1.717 | 14.313 | 32.325 | 1.00 | 18.09 |
| | ATOM | 897 | O | ILE | 126 | -1.991 | 15.205 | 33.123 | 1.00 | 16.68 |
| | ATOM | 898 | N | SER | 127 | -1.108 | 14.532 | 31.172 | 1.00 | 19.12 |
| | ATOM | 899 | CA | SER | 127 | -0.747 | 15.877 | 30.789 | 1.00 | 20.96 |
| | ATOM | 900 | CB | SER | 127 | -0.057 | 15.857 | 29.432 | 1.00 | 19.89 |
| 10 | ATOM | 901 | OG | SER | 127 | 0.569 | 17.100 | 29.190 | 1.00 | 22.20 |
| | ATOM | 902 | C | SER | 127 | -2.011 | 16.742 | 30.746 | 1.00 | 21.92 |
| | ATOM | 903 | O | SER | 127 | -2.177 | 17.658 | 31.551 | 1.00 | 20.25 |
| | ATOM | 904 | N | GLU | 128 | -2.902 | 16.431 | 29.813 | 1.00 | 23.87 |
| | ATOM | 905 | CA | GLU | 128 | -4.152 | 17.161 | 29.670 | 1.00 | 26.98 |
| 15 | ATOM | 906 | CB | GLU | 128 | -5.111 | 16.353 | 28.802 | 1.00 | 33.10 |
| | ATOM | 907 | CG | GLU | 128 | -6.471 | 16.990 | 28.544 | 1.00 | 39.51 |
| | ATOM | 908 | CD | GLU | 128 | -7.280 | 16.175 | 27.544 | 1.00 | 44.52 |
| | ATOM | 909 | OE1 | GLU | 128 | -7.211 | 16.481 | 26.327 | 1.00 | 46.11 |
| | ATOM | 910 | OE2 | GLU | 128 | -7.963 | 15.218 | 27.980 | 1.00 | 43.93 |
| 20 | ATOM | 911 | C | GLU | 128 | -4.797 | 17.431 | 31.020 | 1.00 | 26.55 |
| | ATOM | 912 | O | GLU | 128 | -5.177 | 18.561 | 31.334 | 1.00 | 26.16 |
| | ATOM | 913 | N | CYS | 129 | -4.929 | 16.384 | 31.820 | 1.00 | 26.36 |
| | ATOM | 914 | CA | CYS | 129 | -5.532 | 16.535 | 33.130 | 1.00 | 26.47 |
| | ATOM | 915 | CB | CYS | 129 | -5.452 | 15.219 | 33.893 | 1.00 | 28.39 |
| 25 | ATOM | 916 | SG | CYS | 129 | -6.450 | 13.922 | 33.126 | 1.00 | 37.58 |
| | ATOM | 917 | C | CYS | 129 | -4.853 | 17.636 | 33.914 | 1.00 | 25.00 |
| | ATOM | 918 | O | CYS | 129 | -5.515 | 18.561 | 34.372 | 1.00 | 24.97 |
| | ATOM | 919 | N | ILE | 130 | -3.532 | 17.536 | 34.059 | 1.00 | 24.74 |
| | ATOM | 920 | CA | ILE | 130 | -2.763 | 18.536 | 34.793 | 1.00 | 21.55 |

- 176 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 921 | CB | ILE | 130 | -1.245 | 18.255 | 34.709 | 1.00 17.55 |
| | ATOM | 922 | CG2 | ILE | 130 | -0.458 | 19.404 | 35.304 | 1.00 15.00 |
| | ATOM | 923 | CG1 | ILE | 130 | -0.915 | 16.984 | 35.490 | 1.00 16.42 |
| | ATOM | 924 | CD1 | ILE | 130 | 0.574 | 16.713 | 35.623 | 1.00 18.34 |
| 5 | ATOM | 925 | C | ILE | 130 | -3.070 | 19.910 | 34.219 | 1.00 23.54 |
| | ATOM | 926 | O | ILE | 130 | -3.572 | 20.780 | 34.926 | 1.00 21.27 |
| | ATOM | 927 | N | SER | 131 | -2.785 | 20.091 | 32.933 | 1.00 26.25 |
| | ATOM | 928 | CA | SER | 131 | -3.048 | 21.353 | 32.270 | 1.00 28.50 |
| | ATOM | 929 | CB | SER | 131 | -3.011 | 21.186 | 30.764 | 1.00 28.76 |
| 10 | ATOM | 930 | OG | SER | 131 | -3.856 | 22.154 | 30.164 | 1.00 32.87 |
| | ATOM | 931 | C | SER | 131 | -4.417 | 21.851 | 32.661 | 1.00 31.48 |
| | ATOM | 932 | O | SER | 131 | -4.586 | 23.002 | 33.057 | 1.00 33.67 |
| | ATOM | 933 | N | ASP | 132 | -5.411 | 20.986 | 32.546 | 1.00 34.56 |
| | ATOM | 934 | CA | ASP | 132 | -6.753 | 21.397 | 32.908 | 1.00 39.04 |
| 15 | ATOM | 935 | CB | ASP | 132 | -7.735 | 20.248 | 32.694 | 1.00 44.84 |
| | ATOM | 936 | CG | ASP | 132 | -9.165 | 20.650 | 32.987 | 1.00 50.51 |
| | ATOM | 937 | OD1 | ASP | 132 | -9.764 | 21.347 | 32.131 | 1.00 53.56 |
| | ATOM | 938 | OD2 | ASP | 132 | -9.674 | 20.283 | 34.078 | 1.00 52.37 |
| | ATOM | 939 | C | ASP | 132 | -6.790 | 21.843 | 34.376 | 1.00 38.23 |
| 20 | ATOM | 940 | O | ASP | 132 | -7.160 | 22.982 | 34.677 | 1.00 36.81 |
| | ATOM | 941 | N | PHE | 133 | -6.394 | 20.932 | 35.270 | 1.00 36.88 |
| | ATOM | 942 | CA | PHE | 133 | -6.372 | 21.170 | 36.713 | 1.00 34.85 |
| | ATOM | 943 | CB | PHE | 133 | -5.604 | 20.060 | 37.433 | 1.00 33.59 |
| | ATOM | 944 | CG | PHE | 133 | -5.343 | 20.362 | 38.878 | 1.00 34.77 |
| 25 | ATOM | 945 | CD1 | PHE | 133 | -6.396 | 20.547 | 39.760 | 1.00 35.58 |
| | ATOM | 946 | CD2 | PHE | 133 | -4.043 | 20.523 | 39.348 | 1.00 37.81 |
| | ATOM | 947 | CE1 | PHE | 133 | -6.159 | 20.896 | 41.091 | 1.00 37.66 |
| | ATOM | 948 | CE2 | PHE | 133 | -3.792 | 20.872 | 40.678 | 1.00 38.00 |
| | ATOM | 949 | CZ | PHE | 133 | -4.850 | 21.059 | 41.548 | 1.00 38.85 |

- 177 -

| | ATOM | 950 | C | PHE | 133 | -5.755 | 22.503 | 37.094 | 1.00 | 34.28 |
|---|------|-----|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 951 | O | PHE | 133 | -6.274 | 23.226 | 37.947 | 1.00 | 33.97 |
| | ATOM | 952 | N | LEU | 134 | -4.622 | 22.813 | 36.482 | 1.00 | 33.97 |
| | ATOM | 953 | CA | LEU | 134 | -3.958 | 24.070 | 36.766 | 1.00 | 31.79 |
| 5 | ATOM | 954 | CB | LEU | 134 | -2.590 | 24.109 | 36.089 | 1.00 | 24.12 |
| | ATOM | 955 | CG | LEU | 134 | -1.618 | 23.026 | 36.545 | 1.00 | 16.64 |
| | ATOM | 956 | CD1 | LEU | 134 | -0.368 | 23.101 | 35.705 | 1.00 | 15.98 |
| | ATOM | 957 | CD2 | LEU | 134 | -1.305 | 23.184 | 38.014 | 1.00 | 10.77 |
| | ATOM | 958 | C | LEU | 134 | -4.855 | 25.176 | 36.234 | 1.00 | 34.44 |
| 10 | ATOM | 959 | O | LEU | 134 | -5.111 | 26.163 | 36.920 | 1.00 | 34.41 |
| | ATOM | 960 | N | ASP | 135 | -5.365 | 24.999 | 35.022 | 1.00 | 37.26 |
| | ATOM | 961 | CA | ASP | 135 | -6.230 | 26.014 | 34.454 | 1.00 | 42.65 |
| | ATOM | 962 | CB | ASP | 135 | -6.815 | 25.565 | 33.121 | 1.00 | 46.76 |
| | ATOM | 963 | CG | ASP | 135 | -7.707 | 26.629 | 32.509 | 1.00 | 52.18 |
| 15 | ATOM | 964 | OD1 | ASP | 135 | -8.659 | 26.271 | 31.772 | 1.00 | 53.75 |
| | ATOM | 965 | OD2 | ASP | 135 | -7.443 | 27.829 | 32.772 | 1.00 | 52.70 |
| | ATOM | 966 | C | ASP | 135 | -7.386 | 26.381 | 35.383 | 1.00 | 43.96 |
| | ATOM | 967 | O | ASP | 135 | -7.643 | 27.563 | 35.619 | 1.00 | 44.98 |
| | ATOM | 968 | N | LYS | 136 | -8.084 | 25.368 | 35.894 | 1.00 | 44.30 |
| 20 | ATOM | 969 | CA | LYS | 136 | -9.225 | 25.578 | 36.780 | 1.00 | 44.56 |
| | ATOM | 970 | CB | LYS | 136 | -9.889 | 24.237 | 37.124 | 1.00 | 46.76 |
| | ATOM | 971 | CG | LYS | 136 | -11.195 | 24.350 | 37.941 | 1.00 | 52.67 |
| | ATOM | 972 | CD | LYS | 136 | -11.910 | 22.981 | 38.128 | 1.00 | 55.98 |
| | ATOM | 973 | CE | LYS | 136 | -13.367 | 23.120 | 38.628 | 1.00 | 55.25 |
| 25 | ATOM | 974 | NZ | LYS | 136 | -14.106 | 21.817 | 38.719 | 1.00 | 51.28 |
| | ATOM | 975 | C | LYS | 136 | -8.862 | 26.306 | 38.069 | 1.00 | 44.85 |
| | ATOM | 976 | O | LYS | 136 | -9.730 | 26.894 | 38.717 | 1.00 | 45.87 |
| | ATOM | 977 | N | HIS | 137 | -7.586 | 26.273 | 38.444 | 1.00 | 44.25 |
| | ATOM | 978 | CA | HIS | 137 | -7.149 | 26.937 | 39.670 | 1.00 | 43.21 |

- 178 -

|  | ATOM | 979 | CB | HIS 137 | -6.434 | 25.937 | 40.585 | 1.00 44.13 |
|---|------|-----|------|---------|--------|--------|--------|-----------|
|  | ATOM | 980 | CG | HIS 137 | -7.344 | 24.915 | 41.199 | 1.00 45.24 |
|  | ATOM | 981 | CD2 | HIS 137 | -7.676 | 24.680 | 42.492 | 1.00 45.35 |
|  | ATOM | 982 | ND1 | HIS 137 | -8.042 | 23.991 | 40.452 | 1.00 45.45 |
| 5 | ATOM | 983 | CE1 | HIS 137 | -8.764 | 23.231 | 41.257 | 1.00 45.40 |
|  | ATOM | 984 | NE2 | HIS 137 | -8.560 | 23.629 | 42.500 | 1.00 44.34 |
|  | ATOM | 985 | C | HIS 137 | -6.242 | 28.132 | 39.400 | 1.00 41.96 |
|  | ATOM | 986 | O | HIS 137 | -5.592 | 28.649 | 40.307 | 1.00 40.24 |
|  | ATOM | 987 | N | GLN 138 | -6.217 | 28.577 | 38.151 | 1.00 42.87 |
| 10 | ATOM | 988 | CA | GLN 138 | -5.390 | 29.706 | 37.766 | 1.00 44.93 |
|  | ATOM | 989 | CB | GLN 138 | -5.949 | 30.993 | 38.373 | 1.00 47.58 |
|  | ATOM | 990 | CG | GLN 138 | -7.258 | 31.448 | 37.749 | 1.00 51.96 |
|  | ATOM | 991 | CD | GLN 138 | -7.416 | 32.966 | 37.766 | 1.00 55.20 |
|  | ATOM | 992 | OE1 | GLN 138 | -6.680 | 33.698 | 37.088 | 1.00 56.05 |
| 15 | ATOM | 993 | NE2 | GLN 138 | -8.375 | 33.445 | 38.546 | 1.00 55.44 |
|  | ATOM | 994 | C | GLN 138 | -3.921 | 29.537 | 38.162 | 1.00 44.67 |
|  | ATOM | 995 | O | GLN 138 | -3.316 | 30.437 | 38.747 | 1.00 45.78 |
|  | ATOM | 996 | N | MET 139 | -3.350 | 28.383 | 37.836 | 1.00 41.86 |
|  | ATOM | 997 | CA | MET 139 | -1.951 | 28.109 | 38.138 | 1.00 38.60 |
| 20 | ATOM | 998 | CB | MET 139 | -1.846 | 27.062 | 39.236 | 1.00 39.19 |
|  | ATOM | 999 | CG | MET 139 | -2.048 | 27.660 | 40.604 | 1.00 41.24 |
|  | ATOM | 1000 | SD | MET 139 | -0.859 | 28.992 | 40.852 | 1.00 47.65 |
|  | ATOM | 1001 | CE | MET 139 | 0.308 | 28.217 | 42.007 | 1.00 44.32 |
|  | ATOM | 1002 | C | MET 139 | -1.232 | 27.653 | 36.881 | 1.00 36.60 |
| 25 | ATOM | 1003 | O | MET 139 | -0.316 | 26.823 | 36.910 | 1.00 35.29 |
|  | ATOM | 1004 | N | LYS 140 | -1.659 | 28.237 | 35.771 | 1.00 34.23 |
|  | ATOM | 1005 | CA | LYS 140 | -1.101 | 27.921 | 34.477 | 1.00 32.15 |
|  | ATOM | 1006 | CB | LYS 140 | -2.198 | 28.062 | 33.417 | 1.00 31.04 |
|  | ATOM | 1007 | CG | LYS 140 | -1.970 | 27.293 | 32.116 | 1.00 31.48 |

- 179 -

|   | ATOM | 1008 | CD  | LYS 140 | -2.184 | 25.780 | 32.275 | 1.00 | 32.43 |
|---|------|------|-----|---------|--------|--------|--------|------|-------|
|   | ATOM | 1009 | CE  | LYS 140 | -2.112 | 25.015 | 30.925 | 1.00 | 30.89 |
|   | ATOM | 1010 | NZ  | LYS 140 | -0.811 | 25.130 | 30.168 | 1.00 | 29.56 |
|   | ATOM | 1011 | C   | LYS 140 | 0.085 | 28.834 | 34.161 | 1.00 | 31.02 |
| 5 | ATOM | 1012 | O   | LYS 140 | 0.047 | 30.045 | 34.412 | 1.00 | 29.99 |
|   | ATOM | 1013 | N   | HIS 141 | 1.143 | 28.228 | 33.627 | 1.00 | 31.35 |
|   | ATOM | 1014 | CA  | HIS 141 | 2.353 | 28.940 | 33.244 | 1.00 | 30.03 |
|   | ATOM | 1015 | CB  | HIS 141 | 1.989 | 30.145 | 32.385 | 1.00 | 30.05 |
|   | ATOM | 1016 | CG  | HIS 141 | 1.001 | 29.836 | 31.305 | 1.00 | 31.15 |
| 10 | ATOM | 1017 | CD2 | HIS 141 | -0.132 | 30.473 | 30.927 | 1.00 | 30.91 |
|   | ATOM | 1018 | ND1 | HIS 141 | 1.148 | 28.769 | 30.448 | 1.00 | 33.49 |
|   | ATOM | 1019 | CE1 | HIS 141 | 0.147 | 28.763 | 29.584 | 1.00 | 35.03 |
|   | ATOM | 1020 | NE2 | HIS 141 | -0.643 | 29.787 | 29.853 | 1.00 | 32.67 |
|   | ATOM | 1021 | C   | HIS 141 | 3.138 | 29.396 | 34.460 | 1.00 | 29.17 |
| 15 | ATOM | 1022 | O   | HIS 141 | 4.211 | 29.983 | 34.341 | 1.00 | 28.17 |
|   | ATOM | 1023 | N   | LYS 142 | 2.601 | 29.108 | 35.635 | 1.00 | 28.81 |
|   | ATOM | 1024 | CA  | LYS 142 | 3.248 | 29.505 | 36.869 | 1.00 | 29.17 |
|   | ATOM | 1025 | CB  | LYS 142 | 2.317 | 29.240 | 38.065 | 1.00 | 33.65 |
|   | ATOM | 1026 | CG  | LYS 142 | 0.986 | 30.042 | 38.072 | 1.00 | 39.35 |
| 20 | ATOM | 1027 | CD  | LYS 142 | 1.194 | 31.561 | 38.214 | 1.00 | 42.74 |
|   | ATOM | 1028 | CE  | LYS 142 | -0.122 | 32.360 | 38.170 | 1.00 | 45.49 |
|   | ATOM | 1029 | NZ  | LYS 142 | 0.110 | 33.844 | 38.325 | 1.00 | 46.19 |
|   | ATOM | 1030 | C   | LYS 142 | 4.575 | 28.785 | 37.075 | 1.00 | 26.49 |
|   | ATOM | 1031 | O   | LYS 142 | 5.340 | 29.138 | 37.966 | 1.00 | 26.10 |
| 25 | ATOM | 1032 | N   | LYS 143 | 4.862 | 27.784 | 36.254 | 1.00 | 24.58 |
|   | ATOM | 1033 | CA  | LYS 143 | 6.106 | 27.042 | 36.416 | 1.00 | 22.67 |
|   | ATOM | 1034 | CB  | LYS 143 | 7.258 | 27.847 | 35.836 | 1.00 | 21.51 |
|   | ATOM | 1035 | CG  | LYS 143 | 8.533 | 27.071 | 35.737 | 1.00 | 22.59 |
|   | ATOM | 1036 | CD  | LYS 143 | 9.319 | 27.510 | 34.516 | 1.00 | 25.81 |

- 180 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1037 | CE | LYS 143 | 10.455 | 26.542 | 34.240 | 1.00 | 28.01 |
| | ATOM | 1038 | NZ | LYS 143 | 11.140 | 26.828 | 32.959 | 1.00 | 27.25 |
| | ATOM | 1039 | C | LYS 143 | 6.383 | 26.732 | 37.896 | 1.00 | 22.14 |
| | ATOM | 1040 | 0 | LYS 143 | 7.133 | 27.459 | 38.556 | 1.00 | 21.99 |
| 5 | ATOM | 1041 | N | LEU 144 | 5.766 | 25.655 | 38.401 | 1.00 | 20.81 |
| | ATOM | 1042 | CA | LEU 144 | 5.910 | 25.214 | 39.797 | 1.00 | 16.90 |
| | ATOM | 1043 | CB | LEU 144 | 4.577 | 25.351 | 40.567 | 1.00 | 16.78 |
| | ATOM | 1044 | CG | LEU 144 | 3.208 | 24.956 | 39.983 | 1.00 | 18.43 |
| | ATOM | 1045 | CD1 | LEU 144 | 2.148 | 24.915 | 41.074 | 1.00 | 17.60 |
| 10 | ATOM | 1046 | CD2 | LEU 144 | 2.795 | 25.960 | 38.929 | 1.00 | 19.20 |
| | ATOM | 1047 | C | LEU 144 | 6.432 | 23.781 | 39.933 | 1.00 | 15.80 |
| | ATOM | 1048 | 0 | LEU 144 | 6.265 | 22.958 | 39.032 | 1.00 | 12.24 |
| | ATOM | 1049 | N | PRO 145 | 7.078 | 23.478 | 41.076 | 1.00 | 16.26 |
| | ATOM | 1050 | CD | PRO 145 | 7.227 | 24.446 | 42.172 | 1.00 | 15.64 |
| 15 | ATOM | 1051 | CA | PRO 145 | 7.678 | 22.196 | 41.467 | 1.00 | 14.17 |
| | ATOM | 1052 | CB | PRO 145 | 8.079 | 22.427 | 42.923 | 1.00 | 18.10 |
| | ATOM | 1053 | CG | PRO 145 | 8.378 | 23.860 | 42.963 | 1.00 | 17.14 |
| | ATOM | 1054 | C | PRO 145 | 6.707 | 21.050 | 41.357 | 1.00 | 12.75 |
| | ATOM | 1055 | 0 | PRO 145 | 5.580 | 21.141 | 41.852 | 1.00 | 12.27 |
| 20 | ATOM | 1056 | N | LEU 146 | 7.160 | 19.957 | 40.758 | 1.00 | 10.29 |
| | ATOM | 1057 | CA | LEU 146 | 6.290 | 18.804 | 40.560 | 1.00 | 11.21 |
| | ATOM | 1058 | CB | LEU 146 | 6.156 | 18.539 | 39.075 | 1.00 | 7.24 |
| | ATOM | 1059 | CG | LEU 146 | 5.160 | 17.439 | 38.824 | 1.00 | 3.01 |
| | ATOM | 1060 | CD1 | LEU 146 | 3.817 | 17.832 | 39.389 | 1.00 | 1.00 |
| 25 | ATOM | 1061 | CD2 | LEU 146 | 5.083 | 17.215 | 37.342 | 1.00 | 3.06 |
| | ATOM | 1062 | C | LEU 146 | 6.696 | 17.502 | 41.233 | 1.00 | 12.36 |
| | ATOM | 1063 | 0 | LEU 146 | 7.629 | 16.851 | 40.790 | 1.00 | 15.11 |
| | ATOM | 1064 | N | GLY 147 | 5.972 | 17.086 | 42.262 | 1.00 | 14.72 |
| | ATOM | 1065 | CA | GLY 147 | 6.333 | 15.851 | 42.937 | 1.00 | 17.81 |

- 181 -

|   | ATOM | 1066 | C   | GLY 147 | 5.716 | 14.586 | 42.371 | 1.00 | 18.51 |
|---|------|------|-----|---------|-------|--------|--------|------|-------|
|   | ATOM | 1067 | O   | GLY 147 | 4.689 | 14.644 | 41.704 | 1.00 | 20.85 |
|   | ATOM | 1068 | N   | PHE 148 | 6.342 | 13.440 | 42.631 | 1.00 | 19.28 |
|   | ATOM | 1069 | CA  | PHE 148 | 5.825 | 12.167 | 42.142 | 1.00 | 20.55 |
| 5 | ATOM | 1070 | CB  | PHE 148 | 6.707 | 11.635 | 41.023 | 1.00 | 16.36 |
|   | ATOM | 1071 | CG  | PHE 148 | 6.593 | 12.409 | 39.759 | 1.00 | 17.72 |
|   | ATOM | 1072 | CD1 | PHE 148 | 6.792 | 13.779 | 39.753 | 1.00 | 17.99 |
|   | ATOM | 1073 | CD2 | PHE 148 | 6.298 | 11.769 | 38.560 | 1.00 | 21.10 |
|   | ATOM | 1074 | CE1 | PHE 148 | 6.695 | 14.509 | 38.570 | 1.00 | 22.37 |
| 10 | ATOM | 1075 | CE2 | PHE 148 | 6.198 | 12.494 | 37.362 | 1.00 | 22.82 |
|   | ATOM | 1076 | CZ  | PHE 148 | 6.398 | 13.864 | 37.366 | 1.00 | 21.67 |
|   | ATOM | 1077 | C   | PHE 148 | 5.712 | 11.104 | 43.222 | 1.00 | 22.75 |
|   | ATOM | 1078 | O   | PHE 148 | 6.691 | 10.783 | 43.885 | 1.00 | 24.66 |
|   | ATOM | 1079 | N   | THR 149 | 4.513 | 10.562 | 43.403 | 1.00 | 24.45 |
| 15 | ATOM | 1080 | CA  | THR 149 | 4.312 | 9.514 | 44.387 | 1.00 | 24.75 |
|   | ATOM | 1081 | CB  | THR 149 | 3.365 | 9.917 | 45.497 | 1.00 | 23.76 |
|   | ATOM | 1082 | OG1 | THR 149 | 2.757 | 11.175 | 45.192 | 1.00 | 25.51 |
|   | ATOM | 1083 | CG2 | THR 149 | 4.107 | 9.989 | 46.786 | 1.00 | 22.63 |
|   | ATOM | 1084 | C   | THR 149 | 3.705 | 8.306 | 43.715 | 1.00 | 27.38 |
| 20 | ATOM | 1085 | O   | THR 149 | 3.093 | 8.405 | 42.647 | 1.00 | 24.58 |
|   | ATOM | 1086 | N   | PHE 150 | 3.857 | 7.160 | 44.361 | 1.00 | 30.07 |
|   | ATOM | 1087 | CA  | PHE 150 | 3.327 | 5.936 | 43.811 | 1.00 | 32.54 |
|   | ATOM | 1088 | CB  | PHE 150 | 4.455 | 5.120 | 43.215 | 1.00 | 29.97 |
|   | ATOM | 1089 | CG  | PHE 150 | 5.172 | 5.820 | 42.119 | 1.00 | 27.55 |
| 25 | ATOM | 1090 | CD1 | PHE 150 | 6.134 | 6.770 | 42.397 | 1.00 | 27.41 |
|   | ATOM | 1091 | CD2 | PHE 150 | 4.850 | 5.561 | 40.798 | 1.00 | 27.56 |
|   | ATOM | 1092 | CE1 | PHE 150 | 6.770 | 7.447 | 41.366 | 1.00 | 28.61 |
|   | ATOM | 1093 | CE2 | PHE 150 | 5.481 | 6.231 | 39.762 | 1.00 | 26.86 |
|   | ATOM | 1094 | CZ  | PHE 150 | 6.437 | 7.177 | 40.045 | 1.00 | 27.37 |

- 182 -

| | ATOM | 1095 | C | PHE | 150 | 2.561 | 5.093 | 44.808 | 1.00 | 35.78 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1096 | O | PHE | 150 | 3.095 | 4.695 | 45.845 | 1.00 | 36.93 |
| | ATOM | 1097 | N | SER | 151 | 1.305 | 4.813 | 44.467 | 1.00 | 38.60 |
| | ATOM | 1098 | CA | SER | 151 | 0.420 | 4.006 | 45.295 | 1.00 | 40.51 |
| 5 | ATOM | 1099 | CB | SER | 151 | -0.830 | 4.802 | 45.641 | 1.00 | 41.51 |
| | ATOM | 1100 | OG | SER | 151 | -1.507 | 5.159 | 44.453 | 1.00 | 47.40 |
| | ATOM | 1101 | C | SER | 151 | 0.038 | 2.736 | 44.533 | 1.00 | 41.75 |
| | ATOM | 1102 | O | SER | 151 | 0.069 | 2.696 | 43.301 | 1.00 | 40.78 |
| | ATOM | 1103 | N | PHE | 152 | -0.336 | 1.704 | 45.278 | 1.00 | 43.86 |
| 10 | ATOM | 1104 | CA | PHE | 152 | -0.684 | 0.421 | 44.687 | 1.00 | 45.76 |
| | ATOM | 1105 | CB | PHE | 152 | 0.465 | -0.557 | 44.965 | 1.00 | 51.67 |
| | ATOM | 1106 | CG | PHE | 152 | 0.429 | -1.808 | 44.133 | 1.00 | 57.82 |
| | ATOM | 1107 | CD1 | PHE | 152 | 0.597 | -1.749 | 42.751 | 1.00 | 59.39 |
| | ATOM | 1108 | CD2 | PHE | 152 | 0.256 | -3.056 | 44.739 | 1.00 | 60.37 |
| 15 | ATOM | 1109 | CE1 | PHE | 152 | 0.598 | -2.915 | 41.979 | 1.00 | 61.23 |
| | ATOM | 1110 | CE2 | PHE | 152 | 0.254 | -4.232 | 43.978 | 1.00 | 61.76 |
| | ATOM | 1111 | CZ | PHE | 152 | 0.426 | -4.161 | 42.593 | 1.00 | 61.46 |
| | ATOM | 1112 | C | PHE | 152 | -2.007 | -0.134 | 45.238 | 1.00 | 43.74 |
| | ATOM | 1113 | O | PHE | 152 | -2.137 | -0.382 | 46.437 | 1.00 | 43.01 |
| 20 | ATOM | 1114 | N | PRO | 153 | -3.005 | -0.322 | 44.359 | 1.00 | 40.65 |
| | ATOM | 1115 | CD | PRO | 153 | -2.993 | 0.179 | 42.979 | 1.00 | 39.35 |
| | ATOM | 1116 | CA | PRO | 153 | -4.330 | -0.844 | 44.685 | 1.00 | 38.88 |
| | ATOM | 1117 | CB | PRO | 153 | -5.045 | -0.803 | 43.352 | 1.00 | 36.16 |
| | ATOM | 1118 | CG | PRO | 153 | -4.454 | 0.359 | 42.711 | 1.00 | 37.38 |
| 25 | ATOM | 1119 | C | PRO | 153 | -4.235 | -2.255 | 45.192 | 1.00 | 41.30 |
| | ATOM | 1120 | O | PRO | 153 | -3.481 | -3.057 | 44.657 | 1.00 | 42.17 |
| | ATOM | 1121 | N | VAL | 154 | -5.013 | -2.565 | 46.215 | 1.00 | 45.30 |
| | ATOM | 1122 | CA | VAL | 154 | -5.016 | -3.905 | 46.767 | 1.00 | 49.50 |
| | ATOM | 1123 | CB | VAL | 154 | -4.124 | -3.989 | 47.990 | 1.00 | 45.75 |

- 183 -

|      | ATOM | 1124 | CG1 | VAL | 154 | -4.297  | -5.331 | 48.638 | 1.00 | 45.79 |
|------|------|------|-----|-----|-----|---------|--------|--------|------|-------|
|      | ATOM | 1125 | CG2 | VAL | 154 | -2.684  | -3.772 | 47.594 | 1.00 | 44.88 |
|      | ATOM | 1126 | C   | VAL | 154 | -6.432  | -4.268 | 47.181 | 1.00 | 55.51 |
|      | ATOM | 1127 | O   | VAL | 154 | -6.963  | -3.683 | 48.119 | 1.00 | 58.30 |
| 5    | ATOM | 1128 | N   | ARG | 155 | -7.042  | -5.232 | 46.495 | 1.00 | 61.06 |
|      | ATOM | 1129 | CA  | ARG | 155 | -8.413  | -5.643 | 46.812 | 1.00 | 67.71 |
|      | ATOM | 1130 | CB  | ARG | 155 | -8.812  | -6.847 | 45.956 | 1.00 | 71.43 |
|      | ATOM | 1131 | CG  | ARG | 155 | -9.033  | -6.501 | 44.501 | 1.00 | 76.11 |
|      | ATOM | 1132 | CD  | ARG | 155 | -9.094  | -7.736 | 43.621 | 1.00 | 78.73 |
| 10   | ATOM | 1133 | NE  | ARG | 155 | -9.292  | -7.352 | 42.226 | 1.00 | 81.59 |
|      | ATOM | 1134 | CZ  | ARG | 155 | -9.138  | -8.168 | 41.190 | 1.00 | 82.83 |
|      | ATOM | 1135 | NH1 | ARG | 155 | -8.778  | -9.432 | 41.386 | 1.00 | 83.55 |
|      | ATOM | 1136 | NH2 | ARG | 155 | -9.340  | -7.717 | 39.956 | 1.00 | 82.01 |
|      | ATOM | 1137 | C   | ARG | 155 | -8.639  | -5.965 | 48.291 | 1.00 | 70.15 |
| 15   | ATOM | 1138 | O   | ARG | 155 | -7.689  | -6.255 | 49.022 | 1.00 | 71.24 |
|      | ATOM | 1139 | N   | HIS | 156 | -9.903  | -5.923 | 48.720 | 1.00 | 71.23 |
|      | ATOM | 1140 | CA  | HIS | 156 | -10.265 | -6.184 | 50.117 | 1.00 | 72.30 |
|      | ATOM | 1141 | CB  | HIS | 156 | -11.724 | -5.769 | 50.365 | 1.00 | 73.82 |
|      | ATOM | 1142 | CG  | HIS | 156 | -12.049 | -5.506 | 51.808 | 1.00 | 76.32 |
| 20   | ATOM | 1143 | CD2 | HIS | 156 | -11.335 | -5.722 | 52.941 | 1.00 | 76.70 |
|      | ATOM | 1144 | ND1 | HIS | 156 | -13.243 | -4.944 | 52.211 | 1.00 | 76.54 |
|      | ATOM | 1145 | CE1 | HIS | 156 | -13.251 | -4.823 | 53.527 | 1.00 | 76.16 |
|      | ATOM | 1146 | NE2 | HIS | 156 | -12.106 | -5.288 | 53.994 | 1.00 | 77.55 |
|      | ATOM | 1147 | C   | HIS | 156 | -10.063 | -7.645 | 50.522 | 1.00 | 72.42 |
| 25   | ATOM | 1148 | O   | HIS | 156 | -9.196  | -7.957 | 51.345 | 1.00 | 71.15 |
|      | ATOM | 1149 | N   | ASN | 180 | 11.816  | 6.551  | 32.482 | 1.00 | 43.22 |
|      | ATOM | 1150 | CA  | ASN | 180 | 11.492  | 7.278  | 33.706 | 1.00 | 42.73 |
|      | ATOM | 1151 | CB  | ASN | 180 | 12.677  | 8.168  | 34.155 | 1.00 | 46.67 |
|      | ATOM | 1152 | CG  | ASN | 180 | 13.189  | 9.094  | 33.052 | 1.00 | 50.13 |

- 184 -

|    | ATOM | 1153 | OD1 | ASN | 180 | 14.152 | 8.777 | 32.336 | 1.00 | 51.24 |
|----|------|------|-----|-----|-----|--------|-------|--------|------|-------|
|    | ATOM | 1154 | ND2 | ASN | 180 | 12.547 | 10.250 | 32.915 | 1.00 | 51.73 |
|    | ATOM | 1155 | C   | ASN | 180 | 10.228 | 8.110 | 33.523 | 1.00 | 38.44 |
|    | ATOM | 1156 | O   | ASN | 180 | 9.941  | 8.600 | 32.431 | 1.00 | 36.40 |
| 5  | ATOM | 1157 | N   | VAL | 181 | 9.473  | 8.257 | 34.603 | 1.00 | 34.02 |
|    | ATOM | 1158 | CA  | VAL | 181 | 8.218  | 8.995 | 34.577 | 1.00 | 31.37 |
|    | ATOM | 1159 | CB  | VAL | 181 | 7.498  | 8.874 | 35.957 | 1.00 | 34.84 |
|    | ATOM | 1160 | CG1 | VAL | 181 | 6.091  | 9.484 | 35.909 | 1.00 | 32.59 |
|    | ATOM | 1161 | CG2 | VAL | 181 | 7.414  | 7.405 | 36.353 | 1.00 | 38.00 |
| 10 | ATOM | 1162 | C   | VAL | 181 | 8.426  | 10.458 | 34.221 | 1.00 | 26.36 |
|    | ATOM | 1163 | O   | VAL | 181 | 7.882  | 10.964 | 33.237 | 1.00 | 23.28 |
|    | ATOM | 1164 | N   | VAL | 182 | 9.228  | 11.131 | 35.030 | 1.00 | 23.56 |
|    | ATOM | 1165 | CA  | VAL | 182 | 9.518  | 12.538 | 34.826 | 1.00 | 18.23 |
|    | ATOM | 1166 | CB  | VAL | 182 | 10.702 | 12.958 | 35.716 | 1.00 | 14.26 |
| 15 | ATOM | 1167 | CG1 | VAL | 182 | 11.905 | 12.084 | 35.426 | 1.00 | 14.73 |
|    | ATOM | 1168 | CG2 | VAL | 182 | 11.001 | 14.403 | 35.508 | 1.00 | 11.08 |
|    | ATOM | 1169 | C   | VAL | 182 | 9.773  | 12.882 | 33.352 | 1.00 | 15.36 |
|    | ATOM | 1170 | O   | VAL | 182 | 9.330  | 13.924 | 32.875 | 1.00 | 15.32 |
|    | ATOM | 1171 | N   | GLY | 183 | 10.467 | 12.009 | 32.632 | 1.00 | 13.34 |
| 20 | ATOM | 1172 | CA  | GLY | 183 | 10.713 | 12.267 | 31.228 | 1.00 | 12.56 |
|    | ATOM | 1173 | C   | GLY | 183 | 9.458  | 12.098 | 30.382 | 1.00 | 13.06 |
|    | ATOM | 1174 | O   | GLY | 183 | 9.104  | 12.978 | 29.601 | 1.00 | 12.05 |
|    | ATOM | 1175 | N   | LEU | 184 | 8.772  | 10.971 | 30.540 | 1.00 | 15.78 |
|    | ATOM | 1176 | CA  | LEU | 184 | 7.549  | 10.708 | 29.777 | 1.00 | 15.21 |
| 25 | ATOM | 1177 | CB  | LEU | 184 | 6.858  | 9.435 | 30.295 | 1.00 | 16.78 |
|    | ATOM | 1178 | CG  | LEU | 184 | 7.613  | 8.108 | 30.075 | 1.00 | 15.45 |
|    | ATOM | 1179 | CD1 | LEU | 184 | 7.037  | 7.023 | 30.951 | 1.00 | 10.71 |
|    | ATOM | 1180 | CD2 | LEU | 184 | 7.548  | 7.708 | 28.608 | 1.00 | 16.62 |
|    | ATOM | 1181 | C   | LEU | 184 | 6.601  | 11.894 | 29.863 | 1.00 | 13.07 |

- 185 -

| | ATOM | 1182 | O | LEU | 184 | 6.041 | 12.311 | 28.855 | 1.00 | 13.90 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1183 | N | LEU | 185 | 6.430 | 12.436 | 31.064 | 1.00 | 11.99 |
| | ATOM | 1184 | CA | LEU | 185 | 5.571 | 13.600 | 31.250 | 1.00 | 12.43 |
| | ATOM | 1185 | CB | LEU | 185 | 5.524 | 13.997 | 32.729 | 1.00 | 13.27 |
| 5 | ATOM | 1186 | CG | LEU | 185 | 4.630 | 15.191 | 33.080 | 1.00 | 11.52 |
| | ATOM | 1187 | CD1 | LEU | 185 | 3.256 | 14.936 | 32.515 | 1.00 | 10.60 |
| | ATOM | 1188 | CD2 | LEU | 185 | 4.553 | 15.395 | 34.600 | 1.00 | 12.16 |
| | ATOM | 1189 | C | LEU | 185 | 6.077 | 14.788 | 30.419 | 1.00 | 12.48 |
| | ATOM | 1190 | O | LEU | 185 | 5.289 | 15.488 | 29.784 | 1.00 | 9.22 |
| 10 | ATOM | 1191 | N | ARG | 186 | 7.388 | 15.020 | 30.428 | 1.00 | 13.24 |
| | ATOM | 1192 | CA | ARG | 186 | 7.946 | 16.123 | 29.661 | 1.00 | 14.83 |
| | ATOM | 1193 | CB | ARG | 186 | 9.478 | 16.135 | 29.727 | 1.00 | 14.69 |
| | ATOM | 1194 | CG | ARG | 186 | 10.112 | 17.274 | 30.526 | 1.00 | 18.47 |
| | ATOM | 1195 | CD | ARG | 186 | 11.633 | 17.063 | 30.663 | 1.00 | 25.71 |
| 15 | ATOM | 1196 | NE | ARG | 186 | 12.325 | 18.069 | 31.484 | 1.00 | 37.62 |
| | ATOM | 1197 | CZ | ARG | 186 | 12.048 | 18.357 | 32.764 | 1.00 | 42.54 |
| | ATOM | 1198 | NH1 | ARG | 186 | 11.070 | 17.721 | 33.407 | 1.00 | 43.86 |
| | ATOM | 1199 | NH2 | ARG | 186 | 12.762 | 19.277 | 33.414 | 1.00 | 39.97 |
| | ATOM | 1200 | C | ARG | 186 | 7.510 | 15.968 | 28.220 | 1.00 | 16.38 |
| 20 | ATOM | 1201 | O | ARG | 186 | 6.857 | 16.851 | 27.673 | 1.00 | 17.00 |
| | ATOM | 1202 | N | ASP | 187 | 7.850 | 14.832 | 27.616 | 1.00 | 19.34 |
| | ATOM | 1203 | CA | ASP | 187 | 7.519 | 14.579 | 26.214 | 1.00 | 24.04 |
| | ATOM | 1204 | CB | ASP | 187 | 7.799 | 13.123 | 25.822 | 1.00 | 30.35 |
| | ATOM | 1205 | CG | ASP | 187 | 9.226 | 12.696 | 26.123 | 1.00 | 37.33 |
| 25 | ATOM | 1206 | OD1 | ASP | 187 | 9.479 | 12.216 | 27.251 | 1.00 | 40.99 |
| | ATOM | 1207 | OD2 | ASP | 187 | 10.096 | 12.845 | 25.234 | 1.00 | 40.65 |
| | ATOM | 1208 | C | ASP | 187 | 6.069 | 14.889 | 25.912 | 1.00 | 23.78 |
| | ATOM | 1209 | O | ASP | 187 | 5.756 | 15.541 | 24.909 | 1.00 | 25.37 |
| | ATOM | 1210 | N | ALA | 188 | 5.185 | 14.413 | 26.780 | 1.00 | 20.98 |

- 186 -

| | ATOM | 1211 | CA | ALA | 188 | 3. 761 | 14. 634 | 26. 603 | 1. 00 | 17. 11 |
|---|------|------|----|-----|-----|--------|---------|---------|-------|--------|
| | ATOM | 1212 | CB | ALA | 188 | 2. 996 | 13. 943 | 27. 722 | 1. 00 | 19. 70 |
| | ATOM | 1213 | C | ALA | 188 | 3. 475 | 16. 130 | 26. 600 | 1. 00 | 14. 48 |
| | ATOM | 1214 | O | ALA | 188 | 2. 911 | 16. 660 | 25. 646 | 1. 00 | 11. 69 |
| 5 | ATOM | 1215 | N | ILE | 189 | 3. 873 | 16. 801 | 27. 677 | 1. 00 | 13. 32 |
| | ATOM | 1216 | CA | ILE | 189 | 3. 682 | 18. 239 | 27. 817 | 1. 00 | 13. 84 |
| | ATOM | 1217 | CB | ILE | 189 | 4. 422 | 18. 754 | 29. 056 | 1. 00 | 12. 34 |
| | ATOM | 1218 | CG2 | ILE | 189 | 4. 368 | 20. 266 | 29. 118 | 1. 00 | 13. 98 |
| | ATOM | 1219 | CG1 | ILE | 189 | 3. 776 | 18. 153 | 30. 302 | 1. 00 | 14. 10 |
| 10 | ATOM | 1220 | CD1 | ILE | 189 | 4. 455 | 18. 530 | 31. 595 | 1. 00 | 14. 04 |
| | ATOM | 1221 | C | ILE | 189 | 4. 223 | 18. 928 | 26. 575 | 1. 00 | 15. 60 |
| | ATOM | 1222 | O | ILE | 189 | 3. 634 | 19. 888 | 26. 058 | 1. 00 | 14. 87 |
| | ATOM | 1223 | N | LYS | 190 | 5. 351 | 18. 408 | 26. 103 | 1. 00 | 16. 13 |
| | ATOM | 1224 | CA | LYS | 190 | 6. 010 | 18. 913 | 24. 918 | 1. 00 | 16. 34 |
| 15 | ATOM | 1225 | CB | LYS | 190 | 7. 361 | 18. 211 | 24. 737 | 1. 00 | 18. 43 |
| | ATOM | 1226 | CG | LYS | 190 | 8. 503 | 19. 081 | 24. 175 | 1. 00 | 24. 32 |
| | ATOM | 1227 | CD | LYS | 190 | 8. 539 | 19. 154 | 22. 631 | 1. 00 | 28. 76 |
| | ATOM | 1228 | CE | LYS | 190 | 9. 830 | 19. 841 | 22. 125 | 1. 00 | 30. 07 |
| | ATOM | 1229 | NZ | LYS | 190 | 10. 060 | 19. 788 | 20. 642 | 1. 00 | 27. 01 |
| 20 | ATOM | 1230 | C | LYS | 190 | 5. 101 | 18. 652 | 23. 718 | 1. 00 | 16. 41 |
| | ATOM | 1231 | O | LYS | 190 | 4. 786 | 19. 575 | 22. 981 | 1. 00 | 17. 80 |
| | ATOM | 1232 | N | ARG | 191 | 4. 656 | 17. 413 | 23. 529 | 1. 00 | 14. 92 |
| | ATOM | 1233 | CA | ARG | 191 | 3. 798 | 17. 107 | 22. 386 | 1. 00 | 15. 62 |
| | ATOM | 1234 | CB | ARG | 191 | 3. 241 | 15. 684 | 22. 491 | 1. 00 | 19. 10 |
| 25 | ATOM | 1235 | CG | ARG | 191 | 4. 071 | 14. 622 | 21. 775 | 1. 00 | 20. 57 |
| | ATOM | 1236 | CD | ARG | 191 | 3. 634 | 13. 221 | 22. 156 | 1. 00 | 19. 26 |
| | ATOM | 1237 | NE | ARG | 191 | 3. 950 | 12. 925 | 23. 547 | 1. 00 | 23. 45 |
| | ATOM | 1238 | CZ | ARG | 191 | 3. 732 | 11. 747 | 24. 119 | 1. 00 | 28. 59 |
| | ATOM | 1239 | NH1 | ARG | 191 | 3. 194 | 10. 767 | 23. 406 | 1. 00 | 32. 19 |

- 187 -

| | ATOM | 1240 | NH2 | ARG | 191 | 4.062 | 11.537 | 25.391 | 1.00 | 29.84 |
|---|------|------|-----|-----|-----|-------|--------|--------|------|-------|
| | ATOM | 1241 | C | ARG | 191 | 2.652 | 18.086 | 22.207 | 1.00 | 15.44 |
| | ATOM | 1242 | O | ARG | 191 | 2.383 | 18.513 | 21.098 | 1.00 | 15.17 |
| | ATOM | 1243 | N | ARG | 192 | 1.980 | 18.441 | 23.295 | 1.00 | 17.09 |
| 5 | ATOM | 1244 | CA | ARG | 192 | 0.853 | 19.372 | 23.253 | 1.00 | 19.02 |
| | ATOM | 1245 | CB | ARG | 192 | 0.588 | 19.885 | 24.647 | 1.00 | 17.94 |
| | ATOM | 1246 | CG | ARG | 192 | 0.579 | 18.785 | 25.635 | 1.00 | 20.35 |
| | ATOM | 1247 | CD | ARG | 192 | -0.812 | 18.328 | 25.855 | 1.00 | 22.03 |
| | ATOM | 1248 | NE | ARG | 192 | -1.565 | 19.332 | 26.586 | 1.00 | 27.30 |
| 10 | ATOM | 1249 | CZ | ARG | 192 | -2.824 | 19.164 | 26.954 | 1.00 | 32.13 |
| | ATOM | 1250 | NH1 | ARG | 192 | -3.437 | 18.028 | 26.639 | 1.00 | 34.51 |
| | ATOM | 1251 | NH2 | ARG | 192 | -3.465 | 20.115 | 27.631 | 1.00 | 33.64 |
| | ATOM | 1252 | C | ARG | 192 | 1.010 | 20.572 | 22.321 | 1.00 | 22.21 |
| | ATOM | 1253 | O | ARG | 192 | 0.017 | 21.184 | 21.937 | 1.00 | 24.03 |
| 15 | ATOM | 1254 | N | GLY | 193 | 2.245 | 20.923 | 21.975 | 1.00 | 24.28 |
| | ATOM | 1255 | CA | GLY | 193 | 2.472 | 22.052 | 21.088 | 1.00 | 25.59 |
| | ATOM | 1256 | C | GLY | 193 | 2.351 | 23.417 | 21.750 | 1.00 | 27.55 |
| | ATOM | 1257 | O | GLY | 193 | 2.734 | 24.437 | 21.163 | 1.00 | 26.53 |
| | ATOM | 1258 | N | ASP | 194 | 1.836 | 23.434 | 22.981 | 1.00 | 28.09 |
| 20 | ATOM | 1259 | CA | ASP | 194 | 1.634 | 24.678 | 23.725 | 1.00 | 28.74 |
| | ATOM | 1260 | CB | ASP | 194 | 0.349 | 24.597 | 24.548 | 1.00 | 32.11 |
| | ATOM | 1261 | CG | ASP | 194 | -0.873 | 24.329 | 23.692 | 1.00 | 36.60 |
| | ATOM | 1262 | OD1 | ASP | 194 | -1.053 | 25.025 | 22.668 | 1.00 | 38.48 |
| | ATOM | 1263 | OD2 | ASP | 194 | -1.659 | 23.424 | 24.046 | 1.00 | 40.23 |
| 25 | ATOM | 1264 | C | ASP | 194 | 2.774 | 25.089 | 24.641 | 1.00 | 27.04 |
| | ATOM | 1265 | O | ASP | 194 | 3.815 | 24.439 | 24.689 | 1.00 | 26.55 |
| | ATOM | 1266 | N | PHE | 195 | 2.565 | 26.181 | 25.370 | 1.00 | 25.47 |
| | ATOM | 1267 | CA | PHE | 195 | 3.582 | 26.691 | 26.274 | 1.00 | 25.41 |
| | ATOM | 1268 | CB | PHE | 195 | 3.083 | 27.932 | 27.016 | 1.00 | 27.05 |

|   | ATOM | 1269 | CG | PHE | 195 | 3.156 | 29.192 | 26.201 | 1.00 | 28.43 |
|---|------|------|-----|-----|-----|-------|--------|--------|------|-------|
|   | ATOM | 1270 | CD1 | PHE | 195 | 2.032 | 29.686 | 25.550 | 1.00 | 31.56 |
|   | ATOM | 1271 | CD2 | PHE | 195 | 4.353 | 29.880 | 26.067 | 1.00 | 29.11 |
|   | ATOM | 1272 | CE1 | PHE | 195 | 2.097 | 30.852 | 24.771 | 1.00 | 30.45 |
| 5 | ATOM | 1273 | CE2 | PHE | 195 | 4.426 | 31.046 | 25.290 | 1.00 | 30.62 |
|   | ATOM | 1274 | CZ | PHE | 195 | 3.294 | 31.528 | 24.644 | 1.00 | 29.47 |
|   | ATOM | 1275 | C | PHE | 195 | 4.024 | 25.642 | 27.267 | 1.00 | 24.15 |
|   | ATOM | 1276 | O | PHE | 195 | 3.214 | 25.083 | 28.000 | 1.00 | 25.61 |
|   | ATOM | 1277 | N | GLU | 196 | 5.324 | 25.385 | 27.280 | 1.00 | 22.49 |
| 10 | ATOM | 1278 | CA | GLU | 196 | 5.897 | 24.394 | 28.166 | 1.00 | 23.12 |
|   | ATOM | 1279 | CB | GLU | 196 | 7.117 | 23.754 | 27.499 | 1.00 | 21.72 |
|   | ATOM | 1280 | CG | GLU | 196 | 6.942 | 23.418 | 26.020 | 1.00 | 22.22 |
|   | ATOM | 1281 | CD | GLU | 196 | 8.121 | 22.629 | 25.477 | 1.00 | 24.60 |
|   | ATOM | 1282 | OE1 | GLU | 196 | 8.336 | 22.601 | 24.241 | 1.00 | 23.54 |
| 15 | ATOM | 1283 | OE2 | GLU | 196 | 8.839 | 22.026 | 26.301 | 1.00 | 26.49 |
|   | ATOM | 1284 | C | GLU | 196 | 6.314 | 25.066 | 29.466 | 1.00 | 24.25 |
|   | ATOM | 1285 | O | GLU | 196 | 7.467 | 24.966 | 29.882 | 1.00 | 26.05 |
|   | ATOM | 1286 | N | MET | 197 | 5.376 | 25.729 | 30.126 | 1.00 | 25.12 |
|   | ATOM | 1287 | CA | MET | 197 | 5.711 | 26.444 | 31.352 | 1.00 | 27.52 |
| 20 | ATOM | 1288 | CB | MET | 197 | 5.546 | 27.942 | 31.096 | 1.00 | 29.51 |
|   | ATOM | 1289 | CG | MET | 197 | 6.758 | 28.782 | 31.466 | 1.00 | 33.61 |
|   | ATOM | 1290 | SD | MET | 197 | 7.208 | 29.992 | 30.181 | 1.00 | 35.72 |
|   | ATOM | 1291 | CE | MET | 197 | 5.967 | 31.256 | 30.466 | 1.00 | 37.45 |
|   | ATOM | 1292 | C | MET | 197 | 4.906 | 26.045 | 32.583 | 1.00 | 27.47 |
| 25 | ATOM | 1293 | O | MET | 197 | 4.921 | 26.749 | 33.597 | 1.00 | 25.63 |
|   | ATOM | 1294 | N | ASP | 198 | 4.230 | 24.903 | 32.502 | 1.00 | 27.57 |
|   | ATOM | 1295 | CA | ASP | 198 | 3.384 | 24.430 | 33.598 | 1.00 | 26.12 |
|   | ATOM | 1296 | CB | ASP | 198 | 2.462 | 23.298 | 33.110 | 1.00 | 29.89 |
|   | ATOM | 1297 | CG | ASP | 198 | 1.326 | 23.796 | 32.232 | 1.00 | 31.76 |

- 189 -

| | ATOM | 1298 | OD1 | ASP | 198 | 0.736 | 24.840 | 32.590 | 1.00 | 30.59 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1299 | OD2 | ASP | 198 | 1.023 | 23.135 | 31.203 | 1.00 | 32.71 |
| | ATOM | 1300 | C | ASP | 198 | 4.110 | 23.959 | 34.853 | 1.00 | 22.26 |
| | ATOM | 1301 | O | ASP | 198 | 3.960 | 24.551 | 35.923 | 1.00 | 18.00 |
| 5 | ATOM | 1302 | N | VAL | 199 | 4.873 | 22.878 | 34.717 | 1.00 | 19.81 |
| | ATOM | 1303 | CA | VAL | 199 | 5.605 | 22.301 | 35.841 | 1.00 | 18.78 |
| | ATOM | 1304 | CB | VAL | 199 | 5.133 | 20.852 | 36.115 | 1.00 | 16.48 |
| | ATOM | 1305 | CG1 | VAL | 199 | 3.736 | 20.859 | 36.696 | 1.00 | 19.07 |
| | ATOM | 1306 | CG2 | VAL | 199 | 5.150 | 20.042 | 34.823 | 1.00 | 10.86 |
| 10 | ATOM | 1307 | C | VAL | 199 | 7.121 | 22.267 | 35.648 | 1.00 | 20.19 |
| | ATOM | 1308 | O | VAL | 199 | 7.665 | 22.752 | 34.655 | 1.00 | 21.16 |
| | ATOM | 1309 | N | VAL | 200 | 7.798 | 21.695 | 36.629 | 1.00 | 20.40 |
| | ATOM | 1310 | CA | VAL | 200 | 9.237 | 21.547 | 36.594 | 1.00 | 22.39 |
| | ATOM | 1311 | CB | VAL | 200 | 9.975 | 22.834 | 37.007 | 1.00 | 24.84 |
| 15 | ATOM | 1312 | CG1 | VAL | 200 | 9.331 | 23.406 | 38.255 | 1.00 | 31.58 |
| | ATOM | 1313 | CG2 | VAL | 200 | 11.465 | 22.539 | 37.266 | 1.00 | 21.54 |
| | ATOM | 1314 | C | VAL | 200 | 9.502 | 20.457 | 37.598 | 1.00 | 23.06 |
| | ATOM | 1315 | O | VAL | 200 | 9.039 | 20.501 | 38.755 | 1.00 | 22.26 |
| | ATOM | 1316 | N | ALA | 201 | 10.229 | 19.460 | 37.120 | 1.00 | 23.03 |
| 20 | ATOM | 1317 | CA | ALA | 201 | 10.569 | 18.300 | 37.907 | 1.00 | 22.74 |
| | ATOM | 1318 | CB | ALA | 201 | 11.460 | 17.418 | 37.112 | 1.00 | 23.66 |
| | ATOM | 1319 | C | ALA | 201 | 11.236 | 18.646 | 39.209 | 1.00 | 24.47 |
| | ATOM | 1320 | O | ALA | 201 | 12.045 | 19.564 | 39.285 | 1.00 | 27.55 |
| | ATOM | 1321 | N | MET | 202 | 10.872 | 17.914 | 40.244 | 1.00 | 25.96 |
| 25 | ATOM | 1322 | CA | MET | 202 | 11.479 | 18.106 | 41.547 | 1.00 | 27.52 |
| | ATOM | 1323 | CB | MET | 202 | 10.720 | 19.124 | 42.386 | 1.00 | 27.45 |
| | ATOM | 1324 | CG | MET | 202 | 11.516 | 19.580 | 43.597 | 1.00 | 27.56 |
| | ATOM | 1325 | SD | MET | 202 | 11.967 | 18.244 | 44.740 | 1.00 | 28.85 |
| | ATOM | 1326 | CE | MET | 202 | 10.732 | 18.486 | 46.045 | 1.00 | 23.74 |

- 190 -

|  | ATOM | 1327 | C | MET | 202 | 11. 436 | 16. 752 | 42. 219 | 1. 00 28. 79 |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1328 | O | MET | 202 | 10. 377 | 16. 290 | 42. 653 | 1. 00 25. 51 |
|  | ATOM | 1329 | N | VAL | 203 | 12. 600 | 16. 118 | 42. 293 | 1. 00 29. 76 |
|  | ATOM | 1330 | CA | VAL | 203 | 12. 695 | 14. 802 | 42. 883 | 1. 00 28. 97 |
| 5 | ATOM | 1331 | CB | VAL | 203 | 12. 943 | 13. 727 | 41. 813 | 1. 00 25. 86 |
|  | ATOM | 1332 | CG1 | VAL | 203 | 11. 936 | 13. 870 | 40. 681 | 1. 00 22. 02 |
|  | ATOM | 1333 | CG2 | VAL | 203 | 14. 361 | 13. 831 | 41. 310 | 1. 00 23. 30 |
|  | ATOM | 1334 | C | VAL | 203 | 13. 815 | 14. 713 | 43. 890 | 1. 00 31. 36 |
|  | ATOM | 1335 | O | VAL | 203 | 13. 934 | 13. 713 | 44. 585 | 1. 00 34. 93 |
| 10 | ATOM | 1336 | N | ASN | 204 | 14. 638 | 15. 745 | 43. 987 | 1. 00 32. 12 |
|  | ATOM | 1337 | CA | ASN | 204 | 15. 741 | 15. 674 | 44. 929 | 1. 00 33. 37 |
|  | ATOM | 1338 | CB | ASN | 204 | 16. 667 | 16. 867 | 44. 736 | 1. 00 36. 19 |
|  | ATOM | 1339 | CG | ASN | 204 | 18. 052 | 16. 601 | 45. 260 | 1. 00 39. 20 |
|  | ATOM | 1340 | OD1 | ASN | 204 | 18. 847 | 15. 905 | 44. 621 | 1. 00 41. 71 |
| 15 | ATOM | 1341 | ND2 | ASN | 204 | 18. 349 | 17. 133 | 46. 440 | 1. 00 39. 72 |
|  | ATOM | 1342 | C | ASN | 204 | 15. 220 | 15. 625 | 46. 363 | 1. 00 32. 02 |
|  | ATOM | 1343 | O | ASN | 204 | 14. 382 | 16. 439 | 46. 751 | 1. 00 28. 87 |
|  | ATOM | 1344 | N | ASP | 205 | 15. 705 | 14. 665 | 47. 149 | 1. 00 31. 97 |
|  | ATOM | 1345 | CA | ASP | 205 | 15. 245 | 14. 538 | 48. 541 | 1. 00 33. 94 |
| 20 | ATOM | 1346 | CB | ASP | 205 | 15. 792 | 13. 266 | 49. 197 | 1. 00 32. 38 |
|  | ATOM | 1347 | CG | ASP | 205 | 15. 163 | 12. 017 | 48. 642 | 1. 00 31. 18 |
|  | ATOM | 1348 | OD1 | ASP | 205 | 15. 386 | 10. 935 | 49. 217 | 1. 00 31. 15 |
|  | ATOM | 1349 | OD2 | ASP | 205 | 14. 450 | 12. 118 | 47. 625 | 1. 00 28. 42 |
|  | ATOM | 1350 | C | ASP | 205 | 15. 626 | 15. 722 | 49. 414 | 1. 00 33. 64 |
| 25 | ATOM | 1351 | O | ASP | 205 | 14. 909 | 16. 080 | 50. 356 | 1. 00 33. 83 |
|  | ATOM | 1352 | N | THR | 206 | 16. 770 | 16. 313 | 49. 092 | 1. 00 31. 15 |
|  | ATOM | 1353 | CA | THR | 206 | 17. 290 | 17. 449 | 49. 826 | 1. 00 25. 09 |
|  | ATOM | 1354 | CB | THR | 206 | 18. 646 | 17. 825 | 49. 278 | 1. 00 25. 45 |
|  | ATOM | 1355 | OG1 | THR | 206 | 19. 423 | 16. 630 | 49. 123 | 1. 00 24. 81 |

- 191 -

|  | ATOM | 1356 | CG2 | THR | 206 | 19. 350 | 18. 769 | 50. 232 | 1. 00 | 26. 26 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1357 | C | THR | 206 | 16. 347 | 18. 634 | 49. 734 | 1. 00 | 20. 16 |
|  | ATOM | 1358 | O | THR | 206 | 15. 923 | 19. 184 | 50. 755 | 1. 00 | 17. 86 |
|  | ATOM | 1359 | N | VAL | 207 | 16. 009 | 19. 016 | 48. 510 | 1. 00 | 12. 86 |
| 5 | ATOM | 1360 | CA | VAL | 207 | 15. 106 | 20. 133 | 48. 308 | 1. 00 | 9. 27 |
|  | ATOM | 1361 | CB | VAL | 207 | 14. 582 | 20. 164 | 46. 867 | 1. 00 | 5. 21 |
|  | ATOM | 1362 | CG1 | VAL | 207 | 13. 555 | 21. 243 | 46. 720 | 1. 00 | 1. 26 |
|  | ATOM | 1363 | CG2 | VAL | 207 | 15. 714 | 20. 397 | 45. 910 | 1. 00 | 4. 57 |
|  | ATOM | 1364 | C | VAL | 207 | 13. 917 | 19. 992 | 49. 255 | 1. 00 | 11. 72 |
| 10 | ATOM | 1365 | O | VAL | 207 | 13. 584 | 20. 909 | 50. 016 | 1. 00 | 9. 00 |
|  | ATOM | 1366 | N | ALA | 208 | 13. 291 | 18. 819 | 49. 212 | 1. 00 | 14. 04 |
|  | ATOM | 1367 | CA | ALA | 208 | 12. 122 | 18. 523 | 50. 041 | 1. 00 | 14. 67 |
|  | ATOM | 1368 | CB | ALA | 208 | 11. 598 | 17. 148 | 49. 702 | 1. 00 | 14. 60 |
|  | ATOM | 1369 | C | ALA | 208 | 12. 422 | 18. 615 | 51. 537 | 1. 00 | 15. 41 |
| 15 | ATOM | 1370 | O | ALA | 208 | 11. 514 | 18. 770 | 52. 362 | 1. 00 | 14. 28 |
|  | ATOM | 1371 | N | THR | 209 | 13. 699 | 18. 498 | 51. 879 | 1. 00 | 13. 94 |
|  | ATOM | 1372 | CA | THR | 209 | 14. 123 | 18. 591 | 53. 261 | 1. 00 | 13. 05 |
|  | ATOM | 1373 | CB | THR | 209 | 15. 567 | 18. 237 | 53. 423 | 1. 00 | 11. 66 |
|  | ATOM | 1374 | OG1 | THR | 209 | 15. 887 | 17. 177 | 52. 525 | 1. 00 | 12. 70 |
| 20 | ATOM | 1375 | CG2 | THR | 209 | 15. 833 | 17. 807 | 54. 846 | 1. 00 | 7. 92 |
|  | ATOM | 1376 | C | THR | 209 | 14. 007 | 20. 041 | 53. 626 | 1. 00 | 14. 97 |
|  | ATOM | 1377 | O | THR | 209 | 13. 554 | 20. 401 | 54. 714 | 1. 00 | 14. 80 |
|  | ATOM | 1378 | N | MET | 210 | 14. 447 | 20. 885 | 52. 707 | 1. 00 | 15. 34 |
|  | ATOM | 1379 | CA | MET | 210 | 14. 363 | 22. 298 | 52. 965 | 1. 00 | 16. 36 |
| 25 | ATOM | 1380 | CB | MET | 210 | 15. 043 | 23. 091 | 51. 845 | 1. 00 | 19. 89 |
|  | ATOM | 1381 | CG | MET | 210 | 15. 119 | 24. 592 | 52. 103 | 1. 00 | 23. 82 |
|  | ATOM | 1382 | SD | MET | 210 | 15. 258 | 25. 542 | 50. 561 | 1. 00 | 29. 33 |
|  | ATOM | 1383 | CE | MET | 210 | 13. 547 | 25. 995 | 50. 325 | 1. 00 | 27. 80 |
|  | ATOM | 1384 | C | MET | 210 | 12. 864 | 22. 592 | 53. 031 | 1. 00 | 14. 33 |

- 192 -

| ATOM | 1385 | O | MET | 210 | 12.332 | 22.896 | 54.102 | 1.00 | 15.04 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ATOM | 1386 | N | ILE | 211 | 12.180 | 22.452 | 51.898 | 1.00 | 11.15 |
| ATOM | 1387 | CA | ILE | 211 | 10.743 | 22.708 | 51.831 | 1.00 | 9.09 |
| ATOM | 1388 | CB | ILE | 211 | 10.157 | 22.122 | 50.566 | 1.00 | 5.39 |
| ATOM | 1389 | CG2 | ILE | 211 | 8.748 | 22.693 | 50.337 | 1.00 | 3.22 |
| ATOM | 1390 | CG1 | ILE | 211 | 11.111 | 22.412 | 49.412 | 1.00 | 2.02 |
| ATOM | 1391 | CD1 | ILE | 211 | 10.580 | 22.065 | 48.067 | 1.00 | 1.00 |
| ATOM | 1392 | C | ILE | 211 | 9.987 | 22.129 | 53.022 | 1.00 | 10.92 |
| ATOM | 1393 | O | ILE | 211 | 9.117 | 22.781 | 53.605 | 1.00 | 7.92 |
| ATOM | 1394 | N | SER | 212 | 10.319 | 20.891 | 53.364 | 1.00 | 12.74 |
| ATOM | 1395 | CA | SER | 212 | 9.701 | 20.254 | 54.489 | 1.00 | 15.18 |
| ATOM | 1396 | CB | SER | 212 | 10.300 | 18.880 | 54.704 | 1.00 | 12.84 |
| ATOM | 1397 | OG | SER | 212 | 10.216 | 18.533 | 56.078 | 1.00 | 19.56 |
| ATOM | 1398 | C | SER | 212 | 9.918 | 21.101 | 55.736 | 1.00 | 19.90 |
| ATOM | 1399 | O | SER | 212 | 8.969 | 21.432 | 56.435 | 1.00 | 21.30 |
| ATOM | 1400 | N | CYS | 213 | 11.161 | 21.476 | 56.016 | 1.00 | 24.22 |
| ATOM | 1401 | CA | CYS | 213 | 11.432 | 22.259 | 57.219 | 1.00 | 28.52 |
| ATOM | 1402 | CB | CYS | 213 | 12.934 | 22.367 | 57.464 | 1.00 | 30.65 |
| ATOM | 1403 | SG | CYS | 213 | 13.713 | 20.766 | 57.805 | 1.00 | 39.09 |
| ATOM | 1404 | C | CYS | 213 | 10.822 | 23.637 | 57.168 | 1.00 | 29.40 |
| ATOM | 1405 | O | CYS | 213 | 10.366 | 24.150 | 58.186 | 1.00 | 30.64 |
| ATOM | 1406 | N | TYR | 214 | 10.816 | 24.229 | 55.981 | 1.00 | 29.50 |
| ATOM | 1407 | CA | TYR | 214 | 10.243 | 25.548 | 55.788 | 1.00 | 29.27 |
| ATOM | 1408 | CB | TYR | 214 | 10.168 | 25.846 | 54.292 | 1.00 | 31.33 |
| ATOM | 1409 | CG | TYR | 214 | 9.637 | 27.212 | 53.985 | 1.00 | 33.15 |
| ATOM | 1410 | CD1 | TYR | 214 | 10.182 | 28.328 | 54.594 | 1.00 | 36.28 |
| ATOM | 1411 | CE1 | TYR | 214 | 9.694 | 29.592 | 54.341 | 1.00 | 39.73 |
| ATOM | 1412 | CD2 | TYR | 214 | 8.582 | 27.390 | 53.100 | 1.00 | 35.23 |
| ATOM | 1413 | CE2 | TYR | 214 | 8.080 | 28.656 | 52.833 | 1.00 | 39.38 |

- 193 -

|   | ATOM | 1414 | CZ | TYR | 214 | 8. 644 | 29. 758 | 53. 463 | 1. 00 | 41. 11 |
|---|------|------|-----|-----|-----|--------|---------|---------|-------|--------|
|   | ATOM | 1415 | OH | TYR | 214 | 8. 168 | 31. 034 | 53. 241 | 1. 00 | 43. 33 |
|   | ATOM | 1416 | C | TYR | 214 | 8. 848 | 25. 649 | 56. 429 | 1. 00 | 28. 57 |
|   | ATOM | 1417 | O | TYR | 214 | 8. 561 | 26. 578 | 57. 185 | 1. 00 | 27. 99 |
| 5 | ATOM | 1418 | N | TYR | 215 | 7. 986 | 24. 685 | 56. 136 | 1. 00 | 27. 91 |
|   | ATOM | 1419 | CA | TYR | 215 | 6. 642 | 24. 685 | 56. 691 | 1. 00 | 27. 12 |
|   | ATOM | 1420 | CB | TYR | 215 | 5. 922 | 23. 403 | 56. 309 | 1. 00 | 21. 95 |
|   | ATOM | 1421 | CG | TYR | 215 | 5. 723 | 23. 235 | 54. 829 | 1. 00 | 18. 06 |
|   | ATOM | 1422 | CD1 | TYR | 215 | 6. 064 | 22. 048 | 54. 197 | 1. 00 | 17. 25 |
| 10 | ATOM | 1423 | CE1 | TYR | 215 | 5. 835 | 21. 867 | 52. 841 | 1. 00 | 17. 47 |
|   | ATOM | 1424 | CD2 | TYR | 215 | 5. 152 | 24. 246 | 54. 065 | 1. 00 | 16. 51 |
|   | ATOM | 1425 | CE2 | TYR | 215 | 4. 917 | 24. 075 | 52. 711 | 1. 00 | 15. 51 |
|   | ATOM | 1426 | CZ | TYR | 215 | 5. 257 | 22. 882 | 52. 109 | 1. 00 | 17. 82 |
|   | ATOM | 1427 | OH | TYR | 215 | 4. 979 | 22. 681 | 50. 785 | 1. 00 | 20. 98 |
| 15 | ATOM | 1428 | C | TYR | 215 | 6. 658 | 24. 810 | 58. 201 | 1. 00 | 30. 19 |
|   | ATOM | 1429 | O | TYR | 215 | 5. 780 | 25. 438 | 58. 778 | 1. 00 | 31. 10 |
|   | ATOM | 1430 | N | GLU | 216 | 7. 640 | 24. 197 | 58. 850 | 1. 00 | 35. 15 |
|   | ATOM | 1431 | CA | GLU | 216 | 7. 725 | 24. 278 | 60. 306 | 1. 00 | 41. 19 |
|   | ATOM | 1432 | CB | GLU | 216 | 8. 560 | 23. 132 | 60. 876 | 1. 00 | 44. 10 |
| 20 | ATOM | 1433 | CG | GLU | 216 | 7. 877 | 21. 767 | 60. 887 | 1. 00 | 52. 19 |
|   | ATOM | 1434 | CD | GLU | 216 | 6. 579 | 21. 749 | 61. 685 | 1. 00 | 54. 93 |
|   | ATOM | 1435 | OE1 | GLU | 216 | 6. 491 | 22. 481 | 62. 702 | 1. 00 | 55. 44 |
|   | ATOM | 1436 | OE2 | GLU | 216 | 5. 658 | 20. 988 | 61. 296 | 1. 00 | 56. 26 |
|   | ATOM | 1437 | C | GLU | 216 | 8. 369 | 25. 591 | 60. 707 | 1. 00 | 43. 33 |
| 25 | ATOM | 1438 | O | GLU | 216 | 7. 787 | 26. 385 | 61. 449 | 1. 00 | 44. 64 |
|   | ATOM | 1439 | N | ASP | 217 | 9. 583 | 25. 802 | 60. 209 | 1. 00 | 44. 35 |
|   | ATOM | 1440 | CA | ASP | 217 | 10. 357 | 27. 007 | 60. 489 | 1. 00 | 44. 65 |
|   | ATOM | 1441 | CB | ASP | 217 | 11. 734 | 26. 623 | 61. 033 | 1. 00 | 47. 71 |
|   | ATOM | 1442 | CG | ASP | 217 | 12. 667 | 27. 806 | 61. 136 | 1. 00 | 50. 46 |

- 194 -

|   | ATOM | 1443 | OD1 | ASP | 217 | 13.252 | 28.205 | 60.106 | 1.00 | 51.95 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 1444 | OD2 | ASP | 217 | 12.804 | 28.346 | 62.252 | 1.00 | 54.06 |
|   | ATOM | 1445 | C   | ASP | 217 | 10.514 | 27.820 | 59.215 | 1.00 | 43.04 |
|   | ATOM | 1446 | O   | ASP | 217 | 11.372 | 27.527 | 58.385 | 1.00 | 44.60 |
| 5 | ATOM | 1447 | N   | HIS | 218 | 9.691  | 28.848 | 59.059 | 1.00 | 41.00 |
|   | ATOM | 1448 | CA  | HIS | 218 | 9.750  | 29.671 | 57.862 | 1.00 | 39.42 |
|   | ATOM | 1449 | CB  | HIS | 218 | 8.569  | 30.630 | 57.826 | 1.00 | 40.46 |
|   | ATOM | 1450 | CG  | HIS | 218 | 7.261  | 29.960 | 58.083 | 1.00 | 44.54 |
|   | ATOM | 1451 | CD2 | HIS | 218 | 6.652  | 28.930 | 57.450 | 1.00 | 45.30 |
| 10 | ATOM | 1452 | ND1 | HIS | 218 | 6.449  | 30.290 | 59.147 | 1.00 | 47.09 |
|   | ATOM | 1453 | CE1 | HIS | 218 | 5.397  | 29.492 | 59.161 | 1.00 | 45.61 |
|   | ATOM | 1454 | NE2 | HIS | 218 | 5.497  | 28.657 | 58.142 | 1.00 | 46.44 |
|   | ATOM | 1455 | C   | HIS | 218 | 11.036 | 30.452 | 57.759 | 1.00 | 37.69 |
|   | ATOM | 1456 | O   | HIS | 218 | 11.120 | 31.381 | 56.974 | 1.00 | 37.21 |
| 15 | ATOM | 1457 | N   | GLN | 219 | 12.041 | 30.076 | 58.537 | 1.00 | 37.38 |
|   | ATOM | 1458 | CA  | GLN | 219 | 13.312 | 30.779 | 58.494 | 1.00 | 38.18 |
|   | ATOM | 1459 | CB  | GLN | 219 | 13.727 | 31.186 | 59.910 | 1.00 | 41.72 |
|   | ATOM | 1460 | CG  | GLN | 219 | 14.577 | 32.451 | 60.011 | 1.00 | 48.69 |
|   | ATOM | 1461 | CD  | GLN | 219 | 13.836 | 33.718 | 59.546 | 1.00 | 55.14 |
| 20 | ATOM | 1462 | OE1 | GLN | 219 | 12.665 | 33.945 | 59.908 | 1.00 | 55.89 |
|   | ATOM | 1463 | NE2 | GLN | 219 | 14.523 | 34.555 | 58.751 | 1.00 | 55.41 |
|   | ATOM | 1464 | C   | GLN | 219 | 14.348 | 29.846 | 57.886 | 1.00 | 36.85 |
|   | ATOM | 1465 | O   | GLN | 219 | 15.508 | 30.200 | 57.735 | 1.00 | 37.28 |
|   | ATOM | 1466 | N   | CYS | 220 | 13.912 | 28.647 | 57.535 | 1.00 | 36.02 |
| 25 | ATOM | 1467 | CA  | CYS | 220 | 14.790 | 27.646 | 56.950 | 1.00 | 37.10 |
|   | ATOM | 1468 | CB  | CYS | 220 | 14.103 | 26.286 | 57.043 | 1.00 | 38.40 |
|   | ATOM | 1469 | SG  | CYS | 220 | 15.067 | 24.916 | 56.396 | 1.00 | 44.24 |
|   | ATOM | 1470 | C   | CYS | 220 | 15.106 | 27.970 | 55.486 | 1.00 | 37.48 |
|   | ATOM | 1471 | O   | CYS | 220 | 14.193 | 28.081 | 54.672 | 1.00 | 40.52 |

- 195 -

| | ATOM | 1472 | N | GLU 221 | 16. 382 | 28. 123 | 55. 137 | 1. 00 | 36. 17 |
|---|------|------|-----|---------|---------|---------|---------|-------|--------|
| | ATOM | 1473 | CA | GLU 221 | 16. 742 | 28. 428 | 53. 746 | 1. 00 | 35. 58 |
| | ATOM | 1474 | CB | GLU 221 | 17. 116 | 29. 911 | 53. 591 | 1. 00 | 38. 60 |
| | ATOM | 1475 | CG | GLU 221 | 15. 921 | 30. 878 | 53. 645 | 1. 00 | 42. 48 |
| 5 | ATOM | 1476 | CD | GLU 221 | 16. 325 | 32. 347 | 53. 760 | 1. 00 | 42. 62 |
| | ATOM | 1477 | OE1 | GLU 221 | 17. 120 | 32. 815 | 52. 909 | 1. 00 | 42. 89 |
| | ATOM | 1478 | OE2 | GLU 221 | 15. 835 | 33. 024 | 54. 700 | 1. 00 | 40. 36 |
| | ATOM | 1479 | C | GLU 221 | 17. 896 | 27. 566 | 53. 260 | 1. 00 | 33. 89 |
| | ATOM | 1480 | O | GLU 221 | 18. 498 | 27. 826 | 52. 217 | 1. 00 | 32. 29 |
| 10 | ATOM | 1481 | N | VAL 222 | 18. 199 | 26. 525 | 54. 018 | 1. 00 | 32. 57 |
| | ATOM | 1482 | CA | VAL 222 | 19. 286 | 25. 654 | 53. 645 | 1. 00 | 31. 01 |
| | ATOM | 1483 | CB | VAL 222 | 20. 548 | 26. 041 | 54. 376 | 1. 00 | 29. 59 |
| | ATOM | 1484 | CG1 | VAL 222 | 21. 673 | 25. 102 | 53. 995 | 1. 00 | 29. 07 |
| | ATOM | 1485 | CG2 | VAL 222 | 20. 895 | 27. 465 | 54. 043 | 1. 00 | 30. 00 |
| 15 | ATOM | 1486 | C | VAL 222 | 18. 983 | 24. 214 | 53. 966 | 1. 00 | 31. 75 |
| | ATOM | 1487 | O | VAL 222 | 18. 872 | 23. 846 | 55. 132 | 1. 00 | 33. 50 |
| | ATOM | 1488 | N | GLY 223 | 18. 858 | 23. 400 | 52. 925 | 1. 00 | 31. 02 |
| | ATOM | 1489 | CA | GLY 223 | 18. 575 | 21. 994 | 53. 119 | 1. 00 | 28. 49 |
| | ATOM | 1490 | C | GLY 223 | 19. 847 | 21. 184 | 53. 026 | 1. 00 | 26. 21 |
| 20 | ATOM | 1491 | O | GLY 223 | 20. 757 | 21. 528 | 52. 267 | 1. 00 | 25. 39 |
| | ATOM | 1492 | N | MET 224 | 19. 911 | 20. 098 | 53. 786 | 1. 00 | 24. 93 |
| | ATOM | 1493 | CA | MET 224 | 21. 101 | 19. 267 | 53. 774 | 1. 00 | 24. 66 |
| | ATOM | 1494 | CB | MET 224 | 22. 164 | 19. 958 | 54. 623 | 1. 00 | 26. 07 |
| | ATOM | 1495 | CG | MET 224 | 23. 584 | 19. 535 | 54. 358 | 1. 00 | 26. 25 |
| 25 | ATOM | 1496 | SD | MET 224 | 24. 664 | 20. 375 | 55. 525 | 1. 00 | 28. 76 |
| | ATOM | 1497 | CE | MET 224 | 24. 493 | 19. 328 | 56. 939 | 1. 00 | 27. 46 |
| | ATOM | 1498 | C | MET 224 | 20. 867 | 17. 819 | 54. 253 | 1. 00 | 23. 62 |
| | ATOM | 1499 | O | MET 224 | 20. 243 | 17. 581 | 55. 294 | 1. 00 | 21. 62 |
| | ATOM | 1500 | N | ILE 225 | 21. 389 | 16. 867 | 53. 478 | 1. 00 | 21. 96 |

- 196 -

|  | ATOM | 1501 | CA | ILE 225 | 21.265 | 15.434 | 53.764 | 1.00 | 21.80 |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1502 | CB | ILE 225 | 20.514 | 14.706 | 52.662 | 1.00 | 23.26 |
|  | ATOM | 1503 | CG2 | ILE 225 | 20.389 | 13.242 | 53.026 | 1.00 | 22.57 |
|  | ATOM | 1504 | CG1 | ILE 225 | 19.142 | 15.332 | 52.463 | 1.00 | 26.22 |
| 5 | ATOM | 1505 | CD1 | ILE 225 | 18.270 | 15.229 | 53.688 | 1.00 | 30.06 |
|  | ATOM | 1506 | C | ILE 225 | 22.595 | 14.702 | 53.904 | 1.00 | 21.76 |
|  | ATOM | 1507 | O | ILE 225 | 23.204 | 14.299 | 52.909 | 1.00 | 20.84 |
|  | ATOM | 1508 | N | VAL 226 | 23.008 | 14.492 | 55.146 | 1.00 | 22.14 |
|  | ATOM | 1509 | CA | VAL 226 | 24.263 | 13.824 | 55.454 | 1.00 | 22.07 |
| 10 | ATOM | 1510 | CB | VAL 226 | 25.031 | 14.613 | 56.514 | 1.00 | 22.20 |
|  | ATOM | 1511 | CG1 | VAL 226 | 26.321 | 13.905 | 56.872 | 1.00 | 20.57 |
|  | ATOM | 1512 | CG2 | VAL 226 | 25.283 | 16.016 | 56.005 | 1.00 | 22.66 |
|  | ATOM | 1513 | C | VAL 226 | 24.060 | 12.411 | 55.972 | 1.00 | 22.96 |
|  | ATOM | 1514 | O | VAL 226 | 24.032 | 12.172 | 57.183 | 1.00 | 23.79 |
| 15 | ATOM | 1515 | N | GLY 227 | 23.924 | 11.470 | 55.054 | 1.00 | 23.08 |
|  | ATOM | 1516 | CA | GLY 227 | 23.738 | 10.094 | 55.459 | 1.00 | 25.20 |
|  | ATOM | 1517 | C | GLY 227 | 24.623 | 9.207 | 54.621 | 1.00 | 25.79 |
|  | ATOM | 1518 | O | GLY 227 | 25.820 | 9.447 | 54.501 | 1.00 | 26.18 |
|  | ATOM | 1519 | N | THR 228 | 24.039 | 8.181 | 54.026 | 1.00 | 27.28 |
| 20 | ATOM | 1520 | CA | THR 228 | 24.822 | 7.291 | 53.200 | 1.00 | 29.44 |
|  | ATOM | 1521 | CB | THR 228 | 23.900 | 6.356 | 52.413 | 1.00 | 28.91 |
|  | ATOM | 1522 | OG1 | THR 228 | 24.691 | 5.441 | 51.650 | 1.00 | 27.54 |
|  | ATOM | 1523 | CG2 | THR 228 | 22.983 | 7.159 | 51.496 | 1.00 | 30.69 |
|  | ATOM | 1524 | C | THR 228 | 25.705 | 8.139 | 52.267 | 1.00 | 30.87 |
| 25 | ATOM | 1525 | O | THR 228 | 26.878 | 7.834 | 52.072 | 1.00 | 32.00 |
|  | ATOM | 1526 | N | GLY 229 | 25.140 | 9.216 | 51.723 | 1.00 | 31.23 |
|  | ATOM | 1527 | CA | GLY 229 | 25.888 | 10.111 | 50.855 | 1.00 | 30.25 |
|  | ATOM | 1528 | C | GLY 229 | 25.716 | 11.501 | 51.434 | 1.00 | 32.12 |
|  | ATOM | 1529 | O | GLY 229 | 25.139 | 11.632 | 52.518 | 1.00 | 33.23 |

- 197 -

|  | ATOM | 1530 | N | CYS 230 | 26. 208 | 12. 535 | 50. 749 | 1. 00 | 31. 95 |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1531 | CA | CYS 230 | 26. 057 | 13. 909 | 51. 247 | 1. 00 | 31. 05 |
|  | ATOM | 1532 | CB | CYS 230 | 27. 344 | 14. 417 | 51. 891 | 1. 00 | 31. 11 |
|  | ATOM | 1533 | SG | CYS 230 | 27. 145 | 16. 090 | 52. 562 | 1. 00 | 40. 64 |
| 5 | ATOM | 1534 | C | CYS 230 | 25. 650 | 14. 909 | 50. 183 | 1. 00 | 29. 04 |
|  | ATOM | 1535 | O | CYS 230 | 26. 202 | 14. 913 | 49. 087 | 1. 00 | 30. 85 |
|  | ATOM | 1536 | N | ASN 231 | 24. 701 | 15. 775 | 50. 513 | 1. 00 | 26. 12 |
|  | ATOM | 1537 | CA | ASN 231 | 24. 267 | 16. 773 | 49. 554 | 1. 00 | 26. 17 |
|  | ATOM | 1538 | CB | ASN 231 | 23. 380 | 16. 130 | 48. 505 | 1. 00 | 24. 13 |
| 10 | ATOM | 1539 | CG | ASN 231 | 23. 146 | 17. 030 | 47. 341 | 1. 00 | 24. 98 |
|  | ATOM | 1540 | OD1 | ASN 231 | 22. 505 | 18. 064 | 47. 463 | 1. 00 | 24. 73 |
|  | ATOM | 1541 | ND2 | ASN 231 | 23. 684 | 16. 656 | 46. 196 | 1. 00 | 29. 51 |
|  | ATOM | 1542 | C | ASN 231 | 23. 529 | 17. 927 | 50. 213 | 1. 00 | 27. 77 |
|  | ATOM | 1543 | O | ASN 231 | 22. 929 | 17. 757 | 51. 275 | 1. 00 | 28. 70 |
| 15 | ATOM | 1544 | N | ALA 232 | 23. 569 | 19. 103 | 49. 587 | 1. 00 | 27. 44 |
|  | ATOM | 1545 | CA | ALA 232 | 22. 890 | 20. 258 | 50. 158 | 1. 00 | 26. 70 |
|  | ATOM | 1546 | CB | ALA 232 | 23. 806 | 20. 963 | 51. 113 | 1. 00 | 26. 89 |
|  | ATOM | 1547 | C | ALA 232 | 22. 366 | 21. 245 | 49. 144 | 1. 00 | 26. 61 |
|  | ATOM | 1548 | O | ALA 232 | 22. 693 | 21. 184 | 47. 963 | 1. 00 | 26. 44 |
| 20 | ATOM | 1549 | N | CYS 233 | 21. 537 | 22. 161 | 49. 617 | 1. 00 | 27. 04 |
|  | ATOM | 1550 | CA | CYS 233 | 20. 976 | 23. 172 | 48. 743 | 1. 00 | 31. 21 |
|  | ATOM | 1551 | CB | CYS 233 | 19. 676 | 22. 666 | 48. 127 | 1. 00 | 31. 60 |
|  | ATOM | 1552 | SG | CYS 233 | 18. 376 | 22. 446 | 49. 348 | 1. 00 | 35. 31 |
|  | ATOM | 1553 | C | CYS 233 | 20. 708 | 24. 408 | 49. 589 | 1. 00 | 31. 98 |
| 25 | ATOM | 1554 | O | CYS 233 | 20. 596 | 24. 303 | 50. 809 | 1. 00 | 32. 62 |
|  | ATOM | 1555 | N | TYR 234 | 20. 621 | 25. 572 | 48. 949 | 1. 00 | 30. 70 |
|  | ATOM | 1556 | CA | TYR 234 | 20. 366 | 26. 822 | 49. 660 | 1. 00 | 30. 60 |
|  | ATOM | 1557 | CB | TYR 234 | 21. 684 | 27. 524 | 50. 026 | 1. 00 | 29. 53 |
|  | ATOM | 1558 | CG | TYR 234 | 22. 464 | 28. 011 | 48. 829 | 1. 00 | 27. 41 |

- 198 -

| ATOM | 1559 | CD1 | TYR | 234 | 22. 363 | 29. 327 | 48. 393 | 1. 00 | 25. 56 |
|------|------|-----|-----|-----|---------|---------|---------|-------|--------|
| ATOM | 1560 | CE1 | TYR | 234 | 22. 981 | 29. 739 | 47. 217 | 1. 00 | 25. 47 |
| ATOM | 1561 | CD2 | TYR | 234 | 23. 218 | 27. 121 | 48. 061 | 1. 00 | 28. 10 |
| ATOM | 1562 | CE2 | TYR | 234 | 23. 838 | 27. 524 | 46. 882 | 1. 00 | 26. 39 |
| ATOM | 1563 | CZ | TYR | 234 | 23. 707 | 28. 830 | 46. 462 | 1. 00 | 25. 77 |
| ATOM | 1564 | OH | TYR | 234 | 24. 240 | 29. 201 | 45. 253 | 1. 00 | 27. 36 |
| ATOM | 1565 | C | TYR | 234 | 19. 531 | 27. 742 | 48. 797 | 1. 00 | 32. 10 |
| ATOM | 1566 | O | TYR | 234 | 19. 211 | 27. 411 | 47. 657 | 1. 00 | 32. 79 |
| ATOM | 1567 | N | MET | 235 | 19. 184 | 28. 897 | 49. 357 | 1. 00 | 34. 08 |
| ATOM | 1568 | CA | MET | 235 | 18. 380 | 29. 908 | 48. 679 | 1. 00 | 34. 57 |
| ATOM | 1569 | CB | MET | 235 | 17. 492 | 30. 617 | 49. 697 | 1. 00 | 34. 74 |
| ATOM | 1570 | CG | MET | 235 | 16. 489 | 29. 699 | 50. 305 | 1. 00 | 34. 74 |
| ATOM | 1571 | SD | MET | 235 | 15. 575 | 28. 985 | 48. 959 | 1. 00 | 35. 81 |
| ATOM | 1572 | CE | MET | 235 | 14. 171 | 30. 092 | 48. 917 | 1. 00 | 34. 50 |
| ATOM | 1573 | C | MET | 235 | 19. 270 | 30. 933 | 48. 009 | 1. 00 | 35. 41 |
| ATOM | 1574 | O | MET | 235 | 19. 631 | 31. 930 | 48. 625 | 1. 00 | 37. 55 |
| ATOM | 1575 | N | GLU | 236 | 19. 626 | 30. 702 | 46. 753 | 1. 00 | 35. 58 |
| ATOM | 1576 | CA | GLU | 236 | 20. 487 | 31. 643 | 46. 049 | 1. 00 | 36. 59 |
| ATOM | 1577 | CB | GLU | 236 | 21. 168 | 30. 949 | 44. 869 | 1. 00 | 38. 16 |
| ATOM | 1578 | CG | GLU | 236 | 22. 051 | 31. 861 | 44. 051 | 1. 00 | 39. 44 |
| ATOM | 1579 | CD | GLU | 236 | 23. 107 | 32. 542 | 44. 890 | 1. 00 | 41. 44 |
| ATOM | 1580 | OE1 | GLU | 236 | 24. 116 | 31. 891 | 45. 240 | 1. 00 | 40. 65 |
| ATOM | 1581 | OE2 | GLU | 236 | 22. 918 | 33. 735 | 45. 208 | 1. 00 | 42. 03 |
| ATOM | 1582 | C | GLU | 236 | 19. 679 | 32. 838 | 45. 564 | 1. 00 | 37. 02 |
| ATOM | 1583 | O | GLU | 236 | 18. 452 | 32. 810 | 45. 580 | 1. 00 | 38. 00 |
| ATOM | 1584 | N | GLU | 237 | 20. 354 | 33. 898 | 45. 149 | 1. 00 | 38. 75 |
| ATOM | 1585 | CA | GLU | 237 | 19. 634 | 35. 062 | 44. 668 | 1. 00 | 41. 18 |
| ATOM | 1586 | CB | GLU | 237 | 20. 482 | 36. 317 | 44. 830 | 1. 00 | 39. 63 |
| ATOM | 1587 | CG | GLU | 237 | 20. 912 | 36. 579 | 46. 258 | 1. 00 | 36. 10 |

- 199 -

| | ATOM | 1588 | CD | GLU 237 | 19. 764 | 37. 022 | 47. 131 | 1. 00 | 35. 20 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1589 | OE1 | GLU 237 | 19. 056 | 37. 971 | 46. 726 | 1. 00 | 34. 49 |
| | ATOM | 1590 | OE2 | GLU 237 | 19. 574 | 36. 434 | 48. 221 | 1. 00 | 33. 72 |
| | ATOM | 1591 | C | GLU 237 | 19. 307 | 34. 836 | 43. 206 | 1. 00 | 43. 71 |
| 5 | ATOM | 1592 | O | GLU 237 | 20. 143 | 34. 351 | 42. 437 | 1. 00 | 43. 65 |
| | ATOM | 1593 | N | MET 238 | 18. 078 | 35. 172 | 42. 832 | 1. 00 | 45. 47 |
| | ATOM | 1594 | CA | MET 238 | 17. 625 | 35. 013 | 41. 457 | 1. 00 | 47. 13 |
| | ATOM | 1595 | CB | MET 238 | 16. 275 | 35. 705 | 41. 275 | 1. 00 | 47. 10 |
| | ATOM | 1596 | CG | MET 238 | 15. 094 | 34. 875 | 41. 721 | 1. 00 | 46. 82 |
| 10 | ATOM | 1597 | SD | MET 238 | 14. 773 | 33. 548 | 40. 554 | 1. 00 | 45. 37 |
| | ATOM | 1598 | CE | MET 238 | 13. 564 | 34. 332 | 39. 412 | 1. 00 | 46. 47 |
| | ATOM | 1599 | C | MET 238 | 18. 629 | 35. 589 | 40. 466 | 1. 00 | 48. 34 |
| | ATOM | 1600 | O | MET 238 | 18. 814 | 35. 061 | 39. 371 | 1. 00 | 49. 97 |
| | ATOM | 1601 | N | GLN 239 | 19. 280 | 36. 672 | 40. 868 | 1. 00 | 48. 44 |
| 15 | ATOM | 1602 | CA | GLN 239 | 20. 252 | 37. 344 | 40. 026 | 1. 00 | 49. 76 |
| | ATOM | 1603 | CB | GLN 239 | 20. 398 | 38. 794 | 40. 491 | 1. 00 | 54. 00 |
| | ATOM | 1604 | CG | GLN 239 | 20. 375 | 38. 963 | 42. 007 | 1. 00 | 58. 66 |
| | ATOM | 1605 | CD | GLN 239 | 20. 056 | 40. 394 | 42. 447 | 1. 00 | 63. 23 |
| | ATOM | 1606 | OE1 | GLN 239 | 19. 660 | 40. 624 | 43. 593 | 1. 00 | 65. 75 |
| 20 | ATOM | 1607 | NE2 | GLN 239 | 20. 233 | 41. 359 | 41. 540 | 1. 00 | 63. 23 |
| | ATOM | 1608 | C | GLN 239 | 21. 612 | 36. 665 | 40. 011 | 1. 00 | 48. 87 |
| | ATOM | 1609 | O | GLN 239 | 22. 611 | 37. 295 | 39. 687 | 1. 00 | 49. 50 |
| | ATOM | 1610 | N | ASN 240 | 21. 656 | 35. 384 | 40. 354 | 1. 00 | 47. 67 |
| | ATOM | 1611 | CA | ASN 240 | 22. 926 | 34. 660 | 40. 379 | 1. 00 | 47. 01 |
| 25 | ATOM | 1612 | CB | ASN 240 | 23. 301 | 34. 278 | 41. 809 | 1. 00 | 47. 66 |
| | ATOM | 1613 | CG | ASN 240 | 24. 101 | 35. 347 | 42. 518 | 1. 00 | 45. 71 |
| | ATOM | 1614 | OD1 | ASN 240 | 23. 553 | 36. 328 | 43. 021 | 1. 00 | 43. 88 |
| | ATOM | 1615 | ND2 | ASN 240 | 25. 414 | 35. 159 | 42. 561 | 1. 00 | 46. 64 |
| | ATOM | 1616 | C | ASN 240 | 22. 861 | 33. 393 | 39. 550 | 1. 00 | 46. 58 |

- 200 -

| | ATOM | 1617 | O | ASN 240 | 23.888 | 32.840 | 39.137 | 1.00 | 46.44 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1618 | N | VAL 241 | 21.643 | 32.919 | 39.340 | 1.00 | 44.69 |
| | ATOM | 1619 | CA | VAL 241 | 21.426 | 31.717 | 38.564 | 1.00 | 43.22 |
| | ATOM | 1620 | CB | VAL 241 | 20.103 | 31.056 | 38.948 | 1.00 | 43.93 |
| 5 | ATOM | 1621 | CG1 | VAL 241 | 20.071 | 29.643 | 38.412 | 1.00 | 44.87 |
| | ATOM | 1622 | CG2 | VAL 241 | 19.922 | 31.091 | 40.456 | 1.00 | 40.98 |
| | ATOM | 1623 | C | VAL 241 | 21.358 | 32.182 | 37.126 | 1.00 | 41.83 |
| | ATOM | 1624 | O | VAL 241 | 20.351 | 32.739 | 36.685 | 1.00 | 42.56 |
| | ATOM | 1625 | N | GLU 242 | 22.433 | 31.974 | 36.386 | 1.00 | 39.79 |
| 10 | ATOM | 1626 | CA | GLU 242 | 22.426 | 32.440 | 35.017 | 1.00 | 38.35 |
| | ATOM | 1627 | CB | GLU 242 | 23.841 | 32.438 | 34.435 | 1.00 | 41.38 |
| | ATOM | 1628 | CG | GLU 242 | 24.874 | 33.080 | 35.345 | 1.00 | 43.21 |
| | ATOM | 1629 | CD | GLU 242 | 26.062 | 33.639 | 34.588 | 1.00 | 46.65 |
| | ATOM | 1630 | OE1 | GLU 242 | 26.489 | 33.026 | 33.581 | 1.00 | 46.29 |
| 15 | ATOM | 1631 | OE2 | GLU 242 | 26.581 | 34.694 | 35.014 | 1.00 | 49.23 |
| | ATOM | 1632 | C | GLU 242 | 21.495 | 31.626 | 34.144 | 1.00 | 34.71 |
| | ATOM | 1633 | O | GLU 242 | 21.135 | 32.057 | 33.054 | 1.00 | 33.08 |
| | ATOM | 1634 | N | LEU 243 | 21.085 | 30.456 | 34.612 | 1.00 | 31.90 |
| | ATOM | 1635 | CA | LEU 243 | 20.194 | 29.652 | 33.794 | 1.00 | 30.72 |
| 20 | ATOM | 1636 | CB | LEU 243 | 20.125 | 28.214 | 34.285 | 1.00 | 29.40 |
| | ATOM | 1637 | CG | LEU 243 | 21.244 | 27.279 | 33.833 | 1.00 | 28.38 |
| | ATOM | 1638 | CD1 | LEU 243 | 21.264 | 27.192 | 32.321 | 1.00 | 23.84 |
| | ATOM | 1639 | CD2 | LEU 243 | 22.570 | 27.786 | 34.381 | 1.00 | 31.28 |
| | ATOM | 1640 | C | LEU 243 | 18.799 | 30.222 | 33.763 | 1.00 | 31.18 |
| 25 | ATOM | 1641 | O | LEU 243 | 18.143 | 30.153 | 32.729 | 1.00 | 32.86 |
| | ATOM | 1642 | N | VAL 244 | 18.350 | 30.779 | 34.887 | 1.00 | 30.11 |
| | ATOM | 1643 | CA | VAL 244 | 17.011 | 31.361 | 34.979 | 1.00 | 30.23 |
| | ATOM | 1644 | CB | VAL 244 | 16.549 | 31.527 | 36.432 | 1.00 | 31.77 |
| | ATOM | 1645 | CG1 | VAL 244 | 15.085 | 31.981 | 36.444 | 1.00 | 31.84 |

- 201 -

|  | ATOM | 1646 | CG2 | VAL | 244 | 16.748 | 30.234 | 37.213 | 1.00 | 31.59 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 1647 | C | VAL | 244 | 16.955 | 32.746 | 34.361 | 1.00 | 30.94 |
|  | ATOM | 1648 | O | VAL | 244 | 17.919 | 33.499 | 34.458 | 1.00 | 31.77 |
|  | ATOM | 1649 | N | GLU | 245 | 15.819 | 33.083 | 33.753 | 1.00 | 32.44 |
| 5 | ATOM | 1650 | CA | GLU | 245 | 15.625 | 34.389 | 33.125 | 1.00 | 36.05 |
|  | ATOM | 1651 | CB | GLU | 245 | 14.384 | 34.384 | 32.237 | 1.00 | 35.98 |
|  | ATOM | 1652 | CG | GLU | 245 | 14.542 | 35.203 | 30.981 | 1.00 | 38.72 |
|  | ATOM | 1653 | CD | GLU | 245 | 15.357 | 34.449 | 29.959 | 1.00 | 41.52 |
|  | ATOM | 1654 | OE1 | GLU | 245 | 15.957 | 33.428 | 30.356 | 1.00 | 40.02 |
| 10 | ATOM | 1655 | OE2 | GLU | 245 | 15.402 | 34.859 | 28.776 | 1.00 | 43.26 |
|  | ATOM | 1656 | C | GLU | 245 | 15.453 | 35.511 | 34.149 | 1.00 | 39.49 |
|  | ATOM | 1657 | O | GLU | 245 | 15.995 | 36.603 | 33.978 | 1.00 | 39.69 |
|  | ATOM | 1658 | N | GLY | 246 | 14.676 | 35.239 | 35.197 | 1.00 | 42.62 |
|  | ATOM | 1659 | CA | GLY | 246 | 14.417 | 36.228 | 36.233 | 1.00 | 44.14 |
| 15 | ATOM | 1660 | C | GLY | 246 | 15.642 | 36.762 | 36.953 | 1.00 | 44.54 |
|  | ATOM | 1661 | O | GLY | 246 | 16.720 | 36.163 | 36.906 | 1.00 | 43.59 |
|  | ATOM | 1662 | N | ASP | 247 | 15.476 | 37.896 | 37.627 | 1.00 | 44.51 |
|  | ATOM | 1663 | CA | ASP | 247 | 16.582 | 38.500 | 38.345 | 1.00 | 45.26 |
|  | ATOM | 1664 | CB | ASP | 247 | 17.179 | 39.654 | 37.540 | 1.00 | 48.06 |
| 20 | ATOM | 1665 | CG | ASP | 247 | 18.102 | 39.173 | 36.436 | 1.00 | 52.60 |
|  | ATOM | 1666 | OD1 | ASP | 247 | 19.016 | 38.376 | 36.744 | 1.00 | 54.76 |
|  | ATOM | 1667 | OD2 | ASP | 247 | 17.923 | 39.584 | 35.265 | 1.00 | 54.15 |
|  | ATOM | 1668 | C | ASP | 247 | 16.213 | 38.993 | 39.720 | 1.00 | 44.83 |
|  | ATOM | 1669 | O | ASP | 247 | 17.087 | 39.306 | 40.518 | 1.00 | 45.80 |
| 25 | ATOM | 1670 | N | GLU | 248 | 14.930 | 39.064 | 40.022 | 1.00 | 44.56 |
|  | ATOM | 1671 | CA | GLU | 248 | 14.561 | 39.546 | 41.336 | 1.00 | 45.70 |
|  | ATOM | 1672 | CB | GLU | 248 | 13.610 | 40.727 | 41.206 | 1.00 | 50.66 |
|  | ATOM | 1673 | CG | GLU | 248 | 12.441 | 40.458 | 40.298 | 1.00 | 60.84 |
|  | ATOM | 1674 | CD | GLU | 248 | 11.394 | 41.556 | 40.355 | 1.00 | 67.29 |

- 202 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1675 | OE1 | GLU | 248 | 10. 742 | 41. 702 | 41. 414 | 1. 00 69. 90 |
| | ATOM | 1676 | OE2 | GLU | 248 | 11. 223 | 42. 273 | 39. 340 | 1. 00 71. 41 |
| | ATOM | 1677 | C | GLU | 248 | 13. 952 | 38. 482 | 42. 224 | 1. 00 43. 15 |
| | ATOM | 1678 | O | GLU | 248 | 12. 986 | 37. 827 | 41. 855 | 1. 00 42. 29 |
| 5 | ATOM | 1679 | N | GLY | 249 | 14. 530 | 38. 315 | 43. 404 | 1. 00 42. 35 |
| | ATOM | 1680 | CA | GLY | 249 | 14. 023 | 37. 327 | 44. 330 | 1. 00 42. 91 |
| | ATOM | 1681 | C | GLY | 249 | 15. 044 | 36. 247 | 44. 625 | 1. 00 43. 93 |
| | ATOM | 1682 | O | GLY | 249 | 16. 177 | 36. 294 | 44. 145 | 1. 00 43. 62 |
| | ATOM | 1683 | N | ARG | 250 | 14. 644 | 35. 267 | 45. 427 | 1. 00 43. 38 |
| 10 | ATOM | 1684 | CA | ARG | 250 | 15. 526 | 34. 160 | 45. 781 | 1. 00 41. 04 |
| | ATOM | 1685 | CB | ARG | 250 | 15. 819 | 34. 207 | 47. 293 | 1. 00 42. 27 |
| | ATOM | 1686 | CG | ARG | 250 | 14. 745 | 34. 934 | 48. 114 | 1. 00 46. 82 |
| | ATOM | 1687 | CD | ARG | 250 | 15. 139 | 35. 142 | 49. 584 | 1. 00 51. 21 |
| | ATOM | 1688 | NE | ARG | 250 | 16. 425 | 35. 828 | 49. 730 | 1. 00 55. 52 |
| 15 | ATOM | 1689 | CZ | ARG | 250 | 16. 864 | 36. 394 | 50. 855 | 1. 00 55. 63 |
| | ATOM | 1690 | NH1 | ARG | 250 | 16. 121 | 36. 375 | 51. 956 | 1. 00 55. 05 |
| | ATOM | 1691 | NH2 | ARG | 250 | 18. 063 | 36. 962 | 50. 885 | 1. 00 54. 32 |
| | ATOM | 1692 | C | ARG | 250 | 14. 905 | 32. 812 | 45. 359 | 1. 00 38. 25 |
| | ATOM | 1693 | O | ARG | 250 | 13. 681 | 32. 640 | 45. 394 | 1. 00 37. 44 |
| 20 | ATOM | 1694 | N | MET | 251 | 15. 760 | 31. 880 | 44. 932 | 1. 00 33. 58 |
| | ATOM | 1695 | CA | MET | 251 | 15. 352 | 30. 543 | 44. 492 | 1. 00 29. 34 |
| | ATOM | 1696 | CB | MET | 251 | 15. 326 | 30. 471 | 42. 966 | 1. 00 24. 54 |
| | ATOM | 1697 | CG | MET | 251 | 15. 180 | 29. 069 | 42. 379 | 1. 00 17. 89 |
| | ATOM | 1698 | SD | MET | 251 | 14. 994 | 29. 090 | 40. 552 | 1. 00 18. 23 |
| 25 | ATOM | 1699 | CE | MET | 251 | 16. 329 | 28. 087 | 40. 075 | 1. 00 12. 48 |
| | ATOM | 1700 | C | MET | 251 | 16. 316 | 29. 481 | 45. 004 | 1. 00 30. 48 |
| | ATOM | 1701 | O | MET | 251 | 17. 529 | 29. 640 | 44. 895 | 1. 00 31. 49 |
| | ATOM | 1702 | N | CYS | 252 | 15. 775 | 28. 392 | 45. 546 | 1. 00 29. 56 |
| | ATOM | 1703 | CA | CYS | 252 | 16. 599 | 27. 298 | 46. 059 | 1. 00 26. 54 |

- 203 -

| | ATOM | 1704 | CB | CYS | 252 | 15. 710 | 26. 185 | 46. 612 | 1. 00 | 27. 29 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1705 | SG | CYS | 252 | 16. 613 | 24. 659 | 46. 927 | 1. 00 | 29. 14 |
| | ATOM | 1706 | C | CYS | 252 | 17. 492 | 26. 704 | 44. 975 | 1. 00 | 23. 38 |
| | ATOM | 1707 | O | CYS | 252 | 17. 104 | 26. 639 | 43. 816 | 1. 00 | 22. 79 |
| 5 | ATOM | 1708 | N | VAL | 253 | 18. 688 | 26. 268 | 45. 349 | 1. 00 | 20. 80 |
| | ATOM | 1709 | CA | VAL | 253 | 19. 584 | 25. 660 | 44. 377 | 1. 00 | 20. 25 |
| | ATOM | 1710 | CB | VAL | 253 | 20. 740 | 26. 583 | 43. 969 | 1. 00 | 19. 02 |
| | ATOM | 1711 | CG1 | VAL | 253 | 21. 623 | 25. 881 | 42. 936 | 1. 00 | 15. 42 |
| | ATOM | 1712 | CG2 | VAL | 253 | 20. 198 | 27. 866 | 43. 411 | 1. 00 | 19. 77 |
| 10 | ATOM | 1713 | C | VAL | 253 | 20. 191 | 24. 374 | 44. 900 | 1. 00 | 22. 35 |
| | ATOM | 1714 | O | VAL | 253 | 20. 705 | 24. 305 | 46. 023 | 1. 00 | 22. 21 |
| | ATOM | 1715 | N | ASN | 254 | 20. 127 | 23. 352 | 44. 060 | 1. 00 | 24. 23 |
| | ATOM | 1716 | CA | ASN | 254 | 20. 661 | 22. 045 | 44. 390 | 1. 00 | 22. 10 |
| | ATOM | 1717 | CB | ASN | 254 | 19. 860 | 20. 975 | 43. 647 | 1. 00 | 21. 49 |
| 15 | ATOM | 1718 | CG | ASN | 254 | 20. 479 | 19. 604 | 43. 747 | 1. 00 | 22. 93 |
| | ATOM | 1719 | OD1 | ASN | 254 | 21. 074 | 19. 232 | 44. 764 | 1. 00 | 20. 03 |
| | ATOM | 1720 | ND2 | ASN | 254 | 20. 325 | 18. 827 | 42. 687 | 1. 00 | 26. 40 |
| | ATOM | 1721 | C | ASN | 254 | 22. 124 | 22. 046 | 43. 975 | 1. 00 | 19. 26 |
| | ATOM | 1722 | O | ASN | 254 | 22. 454 | 22. 155 | 42. 795 | 1. 00 | 15. 88 |
| 20 | ATOM | 1723 | N | THR | 255 | 23. 001 | 21. 949 | 44. 961 | 1. 00 | 15. 23 |
| | ATOM | 1724 | CA | THR | 255 | 24. 428 | 21. 962 | 44. 691 | 1. 00 | 15. 03 |
| | ATOM | 1725 | CB | THR | 255 | 25. 193 | 22. 217 | 45. 944 | 1. 00 | 13. 56 |
| | ATOM | 1726 | OG1 | THR | 255 | 25. 035 | 21. 087 | 46. 808 | 1. 00 | 14. 56 |
| | ATOM | 1727 | CG2 | THR | 255 | 24. 670 | 23. 458 | 46. 617 | 1. 00 | 14. 18 |
| 25 | ATOM | 1728 | C | THR | 255 | 24. 957 | 20. 665 | 44. 127 | 1. 00 | 15. 21 |
| | ATOM | 1729 | O | THR | 255 | 25. 675 | 20. 647 | 43. 126 | 1. 00 | 12. 07 |
| | ATOM | 1730 | N | GLU | 256 | 24. 594 | 19. 570 | 44. 777 | 1. 00 | 18. 83 |
| | ATOM | 1731 | CA | GLU | 256 | 25. 076 | 18. 268 | 44. 355 | 1. 00 | 22. 28 |
| | ATOM | 1732 | CB | GLU | 256 | 24. 795 | 18. 025 | 42. 876 | 1. 00 | 25. 93 |

- 204 -

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ATOM | 1733 | CG | GLU | 256 | 23.377 | 18.345 | 42.454 | 1.00 31.90 |
| ATOM | 1734 | CD | GLU | 256 | 22.500 | 17.121 | 42.336 | 1.00 34.74 |
| ATOM | 1735 | OE1 | GLU | 256 | 22.191 | 16.510 | 43.386 | 1.00 36.97 |
| ATOM | 1736 | OE2 | GLU | 256 | 22.122 | 16.777 | 41.188 | 1.00 35.26 |
| ATOM | 1737 | C | GLU | 256 | 26.562 | 18.402 | 44.559 | 1.00 21.32 |
| ATOM | 1738 | O | GLU | 256 | 27.359 | 18.032 | 43.701 | 1.00 23.09 |
| ATOM | 1739 | N | TRP | 257 | 26.931 | 18.966 | 45.699 | 1.00 17.36 |
| ATOM | 1740 | CA | TRP | 257 | 28.327 | 19.141 | 45.985 | 1.00 14.83 |
| ATOM | 1741 | CB | TRP | 257 | 28.514 | 20.074 | 47.176 | 1.00 11.59 |
| ATOM | 1742 | CG | TRP | 257 | 28.038 | 19.561 | 48.478 | 1.00 8.69 |
| ATOM | 1743 | CD2 | TRP | 257 | 27.830 | 20.332 | 49.676 | 1.00 9.05 |
| ATOM | 1744 | CE2 | TRP | 257 | 27.562 | 19.410 | 50.715 | 1.00 7.00 |
| ATOM | 1745 | CE3 | TRP | 257 | 27.845 | 21.703 | 49.964 | 1.00 7.18 |
| ATOM | 1746 | CD1 | TRP | 257 | 27.881 | 18.265 | 48.827 | 1.00 7.58 |
| ATOM | 1747 | NE1 | TRP | 257 | 27.602 | 18.163 | 50.172 | 1.00 7.99 |
| ATOM | 1748 | CZ2 | TRP | 257 | 27.325 | 19.818 | 52.038 | 1.00 4.73 |
| ATOM | 1749 | CZ3 | TRP | 257 | 27.605 | 22.108 | 51.280 | 1.00 7.12 |
| ATOM | 1750 | CH2 | TRP | 257 | 27.346 | 21.164 | 52.300 | 1.00 5.47 |
| ATOM | 1751 | C | TRP | 257 | 29.033 | 17.813 | 46.224 | 1.00 17.81 |
| ATOM | 1752 | O | TRP | 257 | 30.221 | 17.776 | 46.523 | 1.00 19.44 |
| ATOM | 1753 | N | GLY | 258 | 28.318 | 16.708 | 46.099 | 1.00 21.88 |
| ATOM | 1754 | CA | GLY | 258 | 28.991 | 15.444 | 46.303 | 1.00 23.25 |
| ATOM | 1755 | C | GLY | 258 | 30.137 | 15.303 | 45.316 | 1.00 23.01 |
| ATOM | 1756 | O | GLY | 258 | 31.133 | 14.629 | 45.600 | 1.00 21.92 |
| ATOM | 1757 | N | ALA | 259 | 29.997 | 15.943 | 44.156 | 1.00 23.11 |
| ATOM | 1758 | CA | ALA | 259 | 31.015 | 15.863 | 43.113 | 1.00 27.74 |
| ATOM | 1759 | CB | ALA | 259 | 30.400 | 16.139 | 41.766 | 1.00 27.03 |
| ATOM | 1760 | C | ALA | 259 | 32.176 | 16.806 | 43.335 | 1.00 30.23 |
| ATOM | 1761 | O | ALA | 259 | 33.178 | 16.748 | 42.622 | 1.00 32.12 |

- 205 -

|      | ATOM | 1762 | N   | PHE 260 | 32. 041 | 17. 680 | 44. 320 | 1. 00 | 32. 43 |
|------|------|------|-----|---------|---------|---------|---------|-------|--------|
|      | ATOM | 1763 | CA  | PHE 260 | 33. 093 | 18. 627 | 44. 611 | 1. 00 | 36. 43 |
|      | ATOM | 1764 | CB  | PHE 260 | 32. 804 | 19. 343 | 45. 924 | 1. 00 | 39. 42 |
|      | ATOM | 1765 | CG  | PHE 260 | 33. 932 | 20. 206 | 46. 411 | 1. 00 | 43. 92 |
| 5    | ATOM | 1766 | CD1 | PHE 260 | 34. 660 | 21. 003 | 45. 534 | 1. 00 | 46. 49 |
|      | ATOM | 1767 | CD2 | PHE 260 | 34. 232 | 20. 263 | 47. 765 | 1. 00 | 45. 64 |
|      | ATOM | 1768 | CE1 | PHE 260 | 35. 672 | 21. 835 | 46. 002 | 1. 00 | 47. 73 |
|      | ATOM | 1769 | CE2 | PHE 260 | 35. 242 | 21. 093 | 48. 242 | 1. 00 | 46. 62 |
|      | ATOM | 1770 | CZ  | PHE 260 | 35. 958 | 21. 882 | 47. 360 | 1. 00 | 47. 27 |
| 10   | ATOM | 1771 | C   | PHE 260 | 34. 412 | 17. 897 | 44. 695 | 1. 00 | 39. 39 |
|      | ATOM | 1772 | O   | PHE 260 | 34. 495 | 16. 800 | 45. 243 | 1. 00 | 40. 20 |
|      | ATOM | 1773 | N   | GLY 261 | 35. 441 | 18. 511 | 44. 127 | 1. 00 | 41. 71 |
|      | ATOM | 1774 | CA  | GLY 261 | 36. 753 | 17. 911 | 44. 152 | 1. 00 | 43. 62 |
|      | ATOM | 1775 | C   | GLY 261 | 36. 967 | 16. 857 | 43. 090 | 1. 00 | 44. 99 |
| 15   | ATOM | 1776 | O   | GLY 261 | 38. 049 | 16. 282 | 43. 015 | 1. 00 | 47. 22 |
|      | ATOM | 1777 | N   | ASP 262 | 35. 961 | 16. 578 | 42. 270 | 1. 00 | 46. 06 |
|      | ATOM | 1778 | CA  | ASP 262 | 36. 143 | 15. 574 | 41. 229 | 1. 00 | 47. 68 |
|      | ATOM | 1779 | CB  | ASP 262 | 34. 800 | 15. 197 | 40. 602 | 1. 00 | 50. 82 |
|      | ATOM | 1780 | CG  | ASP 262 | 34. 024 | 14. 187 | 41. 445 | 1. 00 | 53. 64 |
| 20   | ATOM | 1781 | OD1 | ASP 262 | 32. 815 | 13. 996 | 41. 191 | 1. 00 | 54. 63 |
|      | ATOM | 1782 | OD2 | ASP 262 | 34. 624 | 13. 578 | 42. 356 | 1. 00 | 54. 71 |
|      | ATOM | 1783 | C   | ASP 262 | 37. 089 | 16. 129 | 40. 177 | 1. 00 | 47. 19 |
|      | ATOM | 1784 | O   | ASP 262 | 37. 539 | 15. 400 | 39. 292 | 1. 00 | 47. 09 |
|      | ATOM | 1785 | N   | SER 263 | 37. 380 | 17. 427 | 40. 298 | 1. 00 | 46. 38 |
| 25   | ATOM | 1786 | CA  | SER 263 | 38. 289 | 18. 147 | 39. 401 | 1. 00 | 44. 53 |
|      | ATOM | 1787 | CB  | SER 263 | 37. 651 | 19. 445 | 38. 903 | 1. 00 | 43. 57 |
|      | ATOM | 1788 | OG  | SER 263 | 36. 341 | 19. 246 | 38. 415 | 1. 00 | 43. 79 |
|      | ATOM | 1789 | C   | SER 263 | 39. 552 | 18. 513 | 40. 174 | 1. 00 | 43. 93 |
|      | ATOM | 1790 | O   | SER 263 | 40. 061 | 19. 632 | 40. 059 | 1. 00 | 44. 40 |

- 206 -

| ATOM | 1791 | N   | GLY 264 | 40.039 | 17.577 | 40.979 | 1.00 | 43.71 |
|------|------|-----|---------|--------|--------|--------|------|-------|
| ATOM | 1792 | CA  | GLY 264 | 41.235 | 17.825 | 41.762 | 1.00 | 42.64 |
| ATOM | 1793 | C   | GLY 264 | 41.133 | 18.889 | 42.845 | 1.00 | 40.75 |
| ATOM | 1794 | O   | GLY 264 | 42.052 | 19.012 | 43.648 | 1.00 | 42.90 |
| ATOM | 1795 | N   | GLU 265 | 40.040 | 19.647 | 42.887 | 1.00 | 38.43 |
| ATOM | 1796 | CA  | GLU 265 | 39.881 | 20.700 | 43.893 | 1.00 | 37.42 |
| ATOM | 1797 | CB  | GLU 265 | 38.437 | 21.227 | 43.907 | 1.00 | 39.11 |
| ATOM | 1798 | CG  | GLU 265 | 37.986 | 21.928 | 42.632 | 1.00 | 40.76 |
| ATOM | 1799 | CD  | GLU 265 | 37.198 | 21.023 | 41.701 | 1.00 | 43.56 |
| ATOM | 1800 | OE1 | GLU 265 | 36.904 | 21.461 | 40.565 | 1.00 | 45.26 |
| ATOM | 1801 | OE2 | GLU 265 | 36.863 | 19.883 | 42.099 | 1.00 | 42.42 |
| ATOM | 1802 | C   | GLU 265 | 40.266 | 20.299 | 45.321 | 1.00 | 36.38 |
| ATOM | 1803 | O   | GLU 265 | 40.410 | 21.160 | 46.185 | 1.00 | 33.59 |
| ATOM | 1804 | N   | LEU 266 | 40.425 | 19.004 | 45.573 | 1.00 | 37.71 |
| ATOM | 1805 | CA  | LEU 266 | 40.783 | 18.534 | 46.912 | 1.00 | 40.56 |
| ATOM | 1806 | CB  | LEU 266 | 39.597 | 17.831 | 47.567 | 1.00 | 40.03 |
| ATOM | 1807 | CG  | LEU 266 | 38.371 | 18.631 | 48.001 | 1.00 | 40.79 |
| ATOM | 1808 | CD1 | LEU 266 | 37.234 | 17.673 | 48.259 | 1.00 | 40.27 |
| ATOM | 1809 | CD2 | LEU 266 | 38.677 | 19.432 | 49.253 | 1.00 | 41.81 |
| ATOM | 1810 | C   | LEU 266 | 41.949 | 17.563 | 46.880 | 1.00 | 43.51 |
| ATOM | 1811 | O   | LEU 266 | 42.363 | 17.045 | 47.919 | 1.00 | 43.63 |
| ATOM | 1812 | N   | ASP 267 | 42.475 | 17.324 | 45.682 | 1.00 | 47.00 |
| ATOM | 1813 | CA  | ASP 267 | 43.584 | 16.393 | 45.480 | 1.00 | 48.18 |
| ATOM | 1814 | CB  | ASP 267 | 44.222 | 16.622 | 44.097 | 1.00 | 50.89 |
| ATOM | 1815 | CG  | ASP 267 | 44.982 | 15.391 | 43.584 | 1.00 | 54.98 |
| ATOM | 1816 | OD1 | ASP 267 | 45.239 | 15.317 | 42.360 | 1.00 | 56.65 |
| ATOM | 1817 | OD2 | ASP 267 | 45.328 | 14.499 | 44.398 | 1.00 | 55.43 |
| ATOM | 1818 | C   | ASP 267 | 44.659 | 16.440 | 46.571 | 1.00 | 46.46 |
| ATOM | 1819 | O   | ASP 267 | 45.205 | 15.397 | 46.960 | 1.00 | 45.37 |

- 207 -

|  | ATOM | 1820 | N | GLU 268 | 44. 957 | 17. 630 | 47. 084 | 1. 00 | 44. 63 |
|---|------|------|------|---------|---------|---------|---------|-------|--------|
|  | ATOM | 1821 | CA | GLU 268 | 45. 990 | 17. 721 | 48. 109 | 1. 00 | 44. 67 |
|  | ATOM | 1822 | CB | GLU 268 | 46. 805 | 19. 024 | 47. 956 | 1. 00 | 44. 68 |
|  | ATOM | 1823 | CG | GLU 268 | 46. 508 | 20. 163 | 48. 934 | 1. 00 | 43. 60 |
| 5 | ATOM | 1824 | CD | GLU 268 | 45. 234 | 20. 915 | 48. 613 | 1. 00 | 43. 53 |
|  | ATOM | 1825 | OE1 | GLU 268 | 45. 020 | 21. 258 | 47. 423 | 1. 00 | 42. 43 |
|  | ATOM | 1826 | OE2 | GLU 268 | 44. 461 | 21. 174 | 49. 561 | 1. 00 | 40. 84 |
|  | ATOM | 1827 | C | GLU 268 | 45. 457 | 17. 569 | 49. 528 | 1. 00 | 43. 45 |
|  | ATOM | 1828 | O | GLU 268 | 46. 102 | 17. 961 | 50. 499 | 1. 00 | 46. 29 |
| 10 | ATOM | 1829 | N | PHE 269 | 44. 286 | 16. 971 | 49. 656 | 1. 00 | 38. 78 |
|  | ATOM | 1830 | CA | PHE 269 | 43. 729 | 16. 785 | 50. 974 | 1. 00 | 33. 75 |
|  | ATOM | 1831 | CB | PHE 269 | 42. 480 | 17. 614 | 51. 135 | 1. 00 | 33. 69 |
|  | ATOM | 1832 | CG | PHE 269 | 42. 733 | 18. 990 | 51. 639 | 1. 00 | 34. 75 |
|  | ATOM | 1833 | CD1 | PHE 269 | 43. 435 | 19. 193 | 52. 822 | 1. 00 | 36. 51 |
| 15 | ATOM | 1834 | CD2 | PHE 269 | 42. 161 | 20. 079 | 51. 001 | 1. 00 | 34. 78 |
|  | ATOM | 1835 | CE1 | PHE 269 | 43. 548 | 20. 469 | 53. 365 | 1. 00 | 37. 39 |
|  | ATOM | 1836 | CE2 | PHE 269 | 42. 266 | 21. 354 | 51. 532 | 1. 00 | 35. 15 |
|  | ATOM | 1837 | CZ | PHE 269 | 42. 955 | 21. 551 | 52. 717 | 1. 00 | 37. 68 |
|  | ATOM | 1838 | C | PHE 269 | 43. 405 | 15. 343 | 51. 225 | 1. 00 | 32. 83 |
| 20 | ATOM | 1839 | O | PHE 269 | 43. 206 | 14. 952 | 52. 365 | 1. 00 | 31. 85 |
|  | ATOM | 1840 | N | LEU 270 | 43. 355 | 14. 555 | 50. 157 | 1. 00 | 33. 85 |
|  | ATOM | 1841 | CA | LEU 270 | 43. 046 | 13. 130 | 50. 259 | 1. 00 | 34. 53 |
|  | ATOM | 1842 | CB | LEU 270 | 42. 712 | 12. 553 | 48. 884 | 1. 00 | 35. 63 |
|  | ATOM | 1843 | CG | LEU 270 | 41. 326 | 12. 857 | 48. 321 | 1. 00 | 37. 61 |
| 25 | ATOM | 1844 | CD1 | LEU 270 | 41. 323 | 14. 293 | 47. 842 | 1. 00 | 35. 85 |
|  | ATOM | 1845 | CD2 | LEU 270 | 40. 966 | 11. 878 | 47. 177 | 1. 00 | 37. 50 |
|  | ATOM | 1846 | C | LEU 270 | 44. 172 | 12. 298 | 50. 845 | 1. 00 | 33. 68 |
|  | ATOM | 1847 | O | LEU 270 | 45. 334 | 12. 640 | 50. 695 | 1. 00 | 35. 64 |
|  | ATOM | 1848 | N | LEU 271 | 43. 829 | 11. 200 | 51. 507 | 1. 00 | 33. 66 |

- 208 -

|   | ATOM | 1849 | CA | LEU 271 | 44.850 | 10.324 | 52.059 | 1.00 | 34.55 |
|---|------|------|-----|---------|--------|--------|--------|------|-------|
|   | ATOM | 1850 | CB | LEU 271 | 44.610 | 10.032 | 53.519 | 1.00 | 30.63 |
|   | ATOM | 1851 | CG | LEU 271 | 44.870 | 11.238 | 54.383 | 1.00 | 29.49 |
|   | ATOM | 1852 | CD1 | LEU 271 | 43.855 | 12.324 | 54.075 | 1.00 | 27.82 |
| 5 | ATOM | 1853 | CD2 | LEU 271 | 44.783 | 10.798 | 55.824 | 1.00 | 31.04 |
|   | ATOM | 1854 | C | LEU 271 | 44.884 | 9.010 | 51.324 | 1.00 | 37.04 |
|   | ATOM | 1855 | O | LEU 271 | 44.009 | 8.715 | 50.513 | 1.00 | 36.79 |
|   | ATOM | 1856 | N | GLU 272 | 45.890 | 8.209 | 51.638 | 1.00 | 40.66 |
|   | ATOM | 1857 | CA | GLU 272 | 46.052 | 6.927 | 50.989 | 1.00 | 44.99 |
| 10 | ATOM | 1858 | CB | GLU 272 | 47.256 | 6.182 | 51.590 | 1.00 | 51.18 |
|   | ATOM | 1859 | CG | GLU 272 | 47.124 | 5.781 | 53.075 | 1.00 | 58.46 |
|   | ATOM | 1860 | CD | GLU 272 | 48.371 | 5.077 | 53.641 | 1.00 | 62.56 |
|   | ATOM | 1861 | OE1 | GLU 272 | 49.393 | 5.772 | 53.876 | 1.00 | 64.96 |
|   | ATOM | 1862 | OE2 | GLU 272 | 48.325 | 3.835 | 53.849 | 1.00 | 61.73 |
| 15 | ATOM | 1863 | C | GLU 272 | 44.789 | 6.080 | 51.092 | 1.00 | 44.62 |
|   | ATOM | 1864 | O | GLU 272 | 44.377 | 5.452 | 50.116 | 1.00 | 44.50 |
|   | ATOM | 1865 | N | TYR 273 | 44.163 | 6.079 | 52.266 | 1.00 | 43.42 |
|   | ATOM | 1866 | CA | TYR 273 | 42.955 | 5.284 | 52.486 | 1.00 | 40.23 |
|   | ATOM | 1867 | CB | TYR 273 | 42.537 | 5.377 | 53.958 | 1.00 | 38.82 |
| 20 | ATOM | 1868 | CG | TYR 273 | 43.709 | 5.401 | 54.923 | 1.00 | 36.38 |
|   | ATOM | 1869 | CD1 | TYR 273 | 44.126 | 6.602 | 55.505 | 1.00 | 35.57 |
|   | ATOM | 1870 | CE1 | TYR 273 | 45.210 | 6.647 | 56.380 | 1.00 | 34.95 |
|   | ATOM | 1871 | CD2 | TYR 273 | 44.413 | 4.231 | 55.243 | 1.00 | 35.34 |
|   | ATOM | 1872 | CE2 | TYR 273 | 45.509 | 4.264 | 56.122 | 1.00 | 34.05 |
| 25 | ATOM | 1873 | CZ | TYR 273 | 45.897 | 5.481 | 56.685 | 1.00 | 34.66 |
|   | ATOM | 1874 | OH | TYR 273 | 46.966 | 5.556 | 57.550 | 1.00 | 33.77 |
|   | ATOM | 1875 | C | TYR 273 | 41.826 | 5.749 | 51.567 | 1.00 | 38.50 |
|   | ATOM | 1876 | O | TYR 273 | 41.264 | 4.967 | 50.804 | 1.00 | 35.21 |
|   | ATOM | 1877 | N | ASP 274 | 41.507 | 7.030 | 51.638 | 1.00 | 38.17 |

- 209 -

| | ATOM | 1878 | CA | ASP | 274 | 40. 473 | 7. 579 | 50. 796 | 1. 00 | 40. 03 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1879 | CB | ASP | 274 | 40. 470 | 9. 083 | 50. 929 | 1. 00 | 41. 17 |
| | ATOM | 1880 | CG | ASP | 274 | 40. 252 | 9. 512 | 52. 341 | 1. 00 | 43. 77 |
| | ATOM | 1881 | OD1 | ASP | 274 | 39. 123 | 9. 327 | 52. 839 | 1. 00 | 46. 59 |
| 5 | ATOM | 1882 | OD2 | ASP | 274 | 41. 212 | 10. 010 | 52. 958 | 1. 00 | 44. 41 |
| | ATOM | 1883 | C | ASP | 274 | 40. 740 | 7. 200 | 49. 359 | 1. 00 | 40. 92 |
| | ATOM | 1884 | O | ASP | 274 | 39. 819 | 6. 937 | 48. 595 | 1. 00 | 41. 41 |
| | ATOM | 1885 | N | ARG | 275 | 42. 007 | 7. 160 | 48. 984 | 1. 00 | 42. 93 |
| | ATOM | 1886 | CA | ARG | 275 | 42. 333 | 6. 819 | 47. 613 | 1. 00 | 45. 81 |
| 10 | ATOM | 1887 | CB | ARG | 275 | 43. 831 | 6. 993 | 47. 365 | 1. 00 | 49. 53 |
| | ATOM | 1888 | CG | ARG | 275 | 44. 191 | 7. 563 | 45. 995 | 1. 00 | 53. 24 |
| | ATOM | 1889 | CD | ARG | 275 | 45. 702 | 7. 772 | 45. 886 | 1. 00 | 58. 85 |
| | ATOM | 1890 | NE | ARG | 275 | 46. 213 | 8. 663 | 46. 933 | 1. 00 | 62. 67 |
| | ATOM | 1891 | CZ | ARG | 275 | 47. 088 | 8. 308 | 47. 876 | 1. 00 | 62. 82 |
| 15 | ATOM | 1892 | NH1 | ARG | 275 | 47. 571 | 7. 068 | 47. 922 | 1. 00 | 61. 28 |
| | ATOM | 1893 | NH2 | ARG | 275 | 47. 476 | 9. 201 | 48. 777 | 1. 00 | 61. 64 |
| | ATOM | 1894 | C | ARG | 275 | 41. 901 | 5. 390 | 47. 316 | 1. 00 | 46. 01 |
| | ATOM | 1895 | O | ARG | 275 | 41. 134 | 5. 160 | 46. 382 | 1. 00 | 45. 19 |
| | ATOM | 1896 | N | LEU | 276 | 42. 382 | 4. 437 | 48. 113 | 1. 00 | 47. 51 |
| 20 | ATOM | 1897 | CA | LEU | 276 | 42. 026 | 3. 030 | 47. 922 | 1. 00 | 48. 68 |
| | ATOM | 1898 | CB | LEU | 276 | 42. 460 | 2. 197 | 49. 134 | 1. 00 | 45. 63 |
| | ATOM | 1899 | CG | LEU | 276 | 43. 971 | 1. 999 | 49. 287 | 1. 00 | 43. 28 |
| | ATOM | 1900 | CD1 | LEU | 276 | 44. 418 | 2. 379 | 50. 686 | 1. 00 | 42. 53 |
| | ATOM | 1901 | CD2 | LEU | 276 | 44. 321 | 0. 557 | 48. 994 | 1. 00 | 42. 97 |
| 25 | ATOM | 1902 | C | LEU | 276 | 40. 520 | 2. 915 | 47. 718 | 1. 00 | 51. 24 |
| | ATOM | 1903 | O | LEU | 276 | 40. 050 | 2. 133 | 46. 891 | 1. 00 | 52. 38 |
| | ATOM | 1904 | N | VAL | 277 | 39. 772 | 3. 710 | 48. 475 | 1. 00 | 53. 11 |
| | ATOM | 1905 | CA | VAL | 277 | 38. 321 | 3. 722 | 48. 372 | 1. 00 | 54. 05 |
| | ATOM | 1906 | CB | VAL | 277 | 37. 703 | 4. 640 | 49. 423 | 1. 00 | 52. 84 |

- 210 -

| | ATOM | 1907 | CG1 | VAL | 277 | 36. 210 | 4. 682 | 49. 249 | 1. 00 | 52. 71 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 1908 | CG2 | VAL | 277 | 38. 069 | 4. 156 | 50. 804 | 1. 00 | 54. 87 |
| | ATOM | 1909 | C | VAL | 277 | 37. 906 | 4. 231 | 46. 999 | 1. 00 | 55. 80 |
| | ATOM | 1910 | O | VAL | 277 | 37. 381 | 3. 474 | 46. 185 | 1. 00 | 57. 15 |
| 5 | ATOM | 1911 | N | ASP | 278 | 38. 146 | 5. 518 | 46. 754 | 1. 00 | 56. 71 |
| | ATOM | 1912 | CA | ASP | 278 | 37. 804 | 6. 146 | 45. 481 | 1. 00 | 57. 65 |
| | ATOM | 1913 | CB | ASP | 278 | 38. 479 | 7. 514 | 45. 353 | 1. 00 | 59. 73 |
| | ATOM | 1914 | CG | ASP | 278 | 38. 243 | 8. 163 | 43. 989 | 1. 00 | 61. 93 |
| | ATOM | 1915 | OD1 | ASP | 278 | 38. 990 | 9. 110 | 43. 642 | 1. 00 | 61. 47 |
| 10 | ATOM | 1916 | OD2 | ASP | 278 | 37. 308 | 7. 733 | 43. 273 | 1. 00 | 62. 11 |
| | ATOM | 1917 | C | ASP | 278 | 38. 263 | 5. 281 | 44. 328 | 1. 00 | 58. 14 |
| | ATOM | 1918 | O | ASP | 278 | 37. 645 | 5. 271 | 43. 266 | 1. 00 | 58. 75 |
| | ATOM | 1919 | N | GLU | 279 | 39. 358 | 4. 563 | 44. 538 | 1. 00 | 58. 33 |
| | ATOM | 1920 | CA | GLU | 279 | 39. 900 | 3. 710 | 43. 498 | 1. 00 | 59. 14 |
| 15 | ATOM | 1921 | CB | GLU | 279 | 41. 437 | 3. 808 | 43. 477 | 1. 00 | 60. 99 |
| | ATOM | 1922 | CG | GLU | 279 | 41. 978 | 5. 219 | 43. 178 | 1. 00 | 61. 92 |
| | ATOM | 1923 | CD | GLU | 279 | 43. 497 | 5. 276 | 43. 014 | 1. 00 | 60. 92 |
| | ATOM | 1924 | OE1 | GLU | 279 | 44. 219 | 4. 874 | 43. 953 | 1. 00 | 60. 85 |
| | ATOM | 1925 | OE2 | GLU | 279 | 43. 965 | 5. 733 | 41. 946 | 1. 00 | 58. 99 |
| 20 | ATOM | 1926 | C | GLU | 279 | 39. 467 | 2. 261 | 43. 664 | 1. 00 | 58. 04 |
| | ATOM | 1927 | O | GLU | 279 | 40. 196 | 1. 346 | 43. 298 | 1. 00 | 59. 38 |
| | ATOM | 1928 | N | SER | 280 | 38. 283 | 2. 044 | 44. 219 | 1. 00 | 57. 21 |
| | ATOM | 1929 | CA | SER | 280 | 37. 798 | 0. 679 | 44. 390 | 1. 00 | 56. 55 |
| | ATOM | 1930 | CB | SER | 280 | 38. 283 | 0. 091 | 45. 719 | 1. 00 | 56. 66 |
| 25 | ATOM | 1931 | OG | SER | 280 | 38. 015 | -1. 298 | 45. 774 | 1. 00 | 54. 41 |
| | ATOM | 1932 | C | SER | 280 | 36. 282 | 0. 671 | 44. 334 | 1. 00 | 55. 29 |
| | ATOM | 1933 | O | SER | 280 | 35. 640 | -0. 371 | 44. 472 | 1. 00 | 53. 68 |
| | ATOM | 1934 | N | SER | 281 | 35. 725 | 1. 854 | 44. 113 | 1. 00 | 54. 58 |
| | ATOM | 1935 | CA | SER | 281 | 34. 288 | 2. 038 | 44. 020 | 1. 00 | 55. 36 |

- 211 -

|      | ATOM | 1936 | CB  | SER | 281 | 33.919 | 3.451  | 44.464 | 1.00 | 56.89 |
|------|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|      | ATOM | 1937 | OG  | SER | 281 | 34.565 | 4.415  | 43.649 | 1.00 | 56.89 |
|      | ATOM | 1938 | C   | SER | 281 | 33.843 | 1.832  | 42.584 | 1.00 | 54.80 |
|      | ATOM | 1939 | O   | SER | 281 | 34.652 | 1.905  | 41.664 | 1.00 | 55.85 |
| 5    | ATOM | 1940 | N   | ALA | 282 | 32.553 | 1.587  | 42.389 | 1.00 | 53.75 |
|      | ATOM | 1941 | CA  | ALA | 282 | 32.025 | 1.379  | 41.050 | 1.00 | 52.42 |
|      | ATOM | 1942 | CB  | ALA | 282 | 30.626 | 0.809  | 41.133 | 1.00 | 52.26 |
|      | ATOM | 1943 | C   | ALA | 282 | 32.012 | 2.679  | 40.250 | 1.00 | 51.83 |
|      | ATOM | 1944 | O   | ALA | 282 | 31.632 | 2.685  | 39.081 | 1.00 | 52.27 |
| 10   | ATOM | 1945 | N   | ASN | 283 | 32.441 | 3.772  | 40.879 | 1.00 | 50.19 |
|      | ATOM | 1946 | CA  | ASN | 283 | 32.465 | 5.089  | 40.239 | 1.00 | 47.37 |
|      | ATOM | 1947 | CB  | ASN | 283 | 31.338 | 5.945  | 40.790 | 1.00 | 47.04 |
|      | ATOM | 1948 | CG  | ASN | 283 | 31.482 | 6.191  | 42.276 | 1.00 | 47.38 |
|      | ATOM | 1949 | OD1 | ASN | 283 | 31.584 | 5.255  | 43.068 | 1.00 | 46.86 |
| 15   | ATOM | 1950 | ND2 | ASN | 283 | 31.497 | 7.455  | 42.662 | 1.00 | 49.96 |
|      | ATOM | 1951 | C   | ASN | 283 | 33.777 | 5.806  | 40.513 | 1.00 | 46.64 |
|      | ATOM | 1952 | O   | ASN | 283 | 33.783 | 6.894  | 41.081 | 1.00 | 48.74 |
|      | ATOM | 1953 | N   | PRO | 284 | 34.905 | 5.214  | 40.110 | 1.00 | 45.15 |
|      | ATOM | 1954 | CD  | PRO | 284 | 35.028 | 3.896  | 39.462 | 1.00 | 44.41 |
| 20   | ATOM | 1955 | CA  | PRO | 284 | 36.227 | 5.814  | 40.327 | 1.00 | 43.24 |
|      | ATOM | 1956 | CB  | PRO | 284 | 37.151 | 4.855  | 39.583 | 1.00 | 44.66 |
|      | ATOM | 1957 | CG  | PRO | 284 | 36.459 | 3.532  | 39.756 | 1.00 | 44.93 |
|      | ATOM | 1958 | C   | PRO | 284 | 36.389 | 7.267  | 39.856 | 1.00 | 41.14 |
|      | ATOM | 1959 | O   | PRO | 284 | 35.978 | 7.624  | 38.755 | 1.00 | 40.17 |
| 25   | ATOM | 1960 | N   | GLY | 285 | 36.994 | 8.099  | 40.695 | 1.00 | 39.45 |
|      | ATOM | 1961 | CA  | GLY | 285 | 37.208 | 9.484  | 40.321 | 1.00 | 40.34 |
|      | ATOM | 1962 | C   | GLY | 285 | 35.964 | 10.343 | 40.401 | 1.00 | 42.06 |
|      | ATOM | 1963 | O   | GLY | 285 | 36.035 | 11.576 | 40.367 | 1.00 | 43.11 |
|      | ATOM | 1964 | N   | GLN | 286 | 34.811 | 9.699  | 40.510 | 1.00 | 42.34 |

- 212 -

|  | ATOM | 1965 | CA | GLN | 286 | 33. 555 | 10. 427 | 40. 601 | 1. 00 | 41. 88 |
|---|------|------|----|-----|-----|---------|---------|---------|-------|--------|
|  | ATOM | 1966 | CB | GLN | 286 | 32. 490 | 9. 717 | 39. 758 | 1. 00 | 44. 97 |
|  | ATOM | 1967 | CG | GLN | 286 | 31. 973 | 10. 544 | 38. 588 | 1. 00 | 49. 89 |
|  | ATOM | 1968 | CD | GLN | 286 | 31. 043 | 11. 668 | 39. 043 | 1. 00 | 54. 72 |
| 5 | ATOM | 1969 | OE1 | GLN | 286 | 29. 911 | 11. 419 | 39. 483 | 1. 00 | 56. 09 |
|  | ATOM | 1970 | NE2 | GLN | 286 | 31. 519 | 12. 911 | 38. 950 | 1. 00 | 54. 20 |
|  | ATOM | 1971 | C | GLN | 286 | 33. 113 | 10. 541 | 42. 063 | 1. 00 | 40. 59 |
|  | ATOM | 1972 | O | GLN | 286 | 33. 396 | 9. 660 | 42. 879 | 1. 00 | 39. 39 |
|  | ATOM | 1973 | N | GLN | 287 | 32. 445 | 11. 648 | 42. 389 | 1. 00 | 39. 59 |
| 10 | ATOM | 1974 | CA | GLN | 287 | 31. 939 | 11. 913 | 43. 741 | 1. 00 | 38. 06 |
|  | ATOM | 1975 | CB | GLN | 287 | 30. 770 | 10. 969 | 44. 053 | 1. 00 | 37. 29 |
|  | ATOM | 1976 | CG | GLN | 287 | 29. 732 | 10. 837 | 42. 939 | 1. 00 | 35. 04 |
|  | ATOM | 1977 | CD | GLN | 287 | 28. 912 | 12. 100 | 42. 736 | 1. 00 | 33. 74 |
|  | ATOM | 1978 | OE1 | GLN | 287 | 28. 906 | 12. 692 | 41. 647 | 1. 00 | 28. 89 |
| 15 | ATOM | 1979 | NE2 | GLN | 287 | 28. 204 | 12. 514 | 43. 786 | 1. 00 | 31. 49 |
|  | ATOM | 1980 | C | GLN | 287 | 33. 015 | 11. 744 | 44. 820 | 1. 00 | 37. 30 |
|  | ATOM | 1981 | O | GLN | 287 | 32. 958 | 10. 813 | 45. 624 | 1. 00 | 37. 53 |
|  | ATOM | 1982 | N | LEU | 288 | 33. 990 | 12. 643 | 44. 856 | 1. 00 | 34. 03 |
|  | ATOM | 1983 | CA | LEU | 288 | 35. 051 | 12. 516 | 45. 844 | 1. 00 | 29. 84 |
| 20 | ATOM | 1984 | CB | LEU | 288 | 36. 351 | 13. 071 | 45. 293 | 1. 00 | 30. 50 |
|  | ATOM | 1985 | CG | LEU | 288 | 37. 285 | 11. 960 | 44. 819 | 1. 00 | 32. 69 |
|  | ATOM | 1986 | CD1 | LEU | 288 | 36. 645 | 11. 102 | 43. 728 | 1. 00 | 31. 90 |
|  | ATOM | 1987 | CD2 | LEU | 288 | 38. 546 | 12. 611 | 44. 323 | 1. 00 | 36. 00 |
|  | ATOM | 1988 | C | LEU | 288 | 34. 729 | 13. 180 | 47. 156 | 1. 00 | 26. 53 |
| 25 | ATOM | 1989 | O | LEU | 288 | 34. 991 | 12. 627 | 48. 218 | 1. 00 | 26. 76 |
|  | ATOM | 1990 | N | TYR | 289 | 34. 172 | 14. 374 | 47. 086 | 1. 00 | 23. 58 |
|  | ATOM | 1991 | CA | TYR | 289 | 33. 809 | 15. 074 | 48. 292 | 1. 00 | 22. 36 |
|  | ATOM | 1992 | CB | TYR | 289 | 33. 086 | 16. 365 | 47. 939 | 1. 00 | 20. 16 |
|  | ATOM | 1993 | CG | TYR | 289 | 32. 716 | 17. 186 | 49. 136 | 1. 00 | 18. 61 |

- 213 -

|   | ATOM | 1994 | CD1 | TYR | 289 | 33.660 | 17.486 | 50.105 | 1.00 | 18.65 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 1995 | CE1 | TYR | 289 | 33.347 | 18.269 | 51.195 | 1.00 | 18.34 |
|   | ATOM | 1996 | CD2 | TYR | 289 | 31.433 | 17.693 | 49.288 | 1.00 | 18.91 |
|   | ATOM | 1997 | CE2 | TYR | 289 | 31.105 | 18.484 | 50.378 | 1.00 | 18.97 |
| 5 | ATOM | 1998 | CZ | TYR | 289 | 32.073 | 18.768 | 51.327 | 1.00 | 20.15 |
|   | ATOM | 1999 | OH | TYR | 289 | 31.788 | 19.565 | 52.408 | 1.00 | 22.93 |
|   | ATOM | 2000 | C | TYR | 289 | 32.894 | 14.165 | 49.105 | 1.00 | 25.30 |
|   | ATOM | 2001 | O | TYR | 289 | 32.991 | 14.106 | 50.337 | 1.00 | 24.21 |
|   | ATOM | 2002 | N | GLU | 290 | 32.005 | 13.448 | 48.411 | 1.00 | 27.35 |
| 10 | ATOM | 2003 | CA | GLU | 290 | 31.071 | 12.532 | 49.084 | 1.00 | 26.68 |
|   | ATOM | 2004 | CB | GLU | 290 | 30.081 | 11.904 | 48.090 | 1.00 | 26.17 |
|   | ATOM | 2005 | CG | GLU | 290 | 28.614 | 12.216 | 48.413 | 1.00 | 25.68 |
|   | ATOM | 2006 | CD | GLU | 290 | 27.617 | 11.404 | 47.591 | 1.00 | 26.93 |
|   | ATOM | 2007 | OE1 | GLU | 290 | 27.735 | 11.363 | 46.337 | 1.00 | 22.27 |
| 15 | ATOM | 2008 | OE2 | GLU | 290 | 26.702 | 10.815 | 48.215 | 1.00 | 27.37 |
|   | ATOM | 2009 | C | GLU | 290 | 31.838 | 11.425 | 49.781 | 1.00 | 25.75 |
|   | ATOM | 2010 | O | GLU | 290 | 31.649 | 11.193 | 50.974 | 1.00 | 26.23 |
|   | ATOM | 2011 | N | LYS | 291 | 32.706 | 10.756 | 49.024 | 1.00 | 24.16 |
|   | ATOM | 2012 | CA | LYS | 291 | 33.526 | 9.666 | 49.538 | 1.00 | 24.45 |
| 20 | ATOM | 2013 | CB | LYS | 291 | 34.342 | 9.063 | 48.408 | 1.00 | 24.19 |
|   | ATOM | 2014 | CG | LYS | 291 | 33.506 | 8.383 | 47.354 | 1.00 | 28.37 |
|   | ATOM | 2015 | CD | LYS | 291 | 34.322 | 8.162 | 46.094 | 1.00 | 31.52 |
|   | ATOM | 2016 | CE | LYS | 291 | 33.533 | 7.434 | 45.030 | 1.00 | 31.16 |
|   | ATOM | 2017 | NZ | LYS | 291 | 34.367 | 7.299 | 43.813 | 1.00 | 33.55 |
| 25 | ATOM | 2018 | C | LYS | 291 | 34.460 | 10.143 | 50.636 | 1.00 | 24.99 |
|   | ATOM | 2019 | O | LYS | 291 | 35.488 | 9.522 | 50.918 | 1.00 | 25.78 |
|   | ATOM | 2020 | N | LEU | 292 | 34.095 | 11.254 | 51.255 | 1.00 | 24.20 |
|   | ATOM | 2021 | CA | LEU | 292 | 34.894 | 11.809 | 52.318 | 1.00 | 25.20 |
|   | ATOM | 2022 | CB | LEU | 292 | 35.544 | 13.106 | 51.843 | 1.00 | 25.62 |

- 214 -

| | ATOM | 2023 | CG | LEU | 292 | 36.904 | 13.450 | 52.464 | 1.00 | 26.59 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2024 | CD1 | LEU | 292 | 37.935 | 12.396 | 52.035 | 1.00 | 26.37 |
| | ATOM | 2025 | CD2 | LEU | 292 | 37.343 | 14.853 | 52.025 | 1.00 | 24.08 |
| | ATOM | 2026 | C | LEU | 292 | 33.999 | 12.063 | 53.528 | 1.00 | 26.58 |
| 5 | ATOM | 2027 | O | LEU | 292 | 34.431 | 11.924 | 54.671 | 1.00 | 27.91 |
| | ATOM | 2028 | N | ILE | 293 | 32.744 | 12.421 | 53.272 | 1.00 | 27.03 |
| | ATOM | 2029 | CA | ILE | 293 | 31.783 | 12.689 | 54.342 | 1.00 | 26.01 |
| | ATOM | 2030 | CB | ILE | 293 | 30.948 | 13.956 | 54.019 | 1.00 | 26.42 |
| | ATOM | 2031 | CG2 | ILE | 293 | 30.184 | 14.431 | 55.247 | 1.00 | 25.08 |
| 10 | ATOM | 2032 | CG1 | ILE | 293 | 31.866 | 15.085 | 53.573 | 1.00 | 24.53 |
| | ATOM | 2033 | CD1 | ILE | 293 | 31.131 | 16.366 | 53.336 | 1.00 | 23.77 |
| | ATOM | 2034 | C | ILE | 293 | 30.827 | 11.503 | 54.489 | 1.00 | 24.65 |
| | ATOM | 2035 | O | ILE | 293 | 30.681 | 10.919 | 55.565 | 1.00 | 23.84 |
| | ATOM | 2036 | N | GLY | 294 | 30.197 | 11.159 | 53.374 | 1.00 | 24.02 |
| 15 | ATOM | 2037 | CA | GLY | 294 | 29.237 | 10.073 | 53.325 | 1.00 | 25.49 |
| | ATOM | 2038 | C | GLY | 294 | 29.454 | 8.815 | 54.142 | 1.00 | 24.75 |
| | ATOM | 2039 | O | GLY | 294 | 30.427 | 8.079 | 53.953 | 1.00 | 26.25 |
| | ATOM | 2040 | N | GLY | 295 | 28.517 | 8.556 | 55.044 | 1.00 | 22.54 |
| | ATOM | 2041 | CA | GLY | 295 | 28.607 | 7.369 | 55.851 | 1.00 | 22.80 |
| 20 | ATOM | 2042 | C | GLY | 295 | 28.530 | 6.125 | 54.986 | 1.00 | 25.08 |
| | ATOM | 2043 | O | GLY | 295 | 28.252 | 5.047 | 55.497 | 1.00 | 27.80 |
| | ATOM | 2044 | N | LYS | 296 | 28.748 | 6.238 | 53.680 | 1.00 | 25.43 |
| | ATOM | 2045 | CA | LYS | 296 | 28.696 | 5.039 | 52.849 | 1.00 | 25.87 |
| | ATOM | 2046 | CB | LYS | 296 | 28.313 | 5.354 | 51.411 | 1.00 | 27.04 |
| 25 | ATOM | 2047 | CG | LYS | 296 | 28.036 | 4.096 | 50.587 | 1.00 | 30.40 |
| | ATOM | 2048 | CD | LYS | 296 | 29.249 | 3.562 | 49.842 | 1.00 | 30.20 |
| | ATOM | 2049 | CE | LYS | 296 | 28.954 | 2.204 | 49.176 | 1.00 | 32.59 |
| | ATOM | 2050 | NZ | LYS | 296 | 29.015 | 1.038 | 50.135 | 1.00 | 32.31 |
| | ATOM | 2051 | C | LYS | 296 | 30.044 | 4.364 | 52.828 | 1.00 | 28.34 |

- 215 -

| | ATOM | 2052 | O | LYS | 296 | 30.158 | 3.185 | 52.507 | 1.00 | 29.08 |
|---|------|------|-----|-----|-----|--------|-------|--------|------|-------|
| | ATOM | 2053 | N | TYR | 297 | 31.075 | 5.122 | 53.163 | 1.00 | 29.56 |
| | ATOM | 2054 | CA | TYR | 297 | 32.414 | 4.582 | 53.147 | 1.00 | 29.25 |
| | ATOM | 2055 | CB | TYR | 297 | 33.208 | 5.230 | 52.022 | 1.00 | 30.07 |
| 5 | ATOM | 2056 | CG | TYR | 297 | 32.620 | 5.025 | 50.650 | 1.00 | 30.84 |
| | ATOM | 2057 | CD1 | TYR | 297 | 32.023 | 6.082 | 49.960 | 1.00 | 32.45 |
| | ATOM | 2058 | CE1 | TYR | 297 | 31.544 | 5.915 | 48.665 | 1.00 | 35.21 |
| | ATOM | 2059 | CD2 | TYR | 297 | 32.715 | 3.789 | 50.015 | 1.00 | 30.51 |
| | ATOM | 2060 | CE2 | TYR | 297 | 32.244 | 3.604 | 48.724 | 1.00 | 34.82 |
| 10 | ATOM | 2061 | CZ | TYR | 297 | 31.661 | 4.673 | 48.049 | 1.00 | 37.82 |
| | ATOM | 2062 | OH | TYR | 297 | 31.219 | 4.504 | 46.753 | 1.00 | 41.74 |
| | ATOM | 2063 | C | TYR | 297 | 33.097 | 4.842 | 54.465 | 1.00 | 27.53 |
| | ATOM | 2064 | O | TYR | 297 | 34.174 | 4.312 | 54.731 | 1.00 | 28.35 |
| | ATOM | 2065 | N | MET | 298 | 32.464 | 5.665 | 55.288 | 1.00 | 24.45 |
| 15 | ATOM | 2066 | CA | MET | 298 | 33.025 | 6.000 | 56.580 | 1.00 | 23.96 |
| | ATOM | 2067 | CB | MET | 298 | 31.959 | 6.652 | 57.454 | 1.00 | 21.69 |
| | ATOM | 2068 | CG | MET | 298 | 32.436 | 6.992 | 58.850 | 1.00 | 20.73 |
| | ATOM | 2069 | SD | MET | 298 | 31.288 | 8.100 | 59.701 | 1.00 | 20.68 |
| | ATOM | 2070 | CE | MET | 298 | 31.435 | 9.523 | 58.620 | 1.00 | 18.32 |
| 20 | ATOM | 2071 | C | MET | 298 | 33.579 | 4.750 | 57.254 | 1.00 | 24.25 |
| | ATOM | 2072 | O | MET | 298 | 34.776 | 4.656 | 57.529 | 1.00 | 24.74 |
| | ATOM | 2073 | N | GLY | 299 | 32.707 | 3.779 | 57.494 | 1.00 | 26.72 |
| | ATOM | 2074 | CA | GLY | 299 | 33.135 | 2.552 | 58.135 | 1.00 | 25.77 |
| | ATOM | 2075 | C | GLY | 299 | 34.301 | 1.906 | 57.424 | 1.00 | 25.50 |
| 25 | ATOM | 2076 | O | GLY | 299 | 35.162 | 1.331 | 58.076 | 1.00 | 26.16 |
| | ATOM | 2077 | N | GLU | 300 | 34.325 | 2.004 | 56.095 | 1.00 | 25.37 |
| | ATOM | 2078 | CA | GLU | 300 | 35.389 | 1.418 | 55.282 | 1.00 | 24.57 |
| | ATOM | 2079 | CB | GLU | 300 | 35.057 | 1.551 | 53.800 | 1.00 | 24.05 |
| | ATOM | 2080 | CG | GLU | 300 | 36.066 | 0.859 | 52.905 | 1.00 | 24.66 |

- 216 -

|  | ATOM | 2081 | CD | GLU | 300 | 36.018 | -0.662 | 53.004 | 1.00 | 24.52 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2082 | OE1 | GLU | 300 | 35.581 | -1.195 | 54.054 | 1.00 | 24.02 |
|  | ATOM | 2083 | OE2 | GLU | 300 | 36.438 | -1.319 | 52.026 | 1.00 | 22.70 |
|  | ATOM | 2084 | C | GLU | 300 | 36.734 | 2.082 | 55.550 | 1.00 | 25.31 |
| 5 | ATOM | 2085 | O | GLU | 300 | 37.769 | 1.408 | 55.663 | 1.00 | 22.71 |
|  | ATOM | 2086 | N | LEU | 301 | 36.712 | 3.409 | 55.622 | 1.00 | 26.47 |
|  | ATOM | 2087 | CA | LEU | 301 | 37.919 | 4.174 | 55.900 | 1.00 | 26.65 |
|  | ATOM | 2088 | CB | LEU | 301 | 37.600 | 5.676 | 55.992 | 1.00 | 26.57 |
|  | ATOM | 2089 | CG | LEU | 301 | 37.165 | 6.395 | 54.701 | 1.00 | 26.02 |
| 10 | ATOM | 2090 | CD1 | LEU | 301 | 36.684 | 7.784 | 55.047 | 1.00 | 27.06 |
|  | ATOM | 2091 | CD2 | LEU | 301 | 38.312 | 6.474 | 53.701 | 1.00 | 25.38 |
|  | ATOM | 2092 | C | LEU | 301 | 38.452 | 3.648 | 57.226 | 1.00 | 26.23 |
|  | ATOM | 2093 | O | LEU | 301 | 39.594 | 3.209 | 57.313 | 1.00 | 26.97 |
|  | ATOM | 2094 | N | VAL | 302 | 37.623 | 3.670 | 58.259 | 1.00 | 26.05 |
| 15 | ATOM | 2095 | CA | VAL | 302 | 38.068 | 3.154 | 59.542 | 1.00 | 27.56 |
|  | ATOM | 2096 | CB | VAL | 302 | 36.911 | 3.034 | 60.524 | 1.00 | 28.13 |
|  | ATOM | 2097 | CG1 | VAL | 302 | 37.354 | 2.285 | 61.777 | 1.00 | 26.62 |
|  | ATOM | 2098 | CG2 | VAL | 302 | 36.433 | 4.424 | 60.882 | 1.00 | 30.95 |
|  | ATOM | 2099 | C | VAL | 302 | 38.723 | 1.786 | 59.386 | 1.00 | 27.42 |
| 20 | ATOM | 2100 | O | VAL | 302 | 39.765 | 1.529 | 59.977 | 1.00 | 29.00 |
|  | ATOM | 2101 | N | ARG | 303 | 38.127 | 0.906 | 58.593 | 1.00 | 25.04 |
|  | ATOM | 2102 | CA | ARG | 303 | 38.723 | -0.395 | 58.417 | 1.00 | 25.12 |
|  | ATOM | 2103 | CB | ARG | 303 | 37.906 | -1.254 | 57.475 | 1.00 | 26.51 |
|  | ATOM | 2104 | CG | ARG | 303 | 38.587 | -2.558 | 57.126 | 1.00 | 28.11 |
| 25 | ATOM | 2105 | CD | ARG | 303 | 37.609 | -3.520 | 56.490 | 1.00 | 31.77 |
|  | ATOM | 2106 | NE | ARG | 303 | 38.260 | -4.456 | 55.583 | 1.00 | 32.46 |
|  | ATOM | 2107 | CZ | ARG | 303 | 38.483 | -4.215 | 54.296 | 1.00 | 34.64 |
|  | ATOM | 2108 | NH1 | ARG | 303 | 38.103 | -3.059 | 53.759 | 1.00 | 33.51 |
|  | ATOM | 2109 | NH2 | ARG | 303 | 39.082 | -5.136 | 53.546 | 1.00 | 35.80 |

- 217 -

| | ATOM | 2110 | C | ARG | 303 | 40.111 | -0.242 | 57.854 | 1.00 | 27.77 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2111 | O | ARG | 303 | 41.073 | -0.788 | 58.401 | 1.00 | 30.47 |
| | ATOM | 2112 | N | LEU | 304 | 40.236 | 0.495 | 56.754 | 1.00 | 27.67 |
| | ATOM | 2113 | CA | LEU | 304 | 41.562 | 0.674 | 56.147 | 1.00 | 24.93 |
| 5 | ATOM | 2114 | CB | LEU | 304 | 41.464 | 1.526 | 54.865 | 1.00 | 22.51 |
| | ATOM | 2115 | CG | LEU | 304 | 40.640 | 0.902 | 53.718 | 1.00 | 19.14 |
| | ATOM | 2116 | CD1 | LEU | 304 | 40.386 | 1.957 | 52.675 | 1.00 | 19.15 |
| | ATOM | 2117 | CD2 | LEU | 304 | 41.352 | -0.295 | 53.105 | 1.00 | 14.45 |
| | ATOM | 2118 | C | LEU | 304 | 42.523 | 1.290 | 57.168 | 1.00 | 21.35 |
| 10 | ATOM | 2119 | O | LEU | 304 | 43.584 | 0.736 | 57.432 | 1.00 | 20.90 |
| | ATOM | 2120 | N | VAL | 305 | 42.142 | 2.406 | 57.770 | 1.00 | 17.52 |
| | ATOM | 2121 | CA | VAL | 305 | 43.003 | 3.011 | 58.758 | 1.00 | 17.43 |
| | ATOM | 2122 | CB | VAL | 305 | 42.316 | 4.162 | 59.423 | 1.00 | 14.40 |
| | ATOM | 2123 | CG1 | VAL | 305 | 43.154 | 4.673 | 60.583 | 1.00 | 14.53 |
| 15 | ATOM | 2124 | CG2 | VAL | 305 | 42.095 | 5.240 | 58.408 | 1.00 | 14.33 |
| | ATOM | 2125 | C | VAL | 305 | 43.400 | 2.010 | 59.829 | 1.00 | 20.92 |
| | ATOM | 2126 | O | VAL | 305 | 44.497 | 2.071 | 60.387 | 1.00 | 22.69 |
| | ATOM | 2127 | N | LEU | 306 | 42.502 | 1.085 | 60.126 | 1.00 | 24.02 |
| | ATOM | 2128 | CA | LEU | 306 | 42.783 | 0.081 | 61.144 | 1.00 | 26.64 |
| 20 | ATOM | 2129 | CB | LEU | 306 | 41.481 | -0.585 | 61.594 | 1.00 | 27.02 |
| | ATOM | 2130 | CG | LEU | 306 | 41.154 | -0.563 | 63.087 | 1.00 | 27.64 |
| | ATOM | 2131 | CD1 | LEU | 306 | 41.094 | 0.873 | 63.592 | 1.00 | 27.51 |
| | ATOM | 2132 | CD2 | LEU | 306 | 39.826 | -1.267 | 63.311 | 1.00 | 28.07 |
| | ATOM | 2133 | C | LEU | 306 | 43.721 | -0.965 | 60.566 | 1.00 | 27.73 |
| 25 | ATOM | 2134 | O | LEU | 306 | 44.745 | -1.303 | 61.157 | 1.00 | 26.86 |
| | ATOM | 2135 | N | LEU | 307 | 43.360 | -1.467 | 59.394 | 1.00 | 28.77 |
| | ATOM | 2136 | CA | LEU | 307 | 44.156 | -2.478 | 58.733 | 1.00 | 32.47 |
| | ATOM | 2137 | CB | LEU | 307 | 43.465 | -2.893 | 57.437 | 1.00 | 29.90 |
| | ATOM | 2138 | CG | LEU | 307 | 43.477 | -4.392 | 57.130 | 1.00 | 29.19 |

- 218 -

| | ATOM | 2139 | CD1 | LEU | 307 | 43. 104 | -5. 210 | 58. 361 | 1. 00 | 28. 38 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2140 | CD2 | LEU | 307 | 42. 495 | -4. 648 | 56. 015 | 1. 00 | 29. 88 |
| | ATOM | 2141 | C | LEU | 307 | 45. 553 | -1. 916 | 58. 466 | 1. 00 | 35. 49 |
| | ATOM | 2142 | O | LEU | 307 | 46. 542 | -2. 645 | 58. 394 | 1. 00 | 36. 50 |
| 5 | ATOM | 2143 | N | ARG | 308 | 45. 622 | -0. 602 | 58. 332 | 1. 00 | 38. 03 |
| | ATOM | 2144 | CA | ARG | 308 | 46. 882 | 0. 080 | 58. 101 | 1. 00 | 41. 29 |
| | ATOM | 2145 | CB | ARG | 308 | 46. 603 | 1. 580 | 57. 936 | 1. 00 | 47. 88 |
| | ATOM | 2146 | CG | ARG | 308 | 47. 706 | 2. 544 | 58. 368 | 1. 00 | 54. 88 |
| | ATOM | 2147 | CD | ARG | 308 | 48. 819 | 2. 693 | 57. 338 | 1. 00 | 60. 14 |
| 10 | ATOM | 2148 | NE | ARG | 308 | 49. 524 | 3. 958 | 57. 540 | 1. 00 | 65. 47 |
| | ATOM | 2149 | CZ | ARG | 308 | 50. 523 | 4. 401 | 56. 784 | 1. 00 | 67. 54 |
| | ATOM | 2150 | NH1 | ARG | 308 | 50. 954 | 3. 673 | 55. 757 | 1. 00 | 68. 57 |
| | ATOM | 2151 | NH2 | ARG | 308 | 51. 074 | 5. 584 | 57. 046 | 1. 00 | 66. 83 |
| | ATOM | 2152 | C | ARG | 308 | 47. 783 | -0. 182 | 59. 301 | 1. 00 | 40. 42 |
| 15 | ATOM | 2153 | O | ARG | 308 | 48. 889 | -0. 694 | 59. 159 | 1. 00 | 40. 04 |
| | ATOM | 2154 | N | LEU | 309 | 47. 287 | 0. 152 | 60. 487 | 1. 00 | 39. 27 |
| | ATOM | 2155 | CA | LEU | 309 | 48. 043 | -0. 027 | 61. 717 | 1. 00 | 38. 92 |
| | ATOM | 2156 | CB | LEU | 309 | 47. 224 | 0. 484 | 62. 895 | 1. 00 | 33. 74 |
| | ATOM | 2157 | CG | LEU | 309 | 46. 852 | 1. 958 | 62. 854 | 1. 00 | 30. 26 |
| 20 | ATOM | 2158 | CD1 | LEU | 309 | 45. 453 | 2. 121 | 63. 368 | 1. 00 | 30. 84 |
| | ATOM | 2159 | CD2 | LEU | 309 | 47. 819 | 2. 766 | 63. 683 | 1. 00 | 27. 57 |
| | ATOM | 2160 | C | LEU | 309 | 48. 461 | -1. 473 | 61. 984 | 1. 00 | 41. 92 |
| | ATOM | 2161 | O | LEU | 309 | 49. 600 | -1. 741 | 62. 364 | 1. 00 | 42. 73 |
| | ATOM | 2162 | N | VAL | 310 | 47. 541 | -2. 406 | 61. 788 | 1. 00 | 44. 59 |
| 25 | ATOM | 2163 | CA | VAL | 310 | 47. 829 | -3. 811 | 62. 039 | 1. 00 | 46. 67 |
| | ATOM | 2164 | CB | VAL | 310 | 46. 606 | -4. 651 | 61. 798 | 1. 00 | 46. 95 |
| | ATOM | 2165 | CG1 | VAL | 310 | 45. 419 | -4. 006 | 62. 479 | 1. 00 | 49. 54 |
| | ATOM | 2166 | CG2 | VAL | 310 | 46. 368 | -4. 779 | 60. 312 | 1. 00 | 47. 77 |
| | ATOM | 2167 | C | VAL | 310 | ·48. 929 | -4. 321 | 61. 139 | 1. 00 | 47. 55 |

- 219 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2168 | O | VAL | 310 | 49.488 | -5.392 | 61.374 | 1.00 48.66 |
| | ATOM | 2169 | N | ASP | 311 | 49.217 | -3.559 | 60.093 | 1.00 48.93 |
| | ATOM | 2170 | CA | ASP | 311 | 50.262 | -3.927 | 59.160 | 1.00 52.04 |
| | ATOM | 2171 | CB | ASP | 311 | 49.993 | -3.298 | 57.793 | 1.00 57.14 |
| 5 | ATOM | 2172 | CG | ASP | 311 | 48.752 | -3.869 | 57.135 | 1.00 61.79 |
| | ATOM | 2173 | OD1 | ASP | 311 | 48.348 | -3.377 | 56.054 | 1.00 63.59 |
| | ATOM | 2174 | OD2 | ASP | 311 | 48.180 | -4.819 | 57.713 | 1.00 63.98 |
| | ATOM | 2175 | C | ASP | 311 | 51.618 | -3.490 | 59.698 | 1.00 51.94 |
| | ATOM | 2176 | O | ASP | 311 | 52.580 | -4.256 | 59.653 | 1.00 53.89 |
| 10 | ATOM | 2177 | N | GLU | 312 | 51.702 | -2.267 | 60.212 | 1.00 49.51 |
| | ATOM | 2178 | CA | GLU | 312 | 52.961 | -1.785 | 60.762 | 1.00 47.68 |
| | ATOM | 2179 | CB | GLU | 312 | 53.071 | -0.272 | 60.632 | 1.00 48.44 |
| | ATOM | 2180 | CG | GLU | 312 | 52.900 | 0.221 | 59.216 | 1.00 51.79 |
| | ATOM | 2181 | CD | GLU | 312 | 53.122 | 1.713 | 59.084 | 1.00 53.56 |
| 15 | ATOM | 2182 | OE1 | GLU | 312 | 52.698 | 2.280 | 58.047 | 1.00 49.90 |
| | ATOM | 2183 | OE2 | GLU | 312 | 53.725 | 2.309 | 60.013 | 1.00 56.82 |
| | ATOM | 2184 | C | GLU | 312 | 53.075 | -2.172 | 62.222 | 1.00 46.11 |
| | ATOM | 2185 | O | GLU | 312 | 53.514 | -1.377 | 63.049 | 1.00 46.75 |
| | ATOM | 2186 | N | ASN | 313 | 52.666 | -3.397 | 62.527 | 1.00 45.02 |
| 20 | ATOM | 2187 | CA | ASN | 313 | 52.720 | -3.938 | 63.879 | 1.00 44.64 |
| | ATOM | 2188 | CB | ASN | 313 | 54.100 | -4.550 | 64.119 | 1.00 43.84 |
| | ATOM | 2189 | CG | ASN | 313 | 54.028 | -5.860 | 64.863 | 1.00 45.16 |
| | ATOM | 2190 | OD1 | ASN | 313 | 53.377 | -5.965 | 65.906 | 1.00 43.79 |
| | ATOM | 2191 | ND2 | ASN | 313 | 54.701 | -6.875 | 64.333 | 1.00 46.05 |
| 25 | ATOM | 2192 | C | ASN | 313 | 52.408 | -2.921 | 64.991 | 1.00 44.49 |
| | ATOM | 2193 | O | ASN | 313 | 53.303 | -2.509 | 65.728 | 1.00 45.19 |
| | ATOM | 2194 | N | LEU | 314 | 51.142 | -2.530 | 65.126 | 1.00 43.02 |
| | ATOM | 2195 | CA | LEU | 314 | 50.743 | -1.563 | 66.159 | 1.00 40.80 |
| | ATOM | 2196 | CB | LEU | 314 | 50.639 | -0.167 | 65.549 | 1.00 34.97 |

- 220 -

| | ATOM | 2197 | CG | LEU | 314 | 51. 940 | 0. 499 | 65. 127 | 1. 00 | 29. 58 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2198 | CD1 | LEU | 314 | 51. 698 | 1. 453 | 63. 981 | 1. 00 | 28. 94 |
| | ATOM | 2199 | CD2 | LEU | 314 | 52. 516 | 1. 212 | 66. 311 | 1. 00 | 28. 16 |
| | ATOM | 2200 | C | LEU | 314 | 49. 396 | -1. 924 | 66. 777 | 1. 00 | 42. 38 |
| 5 | ATOM | 2201 | O | LEU | 314 | 49. 026 | -1. 422 | 67. 848 | 1. 00 | 39. 73 |
| | ATOM | 2202 | N | LEU | 315 | 48. 689 | -2. 812 | 66. 078 | 1. 00 | 44. 49 |
| | ATOM | 2203 | CA | LEU | 315 | 47. 352 | -3. 268 | 66. 439 | 1. 00 | 45. 22 |
| | ATOM | 2204 | CB | LEU | 315 | 46. 354 | -2. 695 | 65. 445 | 1. 00 | 43. 49 |
| | ATOM | 2205 | CG | LEU | 315 | 45. 121 | -2. 063 | 66. 045 | 1. 00 | 43. 28 |
| 10 | ATOM | 2206 | CD1 | LEU | 315 | 44. 055 | -1. 976 | 64. 972 | 1. 00 | 43. 01 |
| | ATOM | 2207 | CD2 | LEU | 315 | 44. 643 | -2. 907 | 67. 209 | 1. 00 | 46. 13 |
| | ATOM | 2208 | C | LEU | 315 | 47. 214 | -4. 781 | 66. 407 | 1. 00 | 46. 34 |
| | ATOM | 2209 | O | LEU | 315 | 47. 828 | -5. 439 | 65. 577 | 1. 00 | 47. 74 |
| | ATOM | 2210 | N | PHE | 316 | 46. 380 | -5. 318 | 67. 292 | 1. 00 | 48. 50 |
| 15 | ATOM | 2211 | CA | PHE | 316 | 46. 125 | -6. 760 | 67. 369 | 1. 00 | 50. 80 |
| | ATOM | 2212 | CB | PHE | 316 | 45. 054 | -7. 186 | 66. 347 | 1. 00 | 48. 89 |
| | ATOM | 2213 | CG | PHE | 316 | 43. 829 | -6. 312 | 66. 331 | 1. 00 | 46. 47 |
| | ATOM | 2214 | CD1 | PHE | 316 | 43. 163 | -5. 999 | 67. 508 | 1. 00 | 45. 93 |
| | ATOM | 2215 | CD2 | PHE | 316 | 43. 350 | -5. 791 | 65. 134 | 1. 00 | 44. 48 |
| 20 | ATOM | 2216 | CE1 | PHE | 316 | 42. 043 | -5. 183 | 67. 491 | 1. 00 | 44. 57 |
| | ATOM | 2217 | CE2 | PHE | 316 | 42. 229 | -4. 974 | 65. 109 | 1. 00 | 43. 59 |
| | ATOM | 2218 | CZ | PHE | 316 | 41. 577 | -4. 669 | 66. 290 | 1. 00 | 44. 05 |
| | ATOM | 2219 | C | PHE | 316 | 47. 371 | -7. 605 | 67. 124 | 1. 00 | 53. 06 |
| | ATOM | 2220 | O | PHE | 316 | 47. 342 | -8. 521 | 66. 299 | 1. 00 | 54. 62 |
| 25 | ATOM | 2221 | N | HIS | 317 | 48. 456 | -7. 304 | 67. 835 | 1. 00 | 54. 60 |
| | ATOM | 2222 | CA | HIS | 317 | 49. 710 | -8. 046 | 67. 691 | 1. 00 | 55. 95 |
| | ATOM | 2223 | CB | HIS | 317 | 49. 676 | -9. 301 | 68. 569 | 1. 00 | 54. 90 |
| | ATOM | 2224 | CG | HIS | 317 | 49. 708 | -9. 004 | 70. 034 | 1. 00 | 55. 21 |
| | ATOM | 2225 | CD2 | HIS | 317 | 49. 686 | -9. 823 | 71. 113 | 1. 00 | 55. 22 |

- 221 -

|      | ATOM | 2226 | ND1 | HIS | 317 | 49. 778 | −7. 718  | 70. 528 | 1. 00 | 54. 55 |
|------|------|------|-----|-----|-----|---------|----------|---------|-------|--------|
|      | ATOM | 2227 | CE1 | HIS | 317 | 49. 798 | −7. 756  | 71. 848 | 1. 00 | 55. 21 |
|      | ATOM | 2228 | NE2 | HIS | 317 | 49. 744 | −9. 020  | 72. 229 | 1. 00 | 56. 90 |
|      | ATOM | 2229 | C   | HIS | 317 | 50. 004 | −8. 426  | 66. 240 | 1. 00 | 58. 27 |
| 5    | ATOM | 2230 | O   | HIS | 317 | 50. 521 | −9. 514  | 65. 950 | 1. 00 | 58. 90 |
|      | ATOM | 2231 | N   | GLY | 318 | 49. 665 | −7. 513  | 65. 335 | 1. 00 | 59. 86 |
|      | ATOM | 2232 | CA  | GLY | 318 | 49. 881 | −7. 734  | 63. 921 | 1. 00 | 60. 72 |
|      | ATOM | 2233 | C   | GLY | 318 | 49. 290 | −9. 022  | 63. 379 | 1. 00 | 62. 25 |
|      | ATOM | 2234 | O   | GLY | 318 | 50. 031 | −9. 956  | 63. 080 | 1. 00 | 63. 75 |
| 10   | ATOM | 2235 | N   | GLU | 319 | 47. 962 | −9. 087  | 63. 277 | 1. 00 | 62. 86 |
|      | ATOM | 2236 | CA  | GLU | 319 | 47. 277 | −10. 257 | 62. 716 | 1. 00 | 62. 72 |
|      | ATOM | 2237 | CB  | GLU | 319 | 47. 663 | −11. 545 | 63. 439 | 1. 00 | 66. 93 |
|      | ATOM | 2238 | CG  | GLU | 319 | 47. 437 | −12. 784 | 62. 575 | 1. 00 | 73. 23 |
|      | ATOM | 2239 | CD  | GLU | 319 | 47. 862 | −14. 068 | 63. 262 | 1. 00 | 78. 58 |
| 15   | ATOM | 2240 | OE1 | GLU | 319 | 49. 020 | −14. 129 | 63. 745 | 1. 00 | 80. 57 |
|      | ATOM | 2241 | OE2 | GLU | 319 | 47. 043 | −15. 019 | 63. 310 | 1. 00 | 81. 49 |
|      | ATOM | 2242 | C   | GLU | 319 | 45. 765 | −10. 097 | 62. 739 | 1. 00 | 59. 42 |
|      | ATOM | 2243 | O   | GLU | 319 | 45. 098 | −10. 387 | 63. 735 | 1. 00 | 57. 03 |
|      | ATOM | 2244 | N   | ALA | 320 | 45. 246 | −9. 643  | 61. 604 | 1. 00 | 55. 74 |
| 20   | ATOM | 2245 | CA  | ALA | 320 | 43. 828 | −9. 394  | 61. 414 | 1. 00 | 54. 02 |
|      | ATOM | 2246 | CB  | ALA | 320 | 43. 657 | −8. 357  | 60. 338 | 1. 00 | 52. 55 |
|      | ATOM | 2247 | C   | ALA | 320 | 43. 052 | −10. 650 | 61. 043 | 1. 00 | 54. 49 |
|      | ATOM | 2248 | O   | ALA | 320 | 43. 620 | −11. 565 | 60. 457 | 1. 00 | 55. 61 |
|      | ATOM | 2249 | N   | SER | 321 | 41. 762 | −10. 698 | 61. 388 | 1. 00 | 55. 01 |
| 25   | ATOM | 2250 | CA  | SER | 321 | 40. 924 | −11. 856 | 61. 050 | 1. 00 | 55. 90 |
|      | ATOM | 2251 | CB  | SER | 321 | 39. 649 | −11. 911 | 61. 895 | 1. 00 | 56. 08 |
|      | ATOM | 2252 | OG  | SER | 321 | 38. 814 | −12. 975 | 61. 445 | 1. 00 | 53. 96 |
|      | ATOM | 2253 | C   | SER | 321 | 40. 513 | −11. 780 | 59. 589 | 1. 00 | 55. 49 |
|      | ATOM | 2254 | O   | SER | 321 | 40. 367 | −10. 689 | 59. 041 | 1. 00 | 54. 92 |

- 222 -

| | ATOM | 2255 | N | GLU 322 | 40. 292 | -12. 933 | 58. 967 | 1. 00 | 54. 84 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2256 | CA | GLU 322 | 39. 917 | -12. 951 | 57. 563 | 1. 00 | 56. 14 |
| | ATOM | 2257 | CB | GLU 322 | 39. 646 | -14. 382 | 57. 092 | 1. 00 | 58. 38 |
| | ATOM | 2258 | CG | GLU 322 | 40. 173 | -14. 697 | 55. 681 | 1. 00 | 63. 26 |
| 5 | ATOM | 2259 | CD | GLU 322 | 41. 712 | -14. 670 | 55. 574 | 1. 00 | 66. 36 |
| | ATOM | 2260 | OE1 | GLU 322 | 42. 296 | -13. 571 | 55. 432 | 1. 00 | 66. 15 |
| | ATOM | 2261 | OE2 | GLU 322 | 42. 339 | -15. 754 | 55. 637 | 1. 00 | 66. 78 |
| | ATOM | 2262 | C | GLU 322 | 38. 685 | -12. 085 | 57. 354 | 1. 00 | 55. 71 |
| | ATOM | 2263 | O | GLU 322 | 38. 343 | -11. 727 | 56. 227 | 1. 00 | 54. 93 |
| 10 | ATOM | 2264 | N | GLN 323 | 38. 027 | -11. 740 | 58. 454 | 1. 00 | 55. 82 |
| | ATOM | 2265 | CA | GLN 323 | 36. 838 | -10. 904 | 58. 393 | 1. 00 | 55. 20 |
| | ATOM | 2266 | CB | GLN 323 | 35. 995 | -11. 101 | 59. 659 | 1. 00 | 57. 22 |
| | ATOM | 2267 | CG | GLN 323 | 35. 737 | -12. 571 | 59. 983 | 1. 00 | 60. 42 |
| | ATOM | 2268 | CD | GLN 323 | 34. 801 | -12. 778 | 61. 164 | 1. 00 | 62. 11 |
| 15 | ATOM | 2269 | OE1 | GLN 323 | 34. 596 | -13. 909 | 61. 612 | 1. 00 | 63. 58 |
| | ATOM | 2270 | NE2 | GLN 323 | 34. 223 | -11. 690 | 61. 668 | 1. 00 | 61. 37 |
| | ATOM | 2271 | C | GLN 323 | 37. 259 | -9. 445 | 58. 249 | 1. 00 | 53. 59 |
| | ATOM | 2272 | O | GLN 323 | 36. 963 | -8. 800 | 57. 242 | 1. 00 | 53. 27 |
| | ATOM | 2273 | N | LEU 324 | 37. 973 | -8. 936 | 59. 248 | 1. 00 | 50. 98 |
| 20 | ATOM | 2274 | CA | LEU 324 | 38. 430 | -7. 553 | 59. 224 | 1. 00 | 48. 40 |
| | ATOM | 2275 | CB | LEU 324 | 39. 396 | -7. 294 | 60. 378 | 1. 00 | 46. 63 |
| | ATOM | 2276 | CG | LEU 324 | 39. 956 | -5. 876 | 60. 498 | 1. 00 | 44. 87 |
| | ATOM | 2277 | CD1 | LEU 324 | 38. 846 | -4. 837 | 60. 390 | 1. 00 | 44. 21 |
| | ATOM | 2278 | CD2 | LEU 324 | 40. 671 | -5. 758 | 61. 827 | 1. 00 | 43. 22 |
| 25 | ATOM | 2279 | C | LEU 324 | 39. 115 | -7. 224 | 57. 911 | 1. 00 | 47. 25 |
| | ATOM | 2280 | O | LEU 324 | 39. 181 | -6. 065 | 57. 505 | 1. 00 | 44. 86 |
| | ATOM | 2281 | N | ARG 325 | 39. 627 | -8. 253 | 57. 252 | 1. 00 | 48. 35 |
| | ATOM | 2282 | CA | ARG 325 | 40. 309 | -8. 057 | 55. 988 | 1. 00 | 50. 22 |
| | ATOM | 2283 | CB | ARG 325 | 41. 473 | -9. 055 | 55. 839 | 1. 00 | 53. 47 |

- 223 -

|  | ATOM | 2284 | CG | ARG | 325 | 42.580 | -8.896 | 56.894 | 1.00 | 57.97 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2285 | CD | ARG | 325 | 43.660 | -9.986 | 56.808 | 1.00 | 61.92 |
|  | ATOM | 2286 | NE | ARG | 325 | 44.564 | -9.957 | 57.966 | 1.00 | 67.95 |
|  | ATOM | 2287 | CZ | ARG | 325 | 45.535 | -10.844 | 58.206 | 1.00 | 70.27 |
| 5 | ATOM | 2288 | NH1 | ARG | 325 | 45.753 | -11.854 | 57.371 | 1.00 | 69.69 |
|  | ATOM | 2289 | NH2 | ARG | 325 | 46.290 | -10.725 | 59.293 | 1.00 | 70.39 |
|  | ATOM | 2290 | C | ARG | 325 | 39.320 | -8.224 | 54.850 | 1.00 | 48.80 |
|  | ATOM | 2291 | O | ARG | 325 | 39.617 | -8.859 | 53.847 | 1.00 | 50.46 |
|  | ATOM | 2292 | N | THR | 326 | 38.131 | -7.663 | 54.999 | 1.00 | 46.54 |
| 10 | ATOM | 2293 | CA | THR | 326 | 37.162 | -7.783 | 53.929 | 1.00 | 45.13 |
|  | ATOM | 2294 | CB | THR | 326 | 36.108 | -8.810 | 54.264 | 1.00 | 44.85 |
|  | ATOM | 2295 | OG1 | THR | 326 | 36.749 | -10.061 | 54.546 | 1.00 | 44.98 |
|  | ATOM | 2296 | CG2 | THR | 326 | 35.160 | -8.973 | 53.092 | 1.00 | 43.46 |
|  | ATOM | 2297 | C | THR | 326 | 36.500 | -6.453 | 53.687 | 1.00 | 44.79 |
| 15 | ATOM | 2298 | O | THR | 326 | 36.256 | -5.705 | 54.626 | 1.00 | 45.01 |
|  | ATOM | 2299 | N | ARG | 327 | 36.216 | -6.143 | 52.430 | 1.00 | 45.02 |
|  | ATOM | 2300 | CA | ARG | 327 | 35.590 | -4.866 | 52.136 | 1.00 | 45.97 |
|  | ATOM | 2301 | CB | ARG | 327 | 35.476 | -4.655 | 50.623 | 1.00 | 48.63 |
|  | ATOM | 2302 | CG | ARG | 327 | 34.961 | -3.283 | 50.229 | 1.00 | 53.97 |
| 20 | ATOM | 2303 | CD | ARG | 327 | 34.975 | -3.072 | 48.722 | 1.00 | 58.44 |
|  | ATOM | 2304 | NE | ARG | 327 | 33.747 | -2.410 | 48.282 | 1.00 | 66.14 |
|  | ATOM | 2305 | CZ | ARG | 327 | 33.387 | -1.178 | 48.648 | 1.00 | 69.53 |
|  | ATOM | 2306 | NH1 | ARG | 327 | 34.167 | -0.471 | 49.458 | 1.00 | 69.84 |
|  | ATOM | 2307 | NH2 | ARG | 327 | 32.242 | -0.652 | 48.220 | 1.00 | 68.29 |
| 25 | ATOM | 2308 | C | ARG | 327 | 34.217 | -4.790 | 52.794 | 1.00 | 44.69 |
|  | ATOM | 2309 | O | ARG | 327 | 33.486 | -5.784 | 52.861 | 1.00 | 44.55 |
|  | ATOM | 2310 | N | GLY | 328 | 33.888 | -3.605 | 53.302 | 1.00 | 42.14 |
|  | ATOM | 2311 | CA | GLY | 328 | 32.606 | -3.394 | 53.952 | 1.00 | 37.48 |
|  | ATOM | 2312 | C | GLY | 328 | 32.480 | -4.007 | 55.334 | 1.00 | 33.00 |

- 224 -

|  | ATOM | 2313 | O | GLY | 328 | 31. 693 | -3. 532 | 56. 148 | 1. 00 | 32. 88 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2314 | N | ALA | 329 | 33. 258 | -5. 049 | 55. 601 | 1. 00 | 29. 02 |
|  | ATOM | 2315 | CA | ALA | 329 | 33. 227 | -5. 743 | 56. 885 | 1. 00 | 26. 22 |
|  | ATOM | 2316 | CB | ALA | 329 | 34. 452 | -6. 623 | 57. 028 | 1. 00 | 28. 65 |
| 5 | ATOM | 2317 | C | ALA | 329 | 33. 092 | -4. 861 | 58. 115 | 1. 00 | 24. 38 |
|  | ATOM | 2318 | O | ALA | 329 | 32. 490 | -5. 276 | 59. 097 | 1. 00 | 26. 43 |
|  | ATOM | 2319 | N | PHE | 330 | 33. 663 | -3. 663 | 58. 091 | 1. 00 | 21. 81 |
|  | ATOM | 2320 | CA | PHE | 330 | 33. 547 | -2. 776 | 59. 242 | 1. 00 | 18. 07 |
|  | ATOM | 2321 | CB | PHE | 330 | 34. 887 | -2. 137 | 59. 558 | 1. 00 | 13. 90 |
| 10 | ATOM | 2322 | CG | PHE | 330 | 34. 913 | -1. 404 | 60. 862 | 1. 00 | 12. 45 |
|  | ATOM | 2323 | CD1 | PHE | 330 | 34. 460 | -0. 096 | 60. 961 | 1. 00 | 12. 64 |
|  | ATOM | 2324 | CD2 | PHE | 330 | 35. 436 | -2. 009 | 61. 995 | 1. 00 | 12. 73 |
|  | ATOM | 2325 | CE1 | PHE | 330 | 34. 535 | 0. 605 | 62. 188 | 1. 00 | 12. 83 |
|  | ATOM | 2326 | CE2 | PHE | 330 | 35. 515 | -1. 315 | 63. 221 | 1. 00 | 11. 49 |
| 15 | ATOM | 2327 | CZ | PHE | 330 | 35. 066 | -0. 008 | 63. 315 | 1. 00 | 8. 96 |
|  | ATOM | 2328 | C | PHE | 330 | 32. 528 | -1. 716 | 58. 886 | 1. 00 | 17. 48 |
|  | ATOM | 2329 | O | PHE | 330 | 32. 855 | -0. 702 | 58. 273 | 1. 00 | 17. 97 |
|  | ATOM | 2330 | N | GLU | 331 | 31. 288 | -1. 976 | 59. 275 | 1. 00 | 16. 36 |
|  | ATOM | 2331 | CA | GLU | 331 | 30. 149 | -1. 105 | 58. 998 | 1. 00 | 18. 14 |
| 20 | ATOM | 2332 | CB | GLU | 331 | 28. 865 | -1. 889 | 59. 308 | 1. 00 | 22. 08 |
|  | ATOM | 2333 | CG | GLU | 331 | 28. 790 | -3. 226 | 58. 546 | 1. 00 | 26. 82 |
|  | ATOM | 2334 | CD | GLU | 331 | 28. 183 | -4. 382 | 59. 346 | 1. 00 | 28. 86 |
|  | ATOM | 2335 | OE1 | GLU | 331 | 28. 381 | -5. 552 | 58. 931 | 1. 00 | 28. 12 |
|  | ATOM | 2336 | OE2 | GLU | 331 | 27. 509 | -4. 129 | 60. 371 | 1. 00 | 30. 16 |
| 25 | ATOM | 2337 | C | GLU | 331 | 30. 126 | 0. 248 | 59. 719 | 1. 00 | 16. 36 |
|  | ATOM | 2338 | O | GLU | 331 | 30. 596 | 0. 380 | 60. 849 | 1. 00 | 16. 97 |
|  | ATOM | 2339 | N | THR | 332 | 29. 583 | 1. 263 | 59. 060 | 1. 00 | 14. 04 |
|  | ATOM | 2340 | CA | THR | 332 | 29. 494 | 2. 568 | 59. 695 | 1. 00 | 14. 47 |
|  | ATOM | 2341 | CB | THR | 332 | 28. 747 | 3. 562 | 58. 825 | 1. 00 | 10. 93 |

- 225 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2342 | OG1 | THR | 332 | 29. 473 | 3. 751 | 57. 611 | 1. 00 | 6. 57 |
| | ATOM | 2343 | CG2 | THR | 332 | 28. 597 | 4. 890 | 59. 550 | 1. 00 | 6. 34 |
| | ATOM | 2344 | C | THR | 332 | 28. 725 | 2. 382 | 60. 994 | 1. 00 | 18. 42 |
| | ATOM | 2345 | O | THR | 332 | 29. 125 | 2. 872 | 62. 052 | 1. 00 | 17. 70 |
| 5 | ATOM | 2346 | N | ARG | 333 | 27. 609 | 1. 671 | 60. 892 | 1. 00 | 21. 79 |
| | ATOM | 2347 | CA | ARG | 333 | 26. 783 | 1. 346 | 62. 040 | 1. 00 | 24. 44 |
| | ATOM | 2348 | CB | ARG | 333 | 26. 095 | 0. 001 | 61. 764 | 1. 00 | 28. 62 |
| | ATOM | 2349 | CG | ARG | 333 | 25. 291 | -0. 590 | 62. 910 | 1. 00 | 34. 65 |
| | ATOM | 2350 | CD | ARG | 333 | 24. 308 | -1. 664 | 62. 401 | 1. 00 | 39. 87 |
| 10 | ATOM | 2351 | NE | ARG | 333 | 24. 953 | -2. 887 | 61. 910 | 1. 00 | 43. 42 |
| | ATOM | 2352 | CZ | ARG | 333 | 25. 198 | -3. 969 | 62. 653 | 1. 00 | 46. 01 |
| | ATOM | 2353 | NH1 | ARG | 333 | 24. 852 | -3. 992 | 63. 940 | 1. 00 | 45. 10 |
| | ATOM | 2354 | NH2 | ARG | 333 | 25. 791 | -5. 030 | 62. 104 | 1. 00 | 43. 75 |
| | ATOM | 2355 | C | ARG | 333 | 27. 638 | 1. 271 | 63. 323 | 1. 00 | 24. 88 |
| 15 | ATOM | 2356 | O | ARG | 333 | 27. 242 | 1. 803 | 64. 358 | 1. 00 | 24. 00 |
| | ATOM | 2357 | N | PHE | 334 | 28. 818 | 0. 635 | 63. 232 | 1. 00 | 23. 97 |
| | ATOM | 2358 | CA | PHE | 334 | 29. 740 | 0. 458 | 64. 371 | 1. 00 | 19. 64 |
| | ATOM | 2359 | CB | PHE | 334 | 30. 877 | -0. 509 | 64. 033 | 1. 00 | 20. 52 |
| | ATOM | 2360 | CG | PHE | 334 | 30. 420 | -1. 813 | 63. 468 | 1. 00 | 24. 74 |
| 20 | ATOM | 2361 | CD1 | PHE | 334 | 29. 469 | -2. 574 | 64. 121 | 1. 00 | 25. 94 |
| | ATOM | 2362 | CD2 | PHE | 334 | 30. 938 | -2. 279 | 62. 262 | 1. 00 | 26. 47 |
| | ATOM | 2363 | CE1 | PHE | 334 | 29. 039 | -3. 780 | 63. 575 | 1. 00 | 28. 43 |
| | ATOM | 2364 | CE2 | PHE | 334 | 30. 514 | -3. 483 | 61. 711 | 1. 00 | 24. 74 |
| | ATOM | 2365 | CZ | PHE | 334 | 29. 565 | -4. 233 | 62. 365 | 1. 00 | 26. 41 |
| 25 | ATOM | 2366 | C | PHE | 334 | 30. 382 | 1. 739 | 64. 842 | 1. 00 | 16. 52 |
| | ATOM | 2367 | O | PHE | 334 | 30. 434 | 2. 020 | 66. 039 | 1. 00 | 16. 16 |
| | ATOM | 2368 | N | VAL | 335 | 30. 907 | 2. 509 | 63. 905 | 1. 00 | 13. 20 |
| | ATOM | 2369 | CA | VAL | 335 | 31. 546 | 3. 752 | 64. 284 | 1. 00 | 11. 36 |
| | ATOM | 2370 | CB | VAL | 335 | 31. 877 | 4. 565 | 63. 033 | 1. 00 | 8. 08 |

- 226 -

|   | ATOM | 2371 | CG1 | VAL | 335 | 32.113 | 6.003 | 63.402 | 1.00 | 8.71 |
|---|------|------|-----|-----|-----|--------|-------|--------|------|------|
|   | ATOM | 2372 | CG2 | VAL | 335 | 33.082 | 3.979 | 62.358 | 1.00 | 1.00 |
|   | ATOM | 2373 | C   | VAL | 335 | 30.653 | 4.558 | 65.249 | 1.00 | 13.02 |
|   | ATOM | 2374 | O   | VAL | 335 | 31.126 | 5.066 | 66.264 | 1.00 | 10.40 |
| 5 | ATOM | 2375 | N   | SER | 336 | 29.359 | 4.640 | 64.934 | 1.00 | 16.23 |
|   | ATOM | 2376 | CA  | SER | 336 | 28.365 | 5.372 | 65.740 | 1.00 | 18.55 |
|   | ATOM | 2377 | CB  | SER | 336 | 27.017 | 5.350 | 65.039 | 1.00 | 19.92 |
|   | ATOM | 2378 | OG  | SER | 336 | 26.611 | 3.999 | 64.866 | 1.00 | 25.40 |
|   | ATOM | 2379 | C   | SER | 336 | 28.162 | 4.766 | 67.118 | 1.00 | 17.99 |
| 10 | ATOM | 2380 | O  | SER | 336 | 27.896 | 5.465 | 68.100 | 1.00 | 14.64 |
|   | ATOM | 2381 | N   | GLN | 337 | 28.239 | 3.445 | 67.159 | 1.00 | 19.48 |
|   | ATOM | 2382 | CA  | GLN | 337 | 28.061 | 2.719 | 68.394 | 1.00 | 21.39 |
|   | ATOM | 2383 | CB  | GLN | 337 | 27.995 | 1.223 | 68.123 | 1.00 | 21.42 |
|   | ATOM | 2384 | CG  | GLN | 337 | 26.829 | 0.800 | 67.264 | 1.00 | 23.07 |
| 15 | ATOM | 2385 | CD | GLN | 337 | 26.920 | -0.654 | 66.895 | 1.00 | 24.96 |
|   | ATOM | 2386 | OE1 | GLN | 337 | 27.243 | -1.496 | 67.735 | 1.00 | 28.83 |
|   | ATOM | 2387 | NE2 | GLN | 337 | 26.633 | -0.966 | 65.638 | 1.00 | 24.29 |
|   | ATOM | 2388 | C   | GLN | 337 | 29.260 | 3.011 | 69.240 | 1.00 | 20.91 |
|   | ATOM | 2389 | O   | GLN | 337 | 29.205 | 2.963 | 70.464 | 1.00 | 23.32 |
| 20 | ATOM | 2390 | N  | VAL | 338 | 30.362 | 3.317 | 68.584 | 1.00 | 20.52 |
|   | ATOM | 2391 | CA  | VAL | 338 | 31.559 | 3.589 | 69.337 | 1.00 | 21.67 |
|   | ATOM | 2392 | CB  | VAL | 338 | 32.812 | 3.470 | 68.443 | 1.00 | 20.93 |
|   | ATOM | 2393 | CG1 | VAL | 338 | 34.065 | 3.624 | 69.279 | 1.00 | 19.79 |
|   | ATOM | 2394 | CG2 | VAL | 338 | 32.811 | 2.126 | 67.739 | 1.00 | 16.69 |
| 25 | ATOM | 2395 | C  | VAL | 338 | 31.480 | 4.973 | 69.977 | 1.00 | 23.61 |
|   | ATOM | 2396 | O   | VAL | 338 | 31.385 | 5.079 | 71.203 | 1.00 | 21.96 |
|   | ATOM | 2397 | N   | GLU | 339 | 31.486 | 6.020 | 69.146 | 1.00 | 25.05 |
|   | ATOM | 2398 | CA  | GLU | 339 | 31.455 | 7.406 | 69.620 | 1.00 | 26.21 |
|   | ATOM | 2399 | CB  | GLU | 339 | 31.460 | 8.402 | 68.440 | 1.00 | 26.37 |

- 227 -

|  | ATOM | 2400 | CG | GLU | 339 | 30.515 | 8.082 | 67.282 | 1.00 | 31.63 |
|---|------|------|-----|-----|-----|--------|-------|--------|------|-------|
|  | ATOM | 2401 | CD | GLU | 339 | 30.287 | 9.267 | 66.311 | 1.00 | 36.86 |
|  | ATOM | 2402 | OE1 | GLU | 339 | 29.542 | 10.219 | 66.663 | 1.00 | 37.19 |
|  | ATOM | 2403 | OE2 | GLU | 339 | 30.850 | 9.243 | 65.187 | 1.00 | 37.90 |
| 5 | ATOM | 2404 | C | GLU | 339 | 30.299 | 7.735 | 70.541 | 1.00 | 26.44 |
|  | ATOM | 2405 | O | GLU | 339 | 30.423 | 8.613 | 71.396 | 1.00 | 27.55 |
|  | ATOM | 2406 | N | SER | 340 | 29.189 | 7.017 | 70.380 | 1.00 | 26.30 |
|  | ATOM | 2407 | CA | SER | 340 | 27.987 | 7.246 | 71.181 | 1.00 | 25.08 |
|  | ATOM | 2408 | CB | SER | 340 | 26.861 | 6.322 | 70.717 | 1.00 | 23.68 |
| 10 | ATOM | 2409 | OG | SER | 340 | 27.191 | 4.970 | 70.957 | 1.00 | 23.58 |
|  | ATOM | 2410 | C | SER | 340 | 28.211 | 7.065 | 72.676 | 1.00 | 26.02 |
|  | ATOM | 2411 | O | SER | 340 | 27.415 | 7.539 | 73.488 | 1.00 | 26.83 |
|  | ATOM | 2412 | N | ASP | 341 | 29.294 | 6.380 | 73.033 | 1.00 | 27.41 |
|  | ATOM | 2413 | CA | ASP | 341 | 29.630 | 6.143 | 74.434 | 1.00 | 27.85 |
| 15 | ATOM | 2414 | CB | ASP | 341 | 28.939 | 4.885 | 74.953 | 1.00 | 27.41 |
|  | ATOM | 2415 | CG | ASP | 341 | 29.253 | 4.621 | 76.410 | 1.00 | 26.49 |
|  | ATOM | 2416 | OD1 | ASP | 341 | 29.628 | 5.591 | 77.107 | 1.00 | 26.07 |
|  | ATOM | 2417 | OD2 | ASP | 341 | 29.117 | 3.463 | 76.862 | 1.00 | 25.64 |
|  | ATOM | 2418 | C | ASP | 341 | 31.128 | 6.008 | 74.672 | 1.00 | 28.59 |
| 20 | ATOM | 2419 | O | ASP | 341 | 31.757 | 5.049 | 74.229 | 1.00 | 30.06 |
|  | ATOM | 2420 | N | THR | 342 | 31.688 | 6.965 | 75.398 | 1.00 | 27.34 |
|  | ATOM | 2421 | CA | THR | 342 | 33.105 | 6.953 | 75.694 | 1.00 | 26.74 |
|  | ATOM | 2422 | CB | THR | 342 | 33.681 | 8.348 | 75.553 | 1.00 | 26.75 |
|  | ATOM | 2423 | OG1 | THR | 342 | 33.072 | 9.217 | 76.511 | 1.00 | 25.10 |
| 25 | ATOM | 2424 | CG2 | THR | 342 | 33.387 | 8.881 | 74.171 | 1.00 | 29.29 |
|  | ATOM | 2425 | C | THR | 342 | 33.292 | 6.477 | 77.114 | 1.00 | 27.84 |
|  | ATOM | 2426 | O | THR | 342 | 34.365 | 6.625 | 77.692 | 1.00 | 27.29 |
|  | ATOM | 2427 | N | GLY | 343 | 32.223 | 5.908 | 77.662 | 1.00 | 30.32 |
|  | ATOM | 2428 | CA | GLY | 343 | 32.234 | 5.398 | 79.020 | 1.00 | 31.31 |

- 228 -

| | ATOM | 2429 | C | GLY 343 | 32.970 | 4.083 | 79.178 | 1.00 | 32.13 |
|---|------|------|------|---------|--------|-------|--------|------|-------|
| | ATOM | 2430 | O | GLY 343 | 33.765 | 3.944 | 80.105 | 1.00 | 34.00 |
| | ATOM | 2431 | N | ASP 344 | 32.712 | 3.114 | 78.304 | 1.00 | 31.93 |
| | ATOM | 2432 | CA | ASP 344 | 33.400 | 1.836 | 78.411 | 1.00 | 34.25 |
| 5 | ATOM | 2433 | CB | ASP 344 | 32.592 | 0.857 | 79.267 | 1.00 | 38.13 |
| | ATOM | 2434 | CG | ASP 344 | 31.205 | 0.646 | 78.744 | 1.00 | 43.49 |
| | ATOM | 2435 | OD1 | ASP 344 | 30.399 | -0.029 | 79.426 | 1.00 | 47.59 |
| | ATOM | 2436 | OD2 | ASP 344 | 30.923 | 1.159 | 77.643 | 1.00 | 46.67 |
| | ATOM | 2437 | C | ASP 344 | 33.744 | 1.196 | 77.075 | 1.00 | 33.85 |
| 10 | ATOM | 2438 | O | ASP 344 | 33.354 | 1.681 | 76.015 | 1.00 | 32.12 |
| | ATOM | 2439 | N | ARG 345 | 34.490 | 0.098 | 77.148 | 1.00 | 34.54 |
| | ATOM | 2440 | CA | ARG 345 | 34.935 | -0.626 | 75.968 | 1.00 | 35.60 |
| | ATOM | 2441 | CB | ARG 345 | 36.297 | -1.278 | 76.233 | 1.00 | 35.33 |
| | ATOM | 2442 | CG | ARG 345 | 37.339 | -0.370 | 76.864 | 1.00 | 35.88 |
| 15 | ATOM | 2443 | CD | ARG 345 | 38.729 | -1.006 | 76.879 | 1.00 | 35.19 |
| | ATOM | 2444 | NE | ARG 345 | 39.507 | -0.597 | 78.054 | 1.00 | 36.95 |
| | ATOM | 2445 | CZ | ARG 345 | 39.984 | 0.629 | 78.275 | 1.00 | 36.97 |
| | ATOM | 2446 | NH1 | ARG 345 | 39.780 | 1.605 | 77.396 | 1.00 | 36.40 |
| | ATOM | 2447 | NH2 | ARG 345 | 40.654 | 0.885 | 79.394 | 1.00 | 36.46 |
| 20 | ATOM | 2448 | C | ARG 345 | 33.961 | -1.716 | 75.551 | 1.00 | 36.31 |
| | ATOM | 2449 | O | ARG 345 | 34.080 | -2.280 | 74.461 | 1.00 | 37.64 |
| | ATOM | 2450 | N | LYS 346 | 33.004 | -2.020 | 76.420 | 1.00 | 35.01 |
| | ATOM | 2451 | CA | LYS 346 | 32.050 | -3.081 | 76.134 | 1.00 | 33.81 |
| | ATOM | 2452 | CB | LYS 346 | 30.824 | -2.975 | 77.041 | 1.00 | 33.64 |
| 25 | ATOM | 2453 | CG | LYS 346 | 29.942 | -4.223 | 76.985 | 1.00 | 33.85 |
| | ATOM | 2454 | CD | LYS 346 | 30.759 | -5.505 | 77.186 | 1.00 | 31.48 |
| | ATOM | 2455 | CE | LYS 346 | 30.061 | -6.699 | 76.542 | 1.00 | 32.39 |
| | ATOM | 2456 | NZ | LYS 346 | 30.855 | -7.968 | 76.542 | 1.00 | 30.01 |
| | ATOM | 2457 | C | LYS 346 | 31.613 | -3.093 | 74.684 | 1.00 | 33.18 |

- 229 -

| | ATOM | 2458 | O | LYS | 346 | 31.746 | -4.101 | 73.995 | 1.00 | 31.98 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2459 | N | GLN | 347 | 31.101 | -1.967 | 74.214 | 1.00 | 33.36 |
| | ATOM | 2460 | CA | GLN | 347 | 30.662 | -1.887 | 72.839 | 1.00 | 34.32 |
| | ATOM | 2461 | CB | GLN | 347 | 30.014 | -0.530 | 72.589 | 1.00 | 37.17 |
| 5 | ATOM | 2462 | CG | GLN | 347 | 28.510 | -0.578 | 72.703 | 1.00 | 39.97 |
| | ATOM | 2463 | CD | GLN | 347 | 27.905 | -1.436 | 71.611 | 1.00 | 43.97 |
| | ATOM | 2464 | OE1 | GLN | 347 | 28.219 | -2.626 | 71.491 | 1.00 | 43.88 |
| | ATOM | 2465 | NE2 | GLN | 347 | 27.039 | -0.835 | 70.799 | 1.00 | 46.46 |
| | ATOM | 2466 | C | GLN | 347 | 31.799 | -2.144 | 71.844 | 1.00 | 34.27 |
| 10 | ATOM | 2467 | O | GLN | 347 | 31.630 | -2.922 | 70.902 | 1.00 | 35.29 |
| | ATOM | 2468 | N | ILE | 348 | 32.952 | -1.502 | 72.054 | 1.00 | 31.49 |
| | ATOM | 2469 | CA | ILE | 348 | 34.109 | -1.679 | 71.165 | 1.00 | 25.43 |
| | ATOM | 2470 | CB | ILE | 348 | 35.309 | -0.826 | 71.614 | 1.00 | 21.01 |
| | ATOM | 2471 | CG2 | ILE | 348 | 36.369 | -0.826 | 70.540 | 1.00 | 15.50 |
| 15 | ATOM | 2472 | CG1 | ILE | 348 | 34.852 | 0.606 | 71.875 | 1.00 | 22.27 |
| | ATOM | 2473 | CD1 | ILE | 348 | 35.914 | 1.509 | 72.462 | 1.00 | 24.55 |
| | ATOM | 2474 | C | ILE | 348 | 34.524 | -3.139 | 71.211 | 1.00 | 24.70 |
| | ATOM | 2475 | O | ILE | 348 | 34.793 | -3.763 | 70.182 | 1.00 | 23.36 |
| | ATOM | 2476 | N | TYR | 349 | 34.560 | -3.681 | 72.421 | 1.00 | 23.30 |
| 20 | ATOM | 2477 | CA | TYR | 349 | 34.933 | -5.061 | 72.597 | 1.00 | 23.65 |
| | ATOM | 2478 | CB | TYR | 349 | 34.727 | -5.491 | 74.047 | 1.00 | 25.21 |
| | ATOM | 2479 | CG | TYR | 349 | 34.779 | -6.989 | 74.221 | 1.00 | 31.27 |
| | ATOM | 2480 | CD1 | TYR | 349 | 35.990 | -7.665 | 74.333 | 1.00 | 33.98 |
| | ATOM | 2481 | CE1 | TYR | 349 | 36.028 | -9.062 | 74.435 | 1.00 | 36.98 |
| 25 | ATOM | 2482 | CD2 | TYR | 349 | 33.607 | -7.740 | 74.216 | 1.00 | 34.38 |
| | ATOM | 2483 | CE2 | TYR | 349 | 33.628 | -9.125 | 74.312 | 1.00 | 36.69 |
| | ATOM | 2484 | CZ | TYR | 349 | 34.837 | -9.786 | 74.421 | 1.00 | 37.89 |
| | ATOM | 2485 | OH | TYR | 349 | 34.834 | -11.165 | 74.512 | 1.00 | 37.12 |
| | ATOM | 2486 | C | TYR | 349 | 34.105 | -5.945 | 71.676 | 1.00 | 23.47 |

- 230 -

| | ATOM | 2487 | O | TYR | 349 | 34. 654 | -6. 602 | 70. 794 | 1. 00 | 21. 02 |
|---|------|------|------|-----|-----|---------|---------|---------|-------|--------|
| | ATOM | 2488 | N | ASN | 350 | 32. 783 | -5. 934 | 71. 872 | 1. 00 | 25. 29 |
| | ATOM | 2489 | CA | ASN | 350 | 31. 850 | -6. 766 | 71. 091 | 1. 00 | 25. 07 |
| | ATOM | 2490 | CB | ASN | 350 | 30. 379 | -6. 500 | 71. 482 | 1. 00 | 23. 90 |
| 5 | ATOM | 2491 | CG | ASN | 350 | 30. 069 | -6. 844 | 72. 941 | 1. 00 | 25. 09 |
| | ATOM | 2492 | OD1 | ASN | 350 | 30. 413 | -7. 924 | 73. 440 | 1. 00 | 22. 84 |
| | ATOM | 2493 | ND2 | ASN | 350 | 29. 398 | -5. 923 | 73. 626 | 1. 00 | 25. 65 |
| | ATOM | 2494 | C | ASN | 350 | 31. 982 | -6. 620 | 69. 580 | 1. 00 | 25. 25 |
| | ATOM | 2495 | O | ASN | 350 | 31. 994 | -7. 619 | 68. 859 | 1. 00 | 25. 84 |
| 10 | ATOM | 2496 | N | ILE | 351 | 32. 068 | -5. 392 | 69. 083 | 1. 00 | 25. 43 |
| | ATOM | 2497 | CA | ILE | 351 | 32. 195 | -5. 227 | 67. 642 | 1. 00 | 25. 64 |
| | ATOM | 2498 | CB | ILE | 351 | 32. 388 | -3. 745 | 67. 248 | 1. 00 | 24. 60 |
| | ATOM | 2499 | CG2 | ILE | 351 | 32. 282 | -3. 600 | 65. 743 | 1. 00 | 23. 69 |
| | ATOM | 2500 | CG1 | ILE | 351 | 31. 305 | -2. 882 | 67. 903 | 1. 00 | 22. 24 |
| 15 | ATOM | 2501 | CD1 | ILE | 351 | 31. 357 | -1. 431 | 67. 509 | 1. 00 | 19. 88 |
| | ATOM | 2502 | C | ILE | 351 | 33. 415 | -6. 047 | 67. 224 | 1. 00 | 26. 73 |
| | ATOM | 2503 | O | ILE | 351 | 33. 282 | -7. 047 | 66. 517 | 1. 00 | 25. 71 |
| | ATOM | 2504 | N | LEU | 352 | 34. 592 | -5. 629 | 67. 695 | 1. 00 | 27. 08 |
| | ATOM | 2505 | CA | LEU | 352 | 35. 847 | -6. 312 | 67. 397 | 1. 00 | 27. 36 |
| 20 | ATOM | 2506 | CB | LEU | 352 | 36. 994 | -5. 700 | 68. 206 | 1. 00 | 24. 45 |
| | ATOM | 2507 | CG | LEU | 352 | 37. 295 | -4. 208 | 68. 090 | 1. 00 | 23. 84 |
| | ATOM | 2508 | CD1 | LEU | 352 | 38. 464 | -3. 838 | 68. 995 | 1. 00 | 21. 54 |
| | ATOM | 2509 | CD2 | LEU | 352 | 37. 620 | -3. 872 | 66. 660 | 1. 00 | 23. 96 |
| | ATOM | 2510 | C | LEU | 352 | 35. 746 | -7. 798 | 67. 737 | 1. 00 | 29. 42 |
| 25 | ATOM | 2511 | O | LEU | 352 | 36. 045 | -8. 670 | 66. 912 | 1. 00 | 29. 43 |
| | ATOM | 2512 | N | SER | 353 | 35. 336 | -8. 087 | 68. 965 | 1. 00 | 30. 73 |
| | ATOM | 2513 | CA | SER | 353 | 35. 206 | -9. 468 | 69. 398 | 1. 00 | 32. 72 |
| | ATOM | 2514 | CB | SER | 353 | 34. 408 | -9. 531 | 70. 711 | 1. 00 | 32. 86 |
| | ATOM | 2515 | OG | SER | 353 | 34. 187 | -10. 870 | 71. 126 | 1. 00 | 35. 10 |

- 231 -

| | ATOM | 2516 | C | SER | 353 | 34.513 | -10.277 | 68.295 | 1.00 | 33.76 |
|---|------|------|-----|-----|-----|--------|---------|--------|------|-------|
| | ATOM | 2517 | O | SER | 353 | 35.123 | -11.149 | 67.670 | 1.00 | 34.42 |
| | ATOM | 2518 | N | THR | 354 | 33.252 | -9.941 | 68.035 | 1.00 | 34.17 |
| | ATOM | 2519 | CA | THR | 354 | 32.437 | -10.621 | 67.031 | 1.00 | 32.96 |
| 5 | ATOM | 2520 | CB | THR | 354 | 30.999 | -10.073 | 67.076 | 1.00 | 33.01 |
| | ATOM | 2521 | OG1 | THR | 354 | 30.120 | -10.980 | 66.408 | 1.00 | 32.52 |
| | ATOM | 2522 | CG2 | THR | 354 | 30.922 | -8.702 | 66.411 | 1.00 | 34.65 |
| | ATOM | 2523 | C | THR | 354 | 33.007 | -10.503 | 65.608 | 1.00 | 32.28 |
| | ATOM | 2524 | O | THR | 354 | 32.444 | -11.038 | 64.646 | 1.00 | 30.58 |
| 10 | ATOM | 2525 | N | LEU | 355 | 34.137 | -9.807 | 65.497 | 1.00 | 31.47 |
| | ATOM | 2526 | CA | LEU | 355 | 34.832 | -9.612 | 64.227 | 1.00 | 30.67 |
| | ATOM | 2527 | CB | LEU | 355 | 35.488 | -8.239 | 64.187 | 1.00 | 28.42 |
| | ATOM | 2528 | CG | LEU | 355 | 34.780 | -7.240 | 63.293 | 1.00 | 27.13 |
| | ATOM | 2529 | CD1 | LEU | 355 | 35.387 | -5.874 | 63.487 | 1.00 | 26.09 |
| 15 | ATOM | 2530 | CD2 | LEU | 355 | 34.898 | -7.698 | 61.859 | 1.00 | 27.39 |
| | ATOM | 2531 | C | LEU | 355 | 35.905 | -10.668 | 64.061 | 1.00 | 31.14 |
| | ATOM | 2532 | O | LEU | 355 | 36.573 | -10.735 | 63.033 | 1.00 | 30.59 |
| | ATOM | 2533 | N | GLY | 356 | 36.074 | -11.484 | 65.091 | 1.00 | 32.64 |
| | ATOM | 2534 | CA | GLY | 356 | 37.068 | -12.530 | 65.030 | 1.00 | 35.49 |
| 20 | ATOM | 2535 | C | GLY | 356 | 38.435 | -12.074 | 65.493 | 1.00 | 37.44 |
| | ATOM | 2536 | O | GLY | 356 | 39.443 | -12.492 | 64.930 | 1.00 | 37.31 |
| | ATOM | 2537 | N | LEU | 357 | 38.471 | -11.222 | 66.516 | 1.00 | 39.40 |
| | ATOM | 2538 | CA | LEU | 357 | 39.729 | -10.717 | 67.057 | 1.00 | 41.85 |
| | ATOM | 2539 | CB | LEU | 357 | 39.898 | -9.239 | 66.705 | 1.00 | 41.35 |
| 25 | ATOM | 2540 | CG | LEU | 357 | 39.816 | -8.876 | 65.218 | 1.00 | 43.17 |
| | ATOM | 2541 | CD1 | LEU | 357 | 39.953 | -7.375 | 65.064 | 1.00 | 42.98 |
| | ATOM | 2542 | CD2 | LEU | 357 | 40.904 | -9.585 | 64.428 | 1.00 | 43.93 |
| | ATOM | 2543 | C | LEU | 357 | 39.759 | -10.888 | 68.571 | 1.00 | 44.59 |
| | ATOM | 2544 | O | LEU | 357 | 38.750 | -11.247 | 69.176 | 1.00 | 45.94 |

- 232 -

| | ATOM | 2545 | N | ARG 358 | 40.919 | -10.643 | 69.178 | 1.00 | 46.55 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2546 | CA | ARG 358 | 41.080 | -10.752 | 70.632 | 1.00 | 48.12 |
| | ATOM | 2547 | CB | ARG 358 | 42.113 | -11.819 | 70.994 | 1.00 | 52.19 |
| | ATOM | 2548 | CG | ARG 358 | 41.649 | -13.258 | 70.839 | 1.00 | 61.21 |
| 5 | ATOM | 2549 | CD | ARG 358 | 40.870 | -13.768 | 72.064 | 1.00 | 68.48 |
| | ATOM | 2550 | NE | ARG 358 | 39.519 | -13.206 | 72.184 | 1.00 | 74.00 |
| | ATOM | 2551 | CZ | ARG 358 | 38.629 | -13.577 | 73.104 | 1.00 | 75.57 |
| | ATOM | 2552 | NH1 | ARG 358 | 38.935 | -14.517 | 73.998 | 1.00 | 75.58 |
| | ATOM | 2553 | NH2 | ARG 358 | 37.431 | -13.005 | 73.131 | 1.00 | 74.54 |
| 10 | ATOM | 2554 | C | ARG 358 | 41.558 | -9.418 | 71.174 | 1.00 | 46.76 |
| | ATOM | 2555 | O | ARG 358 | 42.702 | -9.284 | 71.580 | 1.00 | 49.52 |
| | ATOM | 2556 | N | PRO 359 | 40.679 | -8.412 | 71.197 | 1.00 | 45.33 |
| | ATOM | 2557 | CD | PRO 359 | 39.271 | -8.532 | 70.791 | 1.00 | 45.90 |
| | ATOM | 2558 | CA | PRO 359 | 40.956 | -7.056 | 71.677 | 1.00 | 44.06 |
| 15 | ATOM | 2559 | CB | PRO 359 | 39.565 | -6.449 | 71.784 | 1.00 | 45.14 |
| | ATOM | 2560 | CG | PRO 359 | 38.865 | -7.086 | 70.643 | 1.00 | 46.70 |
| | ATOM | 2561 | C | PRO 359 | 41.725 | -6.936 | 72.986 | 1.00 | 42.11 |
| | ATOM | 2562 | O | PRO 359 | 41.662 | -7.797 | 73.860 | 1.00 | 42.98 |
| | ATOM | 2563 | N | SER 360 | 42.449 | -5.840 | 73.118 | 1.00 | 38.55 |
| 20 | ATOM | 2564 | CA | SER 360 | 43.209 | -5.608 | 74.321 | 1.00 | 35.42 |
| | ATOM | 2565 | CB | SER 360 | 44.701 | -5.624 | 74.014 | 1.00 | 38.45 |
| | ATOM | 2566 | OG | SER 360 | 45.100 | -4.379 | 73.453 | 1.00 | 37.32 |
| | ATOM | 2567 | C | SER 360 | 42.847 | -4.234 | 74.818 | 1.00 | 33.26 |
| | ATOM | 2568 | O | SER 360 | 42.530 | -3.345 | 74.028 | 1.00 | 30.55 |
| 25 | ATOM | 2569 | N | THR 361 | 42.907 | -4.060 | 76.128 | 1.00 | 31.87 |
| | ATOM | 2570 | CA | THR 361 | 42.625 | -2.771 | 76.721 | 1.00 | 33.02 |
| | ATOM | 2571 | CB | THR 361 | 43.285 | -2.646 | 78.083 | 1.00 | 32.00 |
| | ATOM | 2572 | OG1 | THR 361 | 42.697 | -3.593 | 78.981 | 1.00 | 31.30 |
| | ATOM | 2573 | CG2 | THR 361 | 43.135 | -1.223 | 78.618 | 1.00 | 28.90 |

- 233 -

| | ATOM | 2574 | C | THR | 361 | 43. 162 | -1. 637 | 75. 853 | 1. 00 | 35. 59 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2575 | O | THR | 361 | 42. 600 | -0. 545 | 75. 837 | 1. 00 | 37. 16 |
| | ATOM | 2576 | N | THR | 362 | 44. 253 | -1. 879 | 75. 135 | 1. 00 | 37. 62 |
| | ATOM | 2577 | CA | THR | 362 | 44. 812 | -0. 819 | 74. 303 | 1. 00 | 37. 63 |
| 5 | ATOM | 2578 | CB | THR | 362 | 46. 341 | -0. 949 | 74. 156 | 1. 00 | 38. 04 |
| | ATOM | 2579 | OG1 | THR | 362 | 46. 950 | -0. 981 | 75. 453 | 1. 00 | 37. 77 |
| | ATOM | 2580 | CG2 | THR | 362 | 46. 890 | 0. 242 | 73. 395 | 1. 00 | 37. 49 |
| | ATOM | 2581 | C | THR | 362 | 44. 183 | -0. 839 | 72. 928 | 1. 00 | 36. 67 |
| | ATOM | 2582 | O | THR | 362 | 43. 758 | 0. 194 | 72. 416 | 1. 00 | 34. 48 |
| 10 | ATOM | 2583 | N | ASP | 363 | 44. 132 | -2. 032 | 72. 345 | 1. 00 | 37. 88 |
| | ATOM | 2584 | CA | ASP | 363 | 43. 555 | -2. 246 | 71. 024 | 1. 00 | 40. 18 |
| | ATOM | 2585 | CB | ASP | 363 | 43. 238 | -3. 729 | 70. 842 | 1. 00 | 42. 13 |
| | ATOM | 2586 | CG | ASP | 363 | 44. 477 | -4. 557 | 70. 666 | 1. 00 | 45. 73 |
| | ATOM | 2587 | OD1 | ASP | 363 | 44. 433 | -5. 779 | 70. 932 | 1. 00 | 49. 54 |
| 15 | ATOM | 2588 | OD2 | ASP | 363 | 45. 500 | -3. 976 | 70. 247 | 1. 00 | 46. 04 |
| | ATOM | 2589 | C | ASP | 363 | 42. 289 | -1. 429 | 70. 841 | 1. 00 | 40. 28 |
| | ATOM | 2590 | O | ASP | 363 | 42. 070 | -0. 801 | 69. 802 | 1. 00 | 38. 03 |
| | ATOM | 2591 | N | CYS | 364 | 41. 455 | -1. 449 | 71. 871 | 1. 00 | 41. 60 |
| | ATOM | 2592 | CA | CYS | 364 | 40. 197 | -0. 724 | 71. 849 | 1. 00 | 41. 33 |
| 20 | ATOM | 2593 | CB | CYS | 364 | 39. 426 | -1. 036 | 73. 131 | 1. 00 | 41. 81 |
| | ATOM | 2594 | SG. | CYS | 364 | 39. 078 | -2. 818 | 73. 225 | 1. 00 | 41. 98 |
| | ATOM | 2595 | C | CYS | 364 | 40. 447 | 0. 766 | 71. 685 | 1. 00 | 39. 78 |
| | ATOM | 2596 | O | CYS | 364 | 39. 991 | 1. 382 | 70. 721 | 1. 00 | 37. 44 |
| | ATOM | 2597 | N | ASP | 365 | 41. 194 | 1. 333 | 72. 622 | 1. 00 | 38. 65 |
| 25 | ATOM | 2598 | CA | ASP | 365 | 41. 525 | 2. 744 | 72. 580 | 1. 00 | 37. 87 |
| | ATOM | 2599 | CB | ASP | 365 | 42. 498 | 3. 060 | 73. 709 | 1. 00 | 39. 53 |
| | ATOM | 2600 | CG | ASP | 365 | 42. 073 | 2. 424 | 75. 014 | 1. 00 | 42. 28 |
| | ATOM | 2601 | OD1 | ASP | 365 | 40. 887 | 2. 000 | 75. 096 | 1. 00 | 43. 06 |
| | ATOM | 2602 | OD2 | ASP | 365 | 42. 908 | 2. 355 | 75. 949 | 1. 00 | 41. 82 |

- 234 -

|  | ATOM | 2603 | C | ASP | 365 | 42.123 | 3.092 | 71.220 | 1.00 | 35.70 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2604 | 0 | ASP | 365 | 41.887 | 4.173 | 70.682 | 1.00 | 35.49 |
|  | ATOM | 2605 | N | ILE | 366 | 42.895 | 2.175 | 70.655 | 1.00 | 32.72 |
|  | ATOM | 2606 | CA | ILE | 366 | 43.469 | 2.428 | 69.347 | 1.00 | 31.21 |
| 5 | ATOM | 2607 | CB | ILE | 366 | 44.345 | 1.241 | 68.891 | 1.00 | 30.98 |
|  | ATOM | 2608 | CG2 | ILE | 366 | 44.878 | 1.488 | 67.482 | 1.00 | 30.08 |
|  | ATOM | 2609 | CG1 | ILE | 366 | 45.472 | 1.010 | 69.907 | 1.00 | 30.05 |
|  | ATOM | 2610 | CD1 | ILE | 366 | 46.426 | 2.165 | 70.071 | 1.00 | 26.19 |
|  | ATOM | 2611 | C | ILE | 366 | 42.292 | 2.622 | 68.384 | 1.00 | 30.65 |
| 10 | ATOM | 2612 | 0 | ILE | 366 | 42.140 | 3.686 | 67.790 | 1.00 | 29.65 |
|  | ATOM | 2613 | N | VAL | 367 | 41.451 | 1.598 | 68.255 | 1.00 | 29.81 |
|  | ATOM | 2614 | CA | VAL | 367 | 40.287 | 1.665 | 67.378 | 1.00 | 27.24 |
|  | ATOM | 2615 | CB | VAL | 367 | 39.397 | 0.424 | 67.541 | 1.00 | 26.77 |
|  | ATOM | 2616 | CG1 | VAL | 367 | 38.193 | 0.520 | 66.630 | 1.00 | 25.16 |
| 15 | ATOM | 2617 | CG2 | VAL | 367 | 40.190 | -0.817 | 67.220 | 1.00 | 27.90 |
|  | ATOM | 2618 | C | VAL | 367 | 39.453 | 2.910 | 67.657 | 1.00 | 26.82 |
|  | ATOM | 2619 | 0 | VAL | 367 | 39.061 | 3.606 | 66.727 | 1.00 | 27.16 |
|  | ATOM | 2620 | N | ARG | 368 | 39.171 | 3.191 | 68.927 | 1.00 | 25.49 |
|  | ATOM | 2621 | CA | ARG | 368 | 38.398 | 4.380 | 69.266 | 1.00 | 24.26 |
| 20 | ATOM | 2622 | CB | ARG | 368 | 38.431 | 4.644 | 70.772 | 1.00 | 23.73 |
|  | ATOM | 2623 | CG | ARG | 368 | 37.765 | 5.951 | 71.217 | 1.00 | 26.32 |
|  | ATOM | 2624 | CD | ARG | 368 | 36.239 | 5.948 | 71.033 | 1.00 | 32.00 |
|  | ATOM | 2625 | NE | ARG | 368 | 35.542 | 5.015 | 71.926 | 1.00 | 33.36 |
|  | ATOM | 2626 | CZ | ARG | 368 | 35.558 | 5.096 | 73.253 | 1.00 | 33.30 |
| 25 | ATOM | 2627 | NH1 | ARG | 368 | 36.237 | 6.069 | 73.843 | 1.00 | 36.87 |
|  | ATOM | 2628 | NH2 | ARG | 368 | 34.904 | 4.209 | 73.990 | 1.00 | 30.08 |
|  | ATOM | 2629 | C | ARG | 368 | 39.034 | 5.545 | 68.539 | 1.00 | 25.24 |
|  | ATOM | 2630 | 0 | ARG | 368 | 38.403 | 6.175 | 67.700 | 1.00 | 26.08 |
|  | ATOM | 2631 | N | ARG | 369 | 40.299 | 5.808 | 68.844 | 1.00 | 26.69 |

- 235 -

|  | ATOM | 2632 | CA | ARG 369 | 41.022 | 6.905 | 68.226 | 1.00 | 28.80 |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2633 | CB | ARG 369 | 42.500 | 6.842 | 68.619 | 1.00 | 33.81 |
|  | ATOM | 2634 | CG | ARG 369 | 42.992 | 8.041 | 69.421 | 1.00 | 41.54 |
|  | ATOM | 2635 | CD | ARG 369 | 44.246 | 8.666 | 68.797 | 1.00 | 47.78 |
| 5 | ATOM | 2636 | NE | ARG 369 | 44.827 | 9.709 | 69.642 | 1.00 | 53.83 |
|  | ATOM | 2637 | CZ | ARG 369 | 45.436 | 9.479 | 70.803 | 1.00 | 57.34 |
|  | ATOM | 2638 | NH1 | ARG 369 | 45.547 | 8.234 | 71.256 | 1.00 | 57.39 |
|  | ATOM | 2639 | NH2 | ARG 369 | 45.925 | 10.492 | 71.517 | 1.00 | 58.51 |
|  | ATOM | 2640 | C | ARG 369 | 40.888 | 6.941 | 66.704 | 1.00 | 27.66 |
| 10 | ATOM | 2641 | O | ARG 369 | 40.898 | 8.017 | 66.116 | 1.00 | 27.35 |
|  | ATOM | 2642 | N | ALA 370 | 40.760 | 5.778 | 66.071 | 1.00 | 28.23 |
|  | ATOM | 2643 | CA | ALA 370 | 40.622 | 5.699 | 64.613 | 1.00 | 29.69 |
|  | ATOM | 2644 | CB | ALA 370 | 40.779 | 4.264 | 64.144 | 1.00 | 27.18 |
|  | ATOM | 2645 | C | ALA 370 | 39.266 | 6.218 | 64.184 | 1.00 | 32.49 |
| 15 | ATOM | 2646 | O | ALA 370 | 39.155 | 7.084 | 63.313 | 1.00 | 33.37 |
|  | ATOM | 2647 | N | CYS 371 | 38.229 | 5.663 | 64.797 | 1.00 | 35.80 |
|  | ATOM | 2648 | CA | CYS 371 | 36.860 | 6.053 | 64.500 | 1.00 | 37.09 |
|  | ATOM | 2649 | CB | CYS 371 | 35.892 | 5.310 | 65.427 | 1.00 | 37.67 |
|  | ATOM | 2650 | SG | CYS 371 | 35.709 | 3.539 | 65.052 | 1.00 | 43.56 |
| 20 | ATOM | 2651 | C | CYS 371 | 36.692 | 7.555 | 64.663 | 1.00 | 36.66 |
|  | ATOM | 2652 | O | CYS 371 | 36.237 | 8.231 | 63.746 | 1.00 | 36.14 |
|  | ATOM | 2653 | N | GLU 372 | 37.079 | 8.065 | 65.829 | 1.00 | 36.70 |
|  | ATOM | 2654 | CA | GLU 372 | 36.962 | 9.482 | 66.140 | 1.00 | 37.83 |
|  | ATOM | 2655 | CB | GLU 372 | 37.440 | 9.741 | 67.569 | 1.00 | 41.72 |
| 25 | ATOM | 2656 | CG | GLU 372 | 37.405 | 11.202 | 67.993 | 1.00 | 50.44 |
|  | ATOM | 2657 | CD | GLU 372 | 38.615 | 11.981 | 67.504 | 1.00 | 56.78 |
|  | ATOM | 2658 | OE1 | GLU 372 | 39.747 | 11.656 | 67.940 | 1.00 | 60.05 |
|  | ATOM | 2659 | OE2 | GLU 372 | 38.437 | 12.914 | 66.685 | 1.00 | 59.31 |
|  | ATOM | 2660 | C | GLU 372 | 37.736 | 10.344 | 65.163 | 1.00 | 36.14 |

- 236 -

| ATOM | 2661 | O | GLU 372 | 37. 280 | 11. 410 | 64. 745 | 1. 00 | 34. 24 |
|------|------|------|---------|---------|---------|---------|-------|--------|
| ATOM | 2662 | N | SER 373 | 38. 917 | 9. 890 | 64. 793 | 1. 00 | 37. 31 |
| ATOM | 2663 | CA | SER 373 | 39. 703 | 10. 662 | 63. 856 | 1. 00 | 39. 48 |
| ATOM | 2664 | CB | SER 373 | 41. 095 | 10. 040 | 63. 694 | 1. 00 | 40. 54 |
| ATOM | 2665 | OG | SER 373 | 41. 014 | 8. 697 | 63. 253 | 1. 00 | 41. 31 |
| ATOM | 2666 | C | SER 373 | 38. 966 | 10. 713 | 62. 516 | 1. 00 | 38. 54 |
| ATOM | 2667 | O | SER 373 | 38. 778 | 11. 790 | 61. 953 | 1. 00 | 39. 30 |
| ATOM | 2668 | N | VAL 374 | 38. 528 | 9. 552 | 62. 029 | 1. 00 | 35. 74 |
| ATOM | 2669 | CA | VAL 374 | 37. 817 | 9. 462 | 60. 755 | 1. 00 | 34. 53 |
| ATOM | 2670 | CB | VAL 374 | 37. 519 | 7. 987 | 60. 388 | 1. 00 | 33. 30 |
| ATOM | 2671 | CG1 | VAL 374 | 36. 688 | 7. 897 | 59. 119 | 1. 00 | 30. 40 |
| ATOM | 2672 | CG2 | VAL 374 | 38. 811 | 7. 257 | 60. 186 | 1. 00 | 34. 78 |
| ATOM | 2673 | C | VAL 374 | 36. 512 | 10. 250 | 60. 736 | 1. 00 | 35. 17 |
| ATOM | 2674 | O | VAL 374 | 36. 253 | 11. 010 | 59. 797 | 1. 00 | 34. 51 |
| ATOM | 2675 | N | SER 375 | 35. 700 | 10. 080 | 61. 775 | 1. 00 | 35. 24 |
| ATOM | 2676 | CA | SER 375 | 34. 416 | 10. 768 | 61. 866 | 1. 00 | 34. 91 |
| ATOM | 2677 | CB | SER 375 | 33. 641 | 10. 312 | 63. 103 | 1. 00 | 35. 91 |
| ATOM | 2678 | OG | SER 375 | 33. 802 | 11. 230 | 64. 178 | 1. 00 | 37. 28 |
| ATOM | 2679 | C | SER 375 | 34. 585 | 12. 272 | 61. 933 | 1. 00 | 34. 67 |
| ATOM | 2680 | O | SER 375 | 33. 865 | 13. 010 | 61. 266 | 1. 00 | 35. 17 |
| ATOM | 2681 | N | THR 376 | 35. 534 | 12. 725 | 62. 743 | 1. 00 | 34. 00 |
| ATOM | 2682 | CA | THR 376 | 35. 768 | 14. 150 | 62. 889 | 1. 00 | 35. 55 |
| ATOM | 2683 | CB | THR 376 | 36. 827 | 14. 421 | 63. 954 | 1. 00 | 38. 06 |
| ATOM | 2684 | OG1 | THR 376 | 36. 461 | 13. 739 | 65. 158 | 1. 00 | 40. 51 |
| ATOM | 2685 | CG2 | THR 376 | 36. 926 | 15. 923 | 64. 239 | 1. 00 | 38. 22 |
| ATOM | 2686 | C | THR 376 | 36. 208 | 14. 788 | 61. 583 | 1. 00 | 34. 80 |
| ATOM | 2687 | O | THR 376 | 35. 794 | 15. 901 | 61. 241 | 1. 00 | 32. 23 |
| ATOM | 2688 | N | ARG 377 | 37. 049 | 14. 078 | 60. 848 | 1. 00 | 36. 51 |
| ATOM | 2689 | CA | ARG 377 | 37. 523 | 14. 601 | 59. 581 | 1. 00 | 38. 20 |

- 237 -

| | ATOM | 2690 | CB | ARG 377 | 38. 535 | 13. 640 | 58. 956 | 1. 00 | 41. 90 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2691 | CG | ARG 377 | 39. 417 | 14. 271 | 57. 892 | 1. 00 | 43. 83 |
| | ATOM | 2692 | CD | ARG 377 | 38. 735 | 14. 280 | 56. 551 | 1. 00 | 46. 24 |
| | ATOM | 2693 | NE | ARG 377 | 38. 467 | 12. 921 | 56. 074 | 1. 00 | 50. 02 |
| 5 | ATOM | 2694 | CZ | ARG 377 | 39. 400 | 12. 058 | 55. 679 | 1. 00 | 48. 89 |
| | ATOM | 2695 | NH1 | ARG 377 | 40. 681 | 12. 405 | 55. 700 | 1. 00 | 47. 77 |
| | ATOM | 2696 | NH2 | ARG 377 | 39. 050 | 10. 849 | 55. 256 | 1. 00 | 48. 65 |
| | ATOM | 2697 | C | ARG 377 | 36. 311 | 14. 759 | 58. 688 | 1. 00 | 37. 15 |
| | ATOM | 2698 | O | ARG 377 | 36. 163 | 15. 780 | 58. 016 | 1. 00 | 37. 23 |
| 10 | ATOM | 2699 | N | ALA 378 | 35. 445 | 13. 744 | 58. 706 | 1. 00 | 36. 43 |
| | ATOM | 2700 | CA | ALA 378 | 34. 212 | 13. 732 | 57. 920 | 1. 00 | 35. 58 |
| | ATOM | 2701 | CB | ALA 378 | 33. 470 | 12. 430 | 58. 130 | 1. 00 | 35. 75 |
| | ATOM | 2702 | C | ALA 378 | 33. 314 | 14. 897 | 58. 304 | 1. 00 | 34. 75 |
| | ATOM | 2703 | O | ALA 378 | 32. 675 | 15. 507 | 57. 451 | 1. 00 | 34. 63 |
| 15 | ATOM | 2704 | N | ALA 379 | 33. 249 | 15. 204 | 59. 590 | 1. 00 | 34. 17 |
| | ATOM | 2705 | CA | ALA 379 | 32. 427 | 16. 317 | 60. 009 | 1. 00 | 34. 54 |
| | ATOM | 2706 | CB | ALA 379 | 32. 281 | 16. 340 | 61. 515 | 1. 00 | 32. 43 |
| | ATOM | 2707 | C | ALA 379 | 33. 073 | 17. 607 | 59. 519 | 1. 00 | 35. 95 |
| | ATOM | 2708 | O | ALA 379 | 32. 465 | 18. 358 | 58. 761 | 1. 00 | 38. 27 |
| 20 | ATOM | 2709 | N | HIS 380 | 34. 314 | 17. 856 | 59. 925 | 1. 00 | 35. 13 |
| | ATOM | 2710 | CA | HIS 380 | 34. 994 | 19. 083 | 59. 526 | 1. 00 | 34. 04 |
| | ATOM | 2711 | CB | HIS 380 | 36. 448 | 19. 031 | 59. 968 | 1. 00 | 37. 01 |
| | ATOM | 2712 | CG | HIS 380 | 36. 628 | 19. 284 | 61. 430 | 1. 00 | 42. 02 |
| | ATOM | 2713 | CD2 | HIS 380 | 35. 734 | 19. 637 | 62. 385 | 1. 00 | 43. 27 |
| 25 | ATOM | 2714 | ND1 | HIS 380 | 37. 852 | 19. 206 | 62. 058 | 1. 00 | 44. 66 |
| | ATOM | 2715 | CE1 | HIS 380 | 37. 704 | 19. 500 | 63. 339 | 1. 00 | 46. 06 |
| | ATOM | 2716 | NE2 | HIS 380 | 36. 429 | 19. 766 | 63. 562 | 1. 00 | 44. 63 |
| | ATOM | 2717 | C | HIS 380 | 34. 894 | 19. 405 | 58. 045 | 1. 00 | 32. 37 |
| | ATOM | 2718 | O | HIS 380 | 34. 581 | 20. 536 | 57. 671 | 1. 00 | 29. 98 |

- 238 -

| | ATOM | 2719 | N | MET 381 | 35. 154 | 18. 417 | 57. 197 | 1. 00 | 30. 55 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2720 | CA | MET 381 | 35. 055 | 18. 640 | 55. 764 | 1. 00 | 30. 35 |
| | ATOM | 2721 | CB | MET 381 | 35. 383 | 17. 365 | 54. 992 | 1. 00 | 28. 41 |
| | ATOM | 2722 | CG | MET 381 | 36. 852 | 17. 181 | 54. 767 | 1. 00 | 28. 31 |
| 5 | ATOM | 2723 | SD | MET 381 | 37. 505 | 18. 684 | 54. 017 | 1. 00 | 31. 73 |
| | ATOM | 2724 | CE | MET 381 | 38. 142 | 18. 070 | 52. 446 | 1. 00 | 30. 02 |
| | ATOM | 2725 | C | MET 381 | 33. 647 | 19. 101 | 55. 415 | 1. 00 | 32. 29 |
| | ATOM | 2726 | 0 | MET 381 | 33. 453 | 19. 930 | 54. 527 | 1. 00 | 32. 42 |
| | ATOM | 2727 | N | CYS 382 | 32. 660 | 18. 566 | 56. 124 | 1. 00 | 33. 02 |
| 10 | ATOM | 2728 | CA | CYS 382 | 31. 279 | 18. 942 | 55. 869 | 1. 00 | 33. 44 |
| | ATOM | 2729 | CB | CYS 382 | 30. 323 | 18. 012 | 56. 625 | 1. 00 | 33. 78 |
| | ATOM | 2730 | SG | CYS 382 | 28. 582 | 18. 152 | 56. 124 | 1. 00 | 40. 21 |
| | ATOM | 2731 | C | CYS 382 | 31. 087 | 20. 387 | 56. 316 | 1. 00 | 33. 02 |
| | ATOM | 2732 | 0 | CYS 382 | 30. 566 | 21. 218 | 55. 563 | 1. 00 | 32. 71 |
| 15 | ATOM | 2733 | N | SER 383 | 31. 528 | 20. 686 | 57. 537 | 1. 00 | 33. 57 |
| | ATOM | 2734 | CA | SER 383 | 31. 418 | 22. 037 | 58. 097 | 1. 00 | 33. 39 |
| | ATOM | 2735 | CB | SER 383 | 32. 232 | 22. 159 | 59. 392 | 1. 00 | 32. 88 |
| | ATOM | 2736 | OG | SER 383 | 33. 605 | 21. 877 | 59. 176 | 1. 00 | 31. 29 |
| | ATOM | 2737 | C | SER 383 | 31. 935 | 23. 042 | 57. 085 | 1. 00 | 32. 50 |
| 20 | ATOM | 2738 | 0 | SER 383 | 31. 314 | 24. 073 | 56. 832 | 1. 00 | 32. 64 |
| | ATOM | 2739 | N | ALA 384 | 33. 082 | 22. 729 | 56. 501 | 1. 00 | 30. 75 |
| | ATOM | 2740 | CA | ALA 384 | 33. 663 | 23. 607 | 55. 510 | 1. 00 | 29. 62 |
| | ATOM | 2741 | CB | ALA 384 | 34. 787 | 22. 885 | 54. 789 | 1. 00 | 29. 04 |
| | ATOM | 2742 | C | ALA 384 | 32. 604 | 24. 095 | 54. 509 | 1. 00 | 29. 94 |
| 25 | ATOM | 2743 | 0 | ALA 384 | 32. 211 | 25. 259 | 54. 544 | 1. 00 | 28. 35 |
| | ATOM | 2744 | N | GLY 385 | 32. 141 | 23. 193 | 53. 639 | 1. 00 | 31. 38 |
| | ATOM | 2745 | CA | GLY 385 | 31. 149 | 23. 525 | 52. 621 | 1. 00 | 30. 00 |
| | ATOM | 2746 | C | GLY 385 | 29. 870 | 24. 198 | 53. 090 | 1. 00 | 30. 54 |
| | ATOM | 2747 | 0 | GLY 385 | 29. 522 | 25. 285 | 52. 613 | 1. 00 | 28. 88 |

- 239 -

|   | ATOM | 2748 | N | LEU 386 | 29.151 | 23.559 | 54.010 | 1.00 | 29.58 |
|---|------|------|-----|---------|--------|--------|--------|------|-------|
|   | ATOM | 2749 | CA | LEU 386 | 27.917 | 24.148 | 54.522 | 1.00 | 28.86 |
|   | ATOM | 2750 | CB | LEU 386 | 27.410 | 23.374 | 55.749 | 1.00 | 25.55 |
|   | ATOM | 2751 | CG | LEU 386 | 26.141 | 23.824 | 56.493 | 1.00 | 21.28 |
| 5 | ATOM | 2752 | CD1 | LEU 386 | 26.504 | 24.768 | 57.605 | 1.00 | 18.56 |
|   | ATOM | 2753 | CD2 | LEU 386 | 25.157 | 24.456 | 55.533 | 1.00 | 17.77 |
|   | ATOM | 2754 | C | LEU 386 | 28.199 | 25.595 | 54.898 | 1.00 | 30.29 |
|   | ATOM | 2755 | O | LEU 386 | 27.344 | 26.458 | 54.728 | 1.00 | 30.86 |
|   | ATOM | 2756 | N | ALA 387 | 29.413 | 25.846 | 55.393 | 1.00 | 32.40 |
| 10 | ATOM | 2757 | CA | ALA 387 | 29.851 | 27.184 | 55.799 | 1.00 | 32.84 |
|   | ATOM | 2758 | CB | ALA 387 | 31.181 | 27.101 | 56.536 | 1.00 | 31.99 |
|   | ATOM | 2759 | C | ALA 387 | 29.991 | 28.098 | 54.585 | 1.00 | 34.20 |
|   | ATOM | 2760 | O | ALA 387 | 29.509 | 29.235 | 54.588 | 1.00 | 34.34 |
|   | ATOM | 2761 | N | GLY 388 | 30.663 | 27.597 | 53.553 | 1.00 | 34.88 |
| 15 | ATOM | 2762 | CA | GLY 388 | 30.831 | 28.378 | 52.344 | 1.00 | 35.13 |
|   | ATOM | 2763 | C | GLY 388 | 29.467 | 28.833 | 51.867 | 1.00 | 35.42 |
|   | ATOM | 2764 | O | GLY 388 | 29.257 | 30.005 | 51.545 | 1.00 | 36.39 |
|   | ATOM | 2765 | N | VAL 389 | 28.524 | 27.898 | 51.839 | 1.00 | 34.42 |
|   | ATOM | 2766 | CA | VAL 389 | 27.167 | 28.202 | 51.402 | 1.00 | 32.28 |
| 20 | ATOM | 2767 | CB | VAL 389 | 26.266 | 26.949 | 51.487 | 1.00 | 31.56 |
|   | ATOM | 2768 | CG1 | VAL 389 | 24.856 | 27.285 | 51.027 | 1.00 | 28.68 |
|   | ATOM | 2769 | CG2 | VAL 389 | 26.853 | 25.836 | 50.638 | 1.00 | 28.05 |
|   | ATOM | 2770 | C | VAL 389 | 26.579 | 29.307 | 52.273 | 1.00 | 30.86 |
|   | ATOM | 2771 | O | VAL 389 | 26.072 | 30.304 | 51.762 | 1.00 | 26.91 |
| 25 | ATOM | 2772 | N | ILE 390 | 26.665 | 29.115 | 53.586 | 1.00 | 31.06 |
|   | ATOM | 2773 | CA | ILE 390 | 26.146 | 30.073 | 54.548 | 1.00 | 34.83 |
|   | ATOM | 2774 | CB | ILE 390 | 26.262 | 29.538 | 56.001 | 1.00 | 32.76 |
|   | ATOM | 2775 | CG2 | ILE 390 | 25.733 | 30.562 | 56.996 | 1.00 | 31.45 |
|   | ATOM | 2776 | CG1 | ILE 390 | 25.425 | 28.274 | 56.154 | 1.00 | 32.06 |

- 240 -

| ATOM | 2777 | CD1 | ILE | 390 | 25.311 | 27.804 | 57.572 | 1.00 | 31.73 |
|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| ATOM | 2778 | C | ILE | 390 | 26.858 | 31.415 | 54.444 | 1.00 | 39.01 |
| ATOM | 2779 | O | ILE | 390 | 26.209 | 32.465 | 54.370 | 1.00 | 42.11 |
| ATOM | 2780 | N | ASN | 391 | 28.186 | 31.398 | 54.437 | 1.00 | 41.07 |
| ATOM | 2781 | CA | ASN | 391 | 28.921 | 32.652 | 54.326 | 1.00 | 42.97 |
| ATOM | 2782 | CB | ASN | 391 | 30.430 | 32.386 | 54.290 | 1.00 | 47.00 |
| ATOM | 2783 | CG | ASN | 391 | 31.061 | 32.452 | 55.678 | 1.00 | 51.32 |
| ATOM | 2784 | OD1 | ASN | 391 | 32.205 | 32.029 | 55.878 | 1.00 | 51.98 |
| ATOM | 2785 | ND2 | ASN | 391 | 30.312 | 32.996 | 56.646 | 1.00 | 51.87 |
| ATOM | 2786 | C | ASN | 391 | 28.459 | 33.377 | 53.070 | 1.00 | 42.59 |
| ATOM | 2787 | O | ASN | 391 | 27.927 | 34.488 | 53.141 | 1.00 | 40.64 |
| ATOM | 2788 | N | ARG | 392 | 28.638 | 32.723 | 51.928 | 1.00 | 43.30 |
| ATOM | 2789 | CA | ARG | 392 | 28.237 | 33.277 | 50.644 | 1.00 | 45.75 |
| ATOM | 2790 | CB | ARG | 392 | 28.328 | 32.182 | 49.571 | 1.00 | 48.20 |
| ATOM | 2791 | CG | ARG | 392 | 27.020 | 31.811 | 48.892 | 1.00 | 54.22 |
| ATOM | 2792 | CD | ARG | 392 | 26.803 | 32.578 | 47.590 | 1.00 | 59.36 |
| ATOM | 2793 | NE | ARG | 392 | 27.491 | 31.984 | 46.437 | 1.00 | 66.46 |
| ATOM | 2794 | CZ | ARG | 392 | 28.794 | 32.098 | 46.156 | 1.00 | 69.91 |
| ATOM | 2795 | NH1 | ARG | 392 | 29.613 | 32.793 | 46.941 | 1.00 | 69.61 |
| ATOM | 2796 | NH2 | ARG | 392 | 29.279 | 31.524 | 45.063 | 1.00 | 70.50 |
| ATOM | 2797 | C | ARG | 392 | 26.822 | 33.854 | 50.711 | 1.00 | 45.30 |
| ATOM | 2798 | O | ARG | 392 | 26.474 | 34.777 | 49.973 | 1.00 | 44.35 |
| ATOM | 2799 | N | MET | 393 | 26.009 | 33.316 | 51.607 | 1.00 | 47.21 |
| ATOM | 2800 | CA | MET | 393 | 24.640 | 33.785 | 51.739 | 1.00 | 50.87 |
| ATOM | 2801 | CB | MET | 393 | 23.761 | 32.687 | 52.346 | 1.00 | 49.84 |
| ATOM | 2802 | CG | MET | 393 | 23.427 | 31.551 | 51.389 | 1.00 | 45.97 |
| ATOM | 2803 | SD | MET | 393 | 22.244 | 30.416 | 52.096 | 1.00 | 42.67 |
| ATOM | 2804 | CE | MET | 393 | 20.761 | 31.465 | 52.244 | 1.00 | 42.67 |
| ATOM | 2805 | C | MET | 393 | 24.559 | 35.046 | 52.581 | 1.00 | 54.43 |

- 241 -

|  | ATOM | 2806 | O | MET 393 | 23.631 | 35.851 | 52.443 | 1.00 | 53.85 |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 2807 | N | ARG 394 | 25.528 | 35.208 | 53.469 | 1.00 | 59.09 |
|  | ATOM | 2808 | CA | ARG 394 | 25.568 | 36.386 | 54.314 | 1.00 | 64.57 |
|  | ATOM | 2809 | CB | ARG 394 | 26.624 | 36.224 | 55.404 | 1.00 | 65.91 |
| 5 | ATOM | 2810 | CG | ARG 394 | 26.830 | 37.477 | 56.228 | 1.00 | 67.95 |
|  | ATOM | 2811 | CD | ARG 394 | 28.048 | 37.364 | 57.130 | 1.00 | 69.02 |
|  | ATOM | 2812 | NE | ARG 394 | 28.499 | 38.673 | 57.600 | 1.00 | 68.97 |
|  | ATOM | 2813 | CZ | ARG 394 | 27.776 | 39.494 | 58.357 | 1.00 | 69.21 |
|  | ATOM | 2814 | NH1 | ARG 394 | 26.553 | 39.151 | 58.743 | 1.00 | 70.35 |
| 10 | ATOM | 2815 | NH2 | ARG 394 | 28.281 | 40.662 | 58.732 | 1.00 | 68.24 |
|  | ATOM | 2816 | C | ARG 394 | 25.952 | 37.537 | 53.404 | 1.00 | 67.94 |
|  | ATOM | 2817 | O | ARG 394 | 25.306 | 38.588 | 53.391 | 1.00 | 67.14 |
|  | ATOM | 2818 | N | GLU 395 | 27.012 | 37.313 | 52.633 | 1.00 | 72.08 |
|  | ATOM | 2819 | CA | GLU 395 | 27.513 | 38.314 | 51.707 | 1.00 | 77.04 |
| 15 | ATOM | 2820 | CB | GLU 395 | 28.578 | 37.691 | 50.784 | 1.00 | 78.09 |
|  | ATOM | 2821 | CG | GLU 395 | 29.425 | 38.685 | 49.955 | 1.00 | 81.99 |
|  | ATOM | 2822 | CD | GLU 395 | 30.402 | 39.533 | 50.789 | 1.00 | 84.19 |
|  | ATOM | 2823 | OE1 | GLU 395 | 29.949 | 40.442 | 51.526 | 1.00 | 83.64 |
|  | ATOM | 2824 | OE2 | GLU 395 | 31.631 | 39.290 | 50.702 | 1.00 | 84.22 |
| 20 | ATOM | 2825 | C | GLU 395 | 26.340 | 38.873 | 50.898 | 1.00 | 79.30 |
|  | ATOM | 2826 | O | GLU 395 | 26.250 | 40.078 | 50.683 | 1.00 | 81.15 |
|  | ATOM | 2827 | N | SER 396 | 25.423 | 38.007 | 50.481 | 1.00 | 81.59 |
|  | ATOM | 2828 | CA | SER 396 | 24.276 | 38.451 | 49.696 | 1.00 | 83.40 |
|  | ATOM | 2829 | CB | SER 396 | 23.379 | 37.264 | 49.366 | 1.00 | 84.05 |
| 25 | ATOM | 2830 | OG | SER 396 | 24.123 | 36.252 | 48.716 | 1.00 | 86.28 |
|  | ATOM | 2831 | C | SER 396 | 23.462 | 39.526 | 50.406 | 1.00 | 84.36 |
|  | ATOM | 2832 | O | SER 396 | 23.578 | 40.708 | 50.092 | 1.00 | 84.49 |
|  | ATOM | 2833 | N | ARG 397 | 22.639 | 39.118 | 51.362 | 1.00 | 86.41 |
|  | ATOM | 2834 | CA | ARG 397 | 21.812 | 40.070 | 52.090 | 1.00 | 88.71 |

- 242 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2835 | CB | ARG | 397 | 20.682 | 39.335 | 52.816 | 1.00 89.74 |
| | ATOM | 2836 | CG | ARG | 397 | 19.579 | 40.241 | 53.346 | 1.00 90.87 |
| | ATOM | 2837 | CD | ARG | 397 | 19.096 | 39.776 | 54.713 | 1.00 91.04 |
| | ATOM | 2838 | NE | ARG | 397 | 20.021 | 40.158 | 55.782 | 1.00 89.87 |
| 5 | ATOM | 2839 | CZ | ARG | 397 | 19.905 | 39.766 | 57.047 | 1.00 89.80 |
| | ATOM | 2840 | NH1 | ARG | 397 | 18.906 | 38.971 | 57.409 | 1.00 91.15 |
| | ATOM | 2841 | NH2 | ARG | 397 | 20.779 | 40.174 | 57.955 | 1.00 87.97 |
| | ATOM | 2842 | C | ARG | 397 | 22.653 | 40.847 | 53.102 | 1.00 89.74 |
| | ATOM | 2843 | 0 | ARG | 397 | 22.585 | 40.588 | 54.305 | 1.00 90.41 |
| 10 | ATOM | 2844 | N | SER | 398 | 23.448 | 41.795 | 52.614 | 1.00 90.58 |
| | ATOM | 2845 | CA | SER | 398 | 24.288 | 42.602 | 53.492 | 1.00 91.09 |
| | ATOM | 2846 | CB | SER | 398 | 24.903 | 43.782 | 52.718 | 1.00 91.14 |
| | ATOM | 2847 | OG | SER | 398 | 25.845 | 43.347 | 51.747 | 1.00 89.49 |
| | ATOM | 2848 | C | SER | 398 | 23.470 | 43.129 | 54.677 | 1.00 91.27 |
| 15 | ATOM | 2849 | 0 | SER | 398 | 22.458 | 43.810 | 54.496 | 1.00 91.10 |
| | ATOM | 2850 | N | GLU | 399 | 23.904 | 42.786 | 55.887 | 1.00 91.43 |
| | ATOM | 2851 | CA | GLU | 399 | 23.238 | 43.233 | 57.108 | 1.00 90.89 |
| | ATOM | 2852 | CB | GLU | 399 | 21.799 | 42.705 | 57.183 | 1.00 91.87 |
| | ATOM | 2853 | CG | GLU | 399 | 20.969 | 43.349 | 58.298 | 1.00 93.31 |
| 20 | ATOM | 2854 | CD | GLU | 399 | 20.726 | 44.836 | 58.064 | 1.00 94.22 |
| | ATOM | 2855 | OE1 | GLU | 399 | 20.270 | 45.533 | 58.999 | 1.00 93.53 |
| | ATOM | 2856 | OE2 | GLU | 399 | 20.986 | 45.307 | 56.936 | 1.00 94.80 |
| | ATOM | 2857 | C | GLU | 399 | 24.013 | 42.774 | 58.339 | 1.00 89.25 |
| | ATOM | 2858 | 0 | GLU | 399 | 24.987 | 42.029 | 58.236 | 1.00 88.96 |
| 25 | ATOM | 2859 | N | ASP | 400 | 23.570 | 43.226 | 59.502 | 1.00 87.38 |
| | ATOM | 2860 | CA | ASP | 400 | 24.214 | 42.883 | 60.754 | 1.00 85.70 |
| | ATOM | 2861 | CB | ASP | 400 | 23.332 | 43.352 | 61.915 | 1.00 88.35 |
| | ATOM | 2862 | CG | ASP | 400 | 22.861 | 44.795 | 61.743 | 1.00 90.64 |
| | ATOM | 2863 | OD1 | ASP | 400 | 22.059 | 45.055 | 60.817 | 1.00 91.42 |

- 243 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2864 | OD2 | ASP | 400 | 23. 297 | 45. 671 | 62. 524 | 1. 00 | 91. 68 |
| ATOM | 2865 | C | ASP | 400 | 24. 496 | 41. 385 | 60. 853 | 1. 00 | 82. 94 |
| ATOM | 2866 | O | ASP | 400 | 25. 506 | 40. 900 | 60. 346 | 1. 00 | 82. 03 |
| ATOM | 2867 | N | VAL | 401 | 23. 593 | 40. 658 | 61. 502 | 1. 00 | 79. 90 |
| ATOM | 2868 | CA | VAL | 401 | 23. 738 | 39. 219 | 61. 682 | 1. 00 | 75. 91 |
| ATOM | 2869 | CB | VAL | 401 | 23. 607 | 38. 841 | 63. 153 | 1. 00 | 74. 20 |
| ATOM | 2870 | CG1 | VAL | 401 | 24. 803 | 39. 343 | 63. 927 | 1. 00 | 73. 12 |
| ATOM | 2871 | CG2 | VAL | 401 | 22. 314 | 39. 430 | 63. 710 | 1. 00 | 72. 79 |
| ATOM | 2872 | C | VAL | 401 | 22. 662 | 38. 458 | 60. 925 | 1. 00 | 74. 63 |
| ATOM | 2873 | O | VAL | 401 | 21. 489 | 38. 846 | 60. 942 | 1. 00 | 75. 56 |
| ATOM | 2874 | N | MET | 402 | 23. 063 | 37. 365 | 60. 278 | 1. 00 | 70. 61 |
| ATOM | 2875 | CA | MET | 402 | 22. 130 | 36. 539 | 59. 521 | 1. 00 | 65. 65 |
| ATOM | 2876 | CB | MET | 402 | 22. 818 | 35. 887 | 58. 325 | 1. 00 | 62. 74 |
| ATOM | 2877 | CG | MET | 402 | 21. 897 | 34. 958 | 57. 543 | 1. 00 | 56. 61 |
| ATOM | 2878 | SD | MET | 402 | 22. 543 | 34. 551 | 55. 906 | 1. 00 | 52. 49 |
| ATOM | 2879 | CE | MET | 402 | 23. 857 | 33. 399 | 56. 323 | 1. 00 | 49. 76 |
| ATOM | 2880 | C | MET | 402 | 21. 532 | 35. 450 | 60. 381 | 1. 00 | 65. 00 |
| ATOM | 2881 | O | MET | 402 | 22. 222 | 34. 513 | 60. 781 | 1. 00 | 65. 18 |
| ATOM | 2882 | N | ARG | 403 | 20. 241 | 35. 575 | 60. 657 | 1. 00 | 63. 62 |
| ATOM | 2883 | CA | ARG | 403 | 19. 535 | 34. 593 | 61. 462 | 1. 00 | 61. 57 |
| ATOM | 2884 | CB | ARG | 403 | 18. 418 | 35. 275 | 62. 262 | 1. 00 | 64. 83 |
| ATOM | 2885 | CG | ARG | 403 | 18. 856 | 36. 547 | 62. 987 | 1. 00 | 70. 01 |
| ATOM | 2886 | CD | ARG | 403 | 17. 691 | 37. 205 | 63. 724 | 1. 00 | 75. 36 |
| ATOM | 2887 | NE | ARG | 403 | 17. 412 | 36. 582 | 65. 018 | 1. 00 | 80. 50 |
| ATOM | 2888 | CZ | ARG | 403 | 16. 305 | 36. 788 | 65. 731 | 1. 00 | 83. 41 |
| ATOM | 2889 | NH1 | ARG | 403 | 15. 358 | 37. 603 | 65. 277 | 1. 00 | 84. 55 |
| ATOM | 2890 | NH2 | ARG | 403 | 16. 147 | 36. 187 | 66. 907 | 1. 00 | 83. 64 |
| ATOM | 2891 | C | ARG | 403 | 18. 946 | 33. 560 | 60. 504 | 1. 00 | 57. 99 |
| ATOM | 2892 | O | ARG | 403 | 17. 775 | 33. 639 | 60. 135 | 1. 00 | 58. 57 |

- 244 -

| | ATOM | 2893 | N | ILE | 404 | 19.762 | 32.597 | 60.091 | 1.00 | 52.97 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 2894 | CA | ILE | 404 | 19.301 | 31.570 | 59.170 | 1.00 | 49.14 |
| | ATOM | 2895 | CB | ILE | 404 | 20.293 | 31.412 | 57.999 | 1.00 | 47.44 |
| | ATOM | 2896 | CG2 | ILE | 404 | 21.538 | 30.680 | 58.458 | 1.00 | 43.94 |
| 5 | ATOM | 2897 | CG1 | ILE | 404 | 19.629 | 30.649 | 56.854 | 1.00 | 48.45 |
| | ATOM | 2898 | CD1 | ILE | 404 | 20.477 | 30.559 | 55.598 | 1.00 | 48.95 |
| | ATOM | 2899 | C | ILE | 404 | 19.126 | 30.222 | 59.879 | 1.00 | 48.34 |
| | ATOM | 2900 | O | ILE | 404 | 19.771 | 29.967 | 60.897 | 1.00 | 48.83 |
| | ATOM | 2901 | N | THR | 405 | 18.236 | 29.380 | 59.346 | 1.00 | 46.42 |
| 10 | ATOM | 2902 | CA | THR | 405 | 17.956 | 28.043 | 59.892 | 1.00 | 42.37 |
| | ATOM | 2903 | CB | THR | 405 | 16.451 | 27.838 | 60.222 | 1.00 | 41.93 |
| | ATOM | 2904 | OG1 | THR | 405 | 16.010 | 28.839 | 61.145 | 1.00 | 43.89 |
| | ATOM | 2905 | CG2 | THR | 405 | 16.227 | 26.475 | 60.849 | 1.00 | 38.85 |
| | ATOM | 2906 | C | THR | 405 | 18.332 | 26.990 | 58.857 | 1.00 | 39.95 |
| 15 | ATOM | 2907 | O | THR | 405 | 18.178 | 27.204 | 57.653 | 1.00 | 38.97 |
| | ATOM | 2908 | N | VAL | 406 | 18.809 | 25.844 | 59.324 | 1.00 | 38.10 |
| | ATOM | 2909 | CA | VAL | 406 | 19.195 | 24.776 | 58.414 | 1.00 | 36.64 |
| | ATOM | 2910 | CB | VAL | 406 | 20.686 | 24.442 | 58.563 | 1.00 | 35.12 |
| | ATOM | 2911 | CG1 | VAL | 406 | 21.069 | 23.342 | 57.600 | 1.00 | 35.29 |
| 20 | ATOM | 2912 | CG2 | VAL | 406 | 21.515 | 25.672 | 58.303 | 1.00 | 35.40 |
| | ATOM | 2913 | C | VAL | 406 | 18.390 | 23.499 | 58.635 | 1.00 | 35.83 |
| | ATOM | 2914 | O | VAL | 406 | 18.214 | 23.058 | 59.765 | 1.00 | 37.06 |
| | ATOM | 2915 | N | GLY | 407 | 17.895 | 22.915 | 57.549 | 1.00 | 34.50 |
| | ATOM | 2916 | CA | GLY | 407 | 17.143 | 21.680 | 57.653 | 1.00 | 32.79 |
| 25 | ATOM | 2917 | C | GLY | 407 | 18.074 | 20.522 | 57.353 | 1.00 | 32.90 |
| | ATOM | 2918 | O | GLY | 407 | 18.704 | 20.467 | 56.294 | 1.00 | 33.85 |
| | ATOM | 2919 | N | VAL | 408 | 18.177 | 19.585 | 58.279 | 1.00 | 31.27 |
| | ATOM | 2920 | CA | VAL | 408 | 19.064 | 18.466 | 58.054 | 1.00 | 29.57 |
| | ATOM | 2921 | CB | VAL | 408 | 20.199 | 18.491 | 59.042 | 1.00 | 29.66 |

- 245 -

|   | ATOM | 2922 | CG1 | VAL | 408 | 21.390 | 17.767 | 58.468 | 1.00 | 31.77 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 2923 | CG2 | VAL | 408 | 20.515 | 19.916 | 59.412 | 1.00 | 29.91 |
|   | ATOM | 2924 | C   | VAL | 408 | 18.366 | 17.135 | 58.206 | 1.00 | 29.58 |
|   | ATOM | 2925 | O   | VAL | 408 | 17.392 | 17.015 | 58.942 | 1.00 | 28.54 |
| 5 | ATOM | 2926 | N   | ASP | 409 | 18.878 | 16.131 | 57.509 | 1.00 | 30.15 |
|   | ATOM | 2927 | CA  | ASP | 409 | 18.324 | 14.789 | 57.598 | 1.00 | 31.95 |
|   | ATOM | 2928 | CB  | ASP | 409 | 17.109 | 14.635 | 56.674 | 1.00 | 35.66 |
|   | ATOM | 2929 | CG  | ASP | 409 | 16.455 | 13.252 | 56.775 | 1.00 | 40.01 |
|   | ATOM | 2930 | OD1 | ASP | 409 | 15.613 | 12.928 | 55.898 | 1.00 | 40.26 |
| 10 | ATOM | 2931 | OD2 | ASP | 409 | 16.773 | 12.499 | 57.728 | 1.00 | 39.33 |
|   | ATOM | 2932 | C   | ASP | 409 | 19.415 | 13.824 | 57.180 | 1.00 | 31.91 |
|   | ATOM | 2933 | O   | ASP | 409 | 20.352 | 14.208 | 56.484 | 1.00 | 32.39 |
|   | ATOM | 2934 | N   | GLY | 410 | 19.300 | 12.574 | 57.607 | 1.00 | 31.09 |
|   | ATOM | 2935 | CA  | GLY | 410 | 20.299 | 11.593 | 57.233 | 1.00 | 29.56 |
| 15 | ATOM | 2936 | C   | GLY | 410 | 20.703 | 10.704 | 58.385 | 1.00 | 29.32 |
|   | ATOM | 2937 | O   | GLY | 410 | 20.510 | 11.041 | 59.558 | 1.00 | 28.27 |
|   | ATOM | 2938 | N   | SER | 411 | 21.282 | 9.559  | 58.053 | 1.00 | 28.24 |
|   | ATOM | 2939 | CA  | SER | 411 | 21.699 | 8.631  | 59.086 | 1.00 | 27.52 |
|   | ATOM | 2940 | CB  | SER | 411 | 22.018 | 7.253  | 58.481 | 1.00 | 29.46 |
| 20 | ATOM | 2941 | OG  | SER | 411 | 23.016 | 7.316  | 57.471 | 1.00 | 31.64 |
|   | ATOM | 2942 | C   | SER | 411 | 22.895 | 9.160  | 59.863 | 1.00 | 25.78 |
|   | ATOM | 2943 | O   | SER | 411 | 22.909 | 9.113  | 61.090 | 1.00 | 25.89 |
|   | ATOM | 2944 | N   | VAL | 412 | 23.890 | 9.687  | 59.161 | 1.00 | 23.18 |
|   | ATOM | 2945 | CA  | VAL | 412 | 25.076 | 10.185 | 59.839 | 1.00 | 21.25 |
| 25 | ATOM | 2946 | CB  | VAL | 412 | 26.099 | 10.669 | 58.841 | 1.00 | 20.56 |
|   | ATOM | 2947 | CG1 | VAL | 412 | 27.372 | 11.084 | 59.564 | 1.00 | 17.73 |
|   | ATOM | 2948 | CG2 | VAL | 412 | 26.378 | 9.552  | 57.857 | 1.00 | 20.59 |
|   | ATOM | 2949 | C   | VAL | 412 | 24.769 | 11.300 | 60.818 | 1.00 | 20.44 |
|   | ATOM | 2950 | O   | VAL | 412 | 25.182 | 11.262 | 61.983 | 1.00 | 21.51 |

- 246 -

| | ATOM | 2951 | N | TYR | 413 | 24.033 | 12.288 | 60.340 | 1.00 | 16.42 |
|---|------|------|-----|-----|-----|--------|--------|--------|------|-------|
| | ATOM | 2952 | CA | TYR | 413 | 23.659 | 13.409 | 61.171 | 1.00 | 16.41 |
| | ATOM | 2953 | CB | TYR | 413 | 23.095 | 14.526 | 60.288 | 1.00 | 16.40 |
| | ATOM | 2954 | CG | TYR | 413 | 22.700 | 15.762 | 61.051 | 1.00 | 14.37 |
| 5 | ATOM | 2955 | CD1 | TYR | 413 | 23.645 | 16.707 | 61.434 | 1.00 | 13.43 |
| | ATOM | 2956 | CE1 | TYR | 413 | 23.296 | 17.789 | 62.226 | 1.00 | 13.93 |
| | ATOM | 2957 | CD2 | TYR | 413 | 21.401 | 15.939 | 61.470 | 1.00 | 13.10 |
| | ATOM | 2958 | CE2 | TYR | 413 | 21.049 | 17.007 | 62.256 | 1.00 | 15.82 |
| | ATOM | 2959 | CZ | TYR | 413 | 21.994 | 17.927 | 62.638 | 1.00 | 14.65 |
| 10 | ATOM | 2960 | OH | TYR | 413 | 21.620 | 18.948 | 63.475 | 1.00 | 16.02 |
| | ATOM | 2961 | C | TYR | 413 | 22.626 | 13.007 | 62.233 | 1.00 | 17.41 |
| | ATOM | 2962 | O | TYR | 413 | 22.364 | 13.758 | 63.172 | 1.00 | 18.36 |
| | ATOM | 2963 | N | LYS | 414 | 22.035 | 11.826 | 62.103 | 1.00 | 18.12 |
| | ATOM | 2964 | CA | LYS | 414 | 21.033 | 11.426 | 63.083 | 1.00 | 19.00 |
| 15 | ATOM | 2965 | CB | LYS | 414 | 19.706 | 11.130 | 62.384 | 1.00 | 19.22 |
| | ATOM | 2966 | CG | LYS | 414 | 18.962 | 12.358 | 61.894 | 1.00 | 18.92 |
| | ATOM | 2967 | CD | LYS | 414 | 17.615 | 11.965 | 61.314 | 1.00 | 21.36 |
| | ATOM | 2968 | CE | LYS | 414 | 16.829 | 13.181 | 60.855 | 1.00 | 25.08 |
| | ATOM | 2969 | NZ | LYS | 414 | 15.567 | 12.829 | 60.132 | 1.00 | 28.46 |
| 20 | ATOM | 2970 | C | LYS | 414 | 21.400 | 10.249 | 63.975 | 1.00 | 20.50 |
| | ATOM | 2971 | O | LYS | 414 | 20.637 | 9.883 | 64.871 | 1.00 | 21.27 |
| | ATOM | 2972 | N | LEU | 415 | 22.565 | 9.655 | 63.753 | 1.00 | 22.22 |
| | ATOM | 2973 | CA | LEU | 415 | 22.958 | 8.511 | 64.565 | 1.00 | 23.27 |
| | ATOM | 2974 | CB | LEU | 415 | 22.679 | 7.218 | 63.784 | 1.00 | 21.47 |
| 25 | ATOM | 2975 | CG | LEU | 415 | 21.234 | 6.978 | 63.313 | 1.00 | 17.45 |
| | ATOM | 2976 | CD1 | LEU | 415 | 21.158 | 5.672 | 62.545 | 1.00 | 16.66 |
| | ATOM | 2977 | CD2 | LEU | 415 | 20.293 | 6.954 | 64.498 | 1.00 | 14.44 |
| | ATOM | 2978 | C | LEU | 415 | 24.418 | 8.566 | 65.033 | 1.00 | 25.05 |
| | ATOM | 2979 | O | LEU | 415 | 24.921 | 7.625 | 65.657 | 1.00 | 26.05 |

- 247 -

|      | ATOM | 2980 | N   | HIS 416 | 25.095 | 9.673  | 64.736 | 1.00 | 24.04 |
|------|------|------|-----|---------|--------|--------|--------|------|-------|
|      | ATOM | 2981 | CA  | HIS 416 | 26.481 | 9.852  | 65.147 | 1.00 | 22.40 |
|      | ATOM | 2982 | CB  | HIS 416 | 27.365 | 9.997  | 63.922 | 1.00 | 23.29 |
|      | ATOM | 2983 | CG  | HIS 416 | 27.383 | 8.774  | 63.069 | 1.00 | 25.75 |
| 5    | ATOM | 2984 | CD2 | HIS 416 | 28.392 | 7.937  | 62.729 | 1.00 | 27.82 |
|      | ATOM | 2985 | ND1 | HIS 416 | 26.241 | 8.248  | 62.506 | 1.00 | 26.69 |
|      | ATOM | 2986 | CE1 | HIS 416 | 26.545 | 7.138  | 61.857 | 1.00 | 28.69 |
|      | ATOM | 2987 | NE2 | HIS 416 | 27.844 | 6.926  | 61.977 | 1.00 | 28.20 |
|      | ATOM | 2988 | C   | HIS 416 | 26.577 | 11.080 | 66.027 | 1.00 | 21.63 |
| 10   | ATOM | 2989 | O   | HIS 416 | 26.808 | 12.184 | 65.558 | 1.00 | 22.44 |
|      | ATOM | 2990 | N   | PRO 417 | 26.386 | 10.898 | 67.331 | 1.00 | 21.25 |
|      | ATOM | 2991 | CD  | PRO 417 | 26.126 | 9.627  | 68.015 | 1.00 | 22.18 |
|      | ATOM | 2992 | CA  | PRO 417 | 26.440 | 11.991 | 68.297 | 1.00 | 22.07 |
|      | ATOM | 2993 | CB  | PRO 417 | 26.447 | 11.258 | 69.627 | 1.00 | 21.52 |
| 15   | ATOM | 2994 | CG  | PRO 417 | 25.565 | 10.108 | 69.340 | 1.00 | 23.41 |
|      | ATOM | 2995 | C   | PRO 417 | 27.655 | 12.874 | 68.113 | 1.00 | 22.46 |
|      | ATOM | 2996 | O   | PRO 417 | 27.519 | 14.076 | 67.878 | 1.00 | 22.18 |
|      | ATOM | 2997 | N   | SER 418 | 28.835 | 12.262 | 68.221 | 1.00 | 20.96 |
|      | ATOM | 2998 | CA  | SER 418 | 30.105 | 12.959 | 68.064 | 1.00 | 18.32 |
| 20   | ATOM | 2999 | CB  | SER 418 | 31.264 | 11.962 | 68.076 | 1.00 | 20.88 |
|      | ATOM | 3000 | OG  | SER 418 | 32.419 | 12.512 | 67.460 | 1.00 | 24.12 |
|      | ATOM | 3001 | C   | SER 418 | 30.099 | 13.720 | 66.757 | 1.00 | 15.71 |
|      | ATOM | 3002 | O   | SER 418 | 30.269 | 14.935 | 66.742 | 1.00 | 16.10 |
|      | ATOM | 3003 | N   | PHE 419 | 29.905 | 13.010 | 65.656 | 1.00 | 11.39 |
| 25   | ATOM | 3004 | CA  | PHE 419 | 29.864 | 13.683 | 64.379 | 1.00 | 10.22 |
|      | ATOM | 3005 | CB  | PHE 419 | 29.243 | 12.789 | 63.335 | 1.00 | 5.53  |
|      | ATOM | 3006 | CG  | PHE 419 | 29.035 | 13.468 | 62.034 | 1.00 | 1.42  |
|      | ATOM | 3007 | CD1 | PHE 419 | 29.814 | 13.137 | 60.942 | 1.00 | 3.13  |
|      | ATOM | 3008 | CD2 | PHE 419 | 28.080 | 14.449 | 61.893 | 1.00 | 1.00  |

- 248 -

|  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 3009 | CE1 | PHE | 419 | 29.648 | 13.773 | 59.712 | 1.00 | 1.47 |
|  | ATOM | 3010 | CE2 | PHE | 419 | 27.909 | 15.088 | 60.670 | 1.00 | 2.68 |
|  | ATOM | 3011 | CZ | PHE | 419 | 28.699 | 14.746 | 59.575 | 1.00 | 1.00 |
|  | ATOM | 3012 | C | PHE | 419 | 29.037 | 14.965 | 64.472 | 1.00 | 12.48 |
| 5 | ATOM | 3013 | O | PHE | 419 | 29.520 | 16.048 | 64.156 | 1.00 | 12.11 |
|  | ATOM | 3014 | N | LYS | 420 | 27.785 | 14.838 | 64.900 | 1.00 | 15.88 |
|  | ATOM | 3015 | CA | LYS | 420 | 26.917 | 16.000 | 64.994 | 1.00 | 20.63 |
|  | ATOM | 3016 | CB | LYS | 420 | 25.525 | 15.610 | 65.522 | 1.00 | 21.26 |
|  | ATOM | 3017 | CG | LYS | 420 | 24.470 | 16.730 | 65.361 | 1.00 | 22.35 |
| 10 | ATOM | 3018 | CD | LYS | 420 | 23.045 | 16.288 | 65.686 | 1.00 | 22.81 |
|  | ATOM | 3019 | CE | LYS | 420 | 22.942 | 15.740 | 67.102 | 1.00 | 25.24 |
|  | ATOM | 3020 | NZ | LYS | 420 | 21.616 | 15.092 | 67.350 | 1.00 | 27.51 |
|  | ATOM | 3021 | C | LYS | 420 | 27.505 | 17.099 | 65.866 | 1.00 | 24.04 |
|  | ATOM | 3022 | O | LYS | 420 | 27.533 | 18.260 | 65.465 | 1.00 | 23.74 |
| 15 | ATOM | 3023 | N | GLU | 421 | 27.978 | 16.733 | 67.053 | 1.00 | 29.67 |
|  | ATOM | 3024 | CA | GLU | 421 | 28.550 | 17.701 | 67.999 | 1.00 | 34.96 |
|  | ATOM | 3025 | CB | GLU | 421 | 29.075 | 16.972 | 69.244 | 1.00 | 36.76 |
|  | ATOM | 3026 | CG | GLU | 421 | 29.292 | 17.843 | 70.480 | 1.00 | 40.52 |
|  | ATOM | 3027 | CD | GLU | 421 | 29.895 | 17.047 | 71.638 | 1.00 | 43.55 |
| 20 | ATOM | 3028 | OE1 | GLU | 421 | 30.981 | 16.467 | 71.445 | 1.00 | 47.03 |
|  | ATOM | 3029 | OE2 | GLU | 421 | 29.294 | 16.990 | 72.734 | 1.00 | 43.28 |
|  | ATOM | 3030 | C | GLU | 421 | 29.680 | 18.512 | 67.369 | 1.00 | 36.40 |
|  | ATOM | 3031 | O | GLU | 421 | 29.689 | 19.745 | 67.442 | 1.00 | 38.37 |
|  | ATOM | 3032 | N | ARG | 422 | 30.629 | 17.816 | 66.751 | 1.00 | 35.66 |
| 25 | ATOM | 3033 | CA | ARG | 422 | 31.755 | 18.477 | 66.124 | 1.00 | 35.13 |
|  | ATOM | 3034 | CB | ARG | 422 | 32.801 | 17.449 | 65.684 | 1.00 | 38.76 |
|  | ATOM | 3035 | CG | ARG | 422 | 33.277 | 16.525 | 66.811 | 1.00 | 46.51 |
|  | ATOM | 3036 | CD | ARG | 422 | 33.915 | 17.286 | 67.980 | 1.00 | 51.67 |
|  | ATOM | 3037 | NE | ARG | 422 | 35.322 | 17.578 | 67.732 | 1.00 | 57.41 |

- 249 -

| | ATOM | 3038 | CZ | ARG | 422 | 36.269 | 16.649 | 67.625 | 1.00 | 60.70 |
|---|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3039 | NH1 | ARG | 422 | 35.956 | 15.364 | 67.749 | 1.00 | 60.82 |
| | ATOM | 3040 | NH2 | ARG | 422 | 37.529 | 17.002 | 67.380 | 1.00 | 61.68 |
| | ATOM | 3041 | C | ARG | 422 | 31.256 | 19.278 | 64.942 | 1.00 | 33.47 |
| 5 | ATOM | 3042 | O | ARG | 422 | 31.585 | 20.450 | 64.803 | 1.00 | 35.28 |
| | ATOM | 3043 | N | PHE | 423 | 30.446 | 18.654 | 64.096 | 1.00 | 32.46 |
| | ATOM | 3044 | CA | PHE | 423 | 29.901 | 19.348 | 62.930 | 1.00 | 30.30 |
| | ATOM | 3045 | CB | PHE | 423 | 28.949 | 18.423 | 62.165 | 1.00 | 27.32 |
| | ATOM | 3046 | CG | PHE | 423 | 28.188 | 19.106 | 61.063 | 1.00 | 23.75 |
| 10 | ATOM | 3047 | CD1 | PHE | 423 | 26.891 | 19.552 | 61.270 | 1.00 | 22.33 |
| | ATOM | 3048 | CD2 | PHE | 423 | 28.765 | 19.293 | 59.814 | 1.00 | 23.98 |
| | ATOM | 3049 | CE1 | PHE | 423 | 26.178 | 20.169 | 60.245 | 1.00 | 22.83 |
| | ATOM | 3050 | CE2 | PHE | 423 | 28.061 | 19.909 | 58.784 | 1.00 | 22.46 |
| | ATOM | 3051 | CZ | PHE | 423 | 26.769 | 20.347 | 59.001 | 1.00 | 22.73 |
| 15 | ATOM | 3052 | C | PHE | 423 | 29.185 | 20.663 | 63.280 | 1.00 | 29.75 |
| | ATOM | 3053 | O | PHE | 423 | 29.328 | 21.652 | 62.568 | 1.00 | 27.58 |
| | ATOM | 3054 | N | HIS | 424 | 28.415 | 20.694 | 64.363 | 1.00 | 30.19 |
| | ATOM | 3055 | CA | HIS | 424 | 27.743 | 21.936 | 64.692 | 1.00 | 32.48 |
| | ATOM | 3056 | CB | HIS | 424 | 26.754 | 21.760 | 65.835 | 1.00 | 32.75 |
| 20 | ATOM | 3057 | CG | HIS | 424 | 25.412 | 21.279 | 65.387 | 1.00 | 31.94 |
| | ATOM | 3058 | CD2 | HIS | 424 | 24.980 | 20.860 | 64.176 | 1.00 | 29.85 |
| | ATOM | 3059 | ND1 | HIS | 424 | 24.341 | 21.147 | 66.243 | 1.00 | 32.28 |
| | ATOM | 3060 | CE1 | HIS | 424 | 23.308 | 20.661 | 65.580 | 1.00 | 30.67 |
| | ATOM | 3061 | NE2 | HIS | 424 | 23.670 | 20.477 | 64.323 | 1.00 | 30.19 |
| 25 | ATOM | 3062 | C | HIS | 424 | 28.737 | 23.011 | 65.048 | 1.00 | 35.15 |
| | ATOM | 3063 | O | HIS | 424 | 28.689 | 24.102 | 64.487 | 1.00 | 36.91 |
| | ATOM | 3064 | N | ALA | 425 | 29.636 | 22.711 | 65.979 | 1.00 | 36.32 |
| | ATOM | 3065 | CA | ALA | 425 | 30.652 | 23.675 | 66.395 | 1.00 | 36.74 |
| | ATOM | 3066 | CB | ALA | 425 | 31.542 | 23.058 | 67.444 | 1.00 | 35.43 |

- 250 -

|  | ATOM | 3067 | C | ALA | 425 | 31. 492 | 24. 149 | 65. 201 | 1. 00 | 37. 82 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 3068 | O | ALA | 425 | 31. 420 | 25. 316 | 64. 809 | 1. 00 | 38. 66 |
|  | ATOM | 3069 | N | SER | 426 | 32. 274 | 23. 243 | 64. 617 | 1. 00 | 37. 75 |
|  | ATOM | 3070 | CA | SER | 426 | 33. 113 | 23. 576 | 63. 466 | 1. 00 | 37. 83 |
| 5 | ATOM | 3071 | CB | SER | 426 | 33. 602 | 22. 289 | 62. 782 | 1. 00 | 38. 67 |
|  | ATOM | 3072 | OG | SER | 426 | 34. 440 | 22. 560 | 61. 667 | 1. 00 | 37. 85 |
|  | ATOM | 3073 | C | SER | 426 | 32. 390 | 24. 461 | 62. 445 | 1. 00 | 37. 21 |
|  | ATOM | 3074 | O | SER | 426 | 33. 025 | 25. 151 | 61. 657 | 1. 00 | 37. 08 |
|  | ATOM | 3075 | N | VAL | 427 | 31. 064 | 24. 443 | 62. 450 | 1. 00 | 37. 84 |
| 10 | ATOM | 3076 | CA | VAL | 427 | 30. 321 | 25. 269 | 61. 510 | 1. 00 | 38. 87 |
|  | ATOM | 3077 | CB | VAL | 427 | 28. 935 | 24. 667 | 61. 194 | 1. 00 | 39. 38 |
|  | ATOM | 3078 | CG1 | VAL | 427 | 28. 000 | 25. 744 | 60. 633 | 1. 00 | 37. 50 |
|  | ATOM | 3079 | CG2 | VAL | 427 | 29. 092 | 23. 534 | 60. 188 | 1. 00 | 36. 83 |
|  | ATOM | 3080 | C | VAL | 427 | 30. 138 | 26. 655 | 62. 090 | 1. 00 | 39. 54 |
| 15 | ATOM | 3081 | O | VAL | 427 | 30. 578 | 27. 639 | 61. 512 | 1. 00 | 40. 58 |
|  | ATOM | 3082 | N | ARG | 428 | 29. 483 | 26. 724 | 63. 238 | 1. 00 | 40. 14 |
|  | ATOM | 3083 | CA | ARG | 428 | 29. 247 | 27. 993 | 63. 897 | 1. 00 | 42. 86 |
|  | ATOM | 3084 | CB | ARG | 428 | 28. 603 | 27. 739 | 65. 258 | 1. 00 | 42. 72 |
|  | ATOM | 3085 | CG | ARG | 428 | 27. 288 | 26. 982 | 65. 186 | 1. 00 | 43. 31 |
| 20 | ATOM | 3086 | CD | ARG | 428 | 27. 139 | 26. 044 | 66. 378 | 1. 00 | 46. 03 |
|  | ATOM | 3087 | NE | ARG | 428 | 25. 802 | 25. 461 | 66. 485 | 1. 00 | 47. 83 |
|  | ATOM | 3088 | CZ | ARG | 428 | 24. 690 | 26. 173 | 66. 648 | 1. 00 | 48. 39 |
|  | ATOM | 3089 | NH1 | ARG | 428 | 24. 757 | 27. 499 | 66. 716 | 1. 00 | 47. 35 |
|  | ATOM | 3090 | NH2 | ARG | 428 | 23. 516 | 25. 559 | 66. 756 | 1. 00 | 47. 34 |
| 25 | ATOM | 3091 | C | ARG | 428 | 30. 561 | 28. 768 | 64. 064 | 1. 00 | 44. 67 |
|  | ATOM | 3092 | O | ARG | 428 | 30. 577 | 30. 001 | 64. 060 | 1. 00 | 45. 05 |
|  | ATOM | 3093 | N | ARG | 429 | 31. 663 | 28. 037 | 64. 195 | 1. 00 | 45. 77 |
|  | ATOM | 3094 | CA | ARG | 429 | 32. 972 | 28. 652 | 64. 378 | 1. 00 | 46. 48 |
|  | ATOM | 3095 | CB | ARG | 429 | 33. 849 | 27. 738 | 65. 244 | 1. 00 | 52. 63 |

- 251 -

|      | ATOM | 3096 | CG  | ARG 429 | 33. 260 | 27. 471 | 66. 648 | 1. 00 | 59. 36 |
|------|------|------|-----|---------|---------|---------|---------|-------|--------|
|      | ATOM | 3097 | CD  | ARG 429 | 33. 828 | 26. 199 | 67. 328 | 1. 00 | 64. 53 |
|      | ATOM | 3098 | NE  | ARG 429 | 35. 247 | 26. 286 | 67. 677 | 1. 00 | 66. 23 |
|      | ATOM | 3099 | CZ  | ARG 429 | 35. 963 | 25. 274 | 68. 159 | 1. 00 | 66. 80 |
| 5    | ATOM | 3100 | NH1 | ARG 429 | 35. 398 | 24. 083 | 68. 357 | 1. 00 | 66. 02 |
|      | ATOM | 3101 | NH2 | ARG 429 | 37. 249 | 25. 455 | 68. 435 | 1. 00 | 68. 38 |
|      | ATOM | 3102 | C   | ARG 429 | 33. 657 | 28. 954 | 63. 049 | 1. 00 | 44. 06 |
|      | ATOM | 3103 | O   | ARG 429 | 34. 885 | 28. 943 | 62. 954 | 1. 00 | 43. 92 |
|      | ATOM | 3104 | N   | LEU 430 | 32. 847 | 29. 221 | 62. 029 | 1. 00 | 41. 46 |
| 10   | ATOM | 3105 | CA  | LEU 430 | 33. 333 | 29. 551 | 60. 692 | 1. 00 | 40. 12 |
|      | ATOM | 3106 | CB  | LEU 430 | 33. 495 | 28. 300 | 59. 830 | 1. 00 | 35. 57 |
|      | ATOM | 3107 | CG  | LEU 430 | 34. 755 | 27. 468 | 60. 042 | 1. 00 | 34. 48 |
|      | ATOM | 3108 | CD1 | LEU 430 | 34. 764 | 26. 279 | 59. 101 | 1. 00 | 32. 77 |
|      | ATOM | 3109 | CD2 | LEU 430 | 35. 965 | 28. 332 | 59. 806 | 1. 00 | 33. 57 |
| 15   | ATOM | 3110 | C   | LEU 430 | 32. 332 | 30. 468 | 60. 029 | 1. 00 | 42. 10 |
|      | ATOM | 3111 | O   | LEU 430 | 32. 503 | 30. 868 | 58. 880 | 1. 00 | 42. 67 |
|      | ATOM | 3112 | N   | THR 431 | 31. 280 | 30. 797 | 60. 763 | 1. 00 | 44. 70 |
|      | ATOM | 3113 | CA  | THR 431 | 30. 238 | 31. 658 | 60. 239 | 1. 00 | 48. 98 |
|      | ATOM | 3114 | CB  | THR 431 | 28. 923 | 30. 928 | 60. 113 | 1. 00 | 49. 80 |
| 20   | ATOM | 3115 | OG1 | THR 431 | 28. 533 | 30. 463 | 61. 410 | 1. 00 | 50. 69 |
|      | ATOM | 3116 | CG2 | THR 431 | 29. 048 | 29. 758 | 59. 159 | 1. 00 | 51. 11 |
|      | ATOM | 3117 | C   | THR 431 | 29. 999 | 32. 820 | 61. 174 | 1. 00 | 51. 66 |
|      | ATOM | 3118 | O   | THR 431 | 28. 986 | 32. 868 | 61. 881 | 1. 00 | 52. 07 |
|      | ATOM | 3119 | N   | PRO 432 | 30. 935 | 33. 774 | 61. 190 | 1. 00 | 52. 95 |
| 25   | ATOM | 3120 | CD  | PRO 432 | 32. 179 | 33. 719 | 60. 403 | 1. 00 | 51. 90 |
|      | ATOM | 3121 | CA  | PRO 432 | 30. 886 | 34. 980 | 62. 020 | 1. 00 | 52. 47 |
|      | ATOM | 3122 | CB  | PRO 432 | 32. 135 | 35. 733 | 61. 587 | 1. 00 | 54. 48 |
|      | ATOM | 3123 | CG  | PRO 432 | 33. 073 | 34. 623 | 61. 176 | 1. 00 | 54. 21 |
|      | ATOM | 3124 | C   | PRO 432 | 29. 620 | 35. 783 | 61. 739 | 1. 00 | 52. 15 |

- 252 -

| | ATOM | 3125 | O | PRO 432 | 29.257 | 35.981 | 60.582 | 1.00 | 49.70 |
|---|------|------|------|---------|--------|--------|--------|------|-------|
| | ATOM | 3126 | N | SER 433 | 28.955 | 36.243 | 62.793 | 1.00 | 53.82 |
| | ATOM | 3127 | CA | SER 433 | 27.734 | 37.042 | 62.652 | 1.00 | 57.56 |
| | ATOM | 3128 | CB | SER 433 | 28.055 | 38.372 | 61.952 | 1.00 | 59.89 |
| 5 | ATOM | 3129 | OG | SER 433 | 28.537 | 38.176 | 60.633 | 1.00 | 62.34 |
| | ATOM | 3130 | C | SER 433 | 26.570 | 36.340 | 61.926 | 1.00 | 57.57 |
| | ATOM | 3131 | O | SER 433 | 25.907 | 36.923 | 61.056 | 1.00 | 57.63 |
| | ATOM | 3132 | N | CYS 434 | 26.327 | 35.088 | 62.306 | 1.00 | 56.67 |
| | ATOM | 3133 | CA | CYS 434 | 25.256 | 34.275 | 61.738 | 1.00 | 54.67 |
| 10 | ATOM | 3134 | CB | CYS 434 | 25.805 | 33.375 | 60.634 | 1.00 | 54.21 |
| | ATOM | 3135 | SG | CYS 434 | 26.729 | 34.213 | 59.354 | 1.00 | 55.95 |
| | ATOM | 3136 | C | CYS 434 | 24.657 | 33.390 | 62.832 | 1.00 | 54.71 |
| | ATOM | 3137 | O | CYS 434 | 25.381 | 32.663 | 63.513 | 1.00 | 54.74 |
| | ATOM | 3138 | N | GLU 435 | 23.344 | 33.454 | 63.011 | 1.00 | 54.63 |
| 15 | ATOM | 3139 | CA | GLU 435 | 22.681 | 32.621 | 64.009 | 1.00 | 54.57 |
| | ATOM | 3140 | CB | GLU 435 | 21.529 | 33.383 | 64.681 | 1.00 | 59.73 |
| | ATOM | 3141 | CG | GLU 435 | 21.927 | 34.615 | 65.511 | 1.00 | 64.17 |
| | ATOM | 3142 | CD | GLU 435 | 20.717 | 35.479 | 65.902 | 1.00 | 67.96 |
| | ATOM | 3143 | OE1 | GLU 435 | 20.905 | 36.554 | 66.521 | 1.00 | 68.24 |
| 20 | ATOM | 3144 | OE2 | GLU 435 | 19.574 | 35.079 | 65.584 | 1.00 | 69.98 |
| | ATOM | 3145 | C | GLU 435 | 22.134 | 31.378 | 63.289 | 1.00 | 51.70 |
| | ATOM | 3146 | O | GLU 435 | 21.058 | 31.412 | 62.685 | 1.00 | 51.14 |
| | ATOM | 3147 | N | ILE 436 | 22.889 | 30.288 | 63.350 | 1.00 | 47.61 |
| | ATOM | 3148 | CA | ILE 436 | 22.497 | 29.046 | 62.702 | 1.00 | 43.09 |
| 25 | ATOM | 3149 | CB | ILE 436 | 23.719 | 28.331 | 62.118 | 1.00 | 38.65 |
| | ATOM | 3150 | CG2 | ILE 436 | 23.278 | 27.138 | 61.300 | 1.00 | 38.13 |
| | ATOM | 3151 | CG1 | ILE 436 | 24.502 | 29.286 | 61.234 | 1.00 | 34.79 |
| | ATOM | 3152 | CD1 | ILE 436 | 25.768 | 28.686 | 60.710 | 1.00 | 34.08 |
| | ATOM | 3153 | C | ILE 436 | 21.798 | 28.088 | 63.664 | 1.00 | 42.96 |

- 253 -

|      | ATOM | 3154 | O   | ILE 436 | 22. 403 | 27. 608 | 64. 621 | 1. 00 | 43. 46 |
|------|------|------|-----|---------|---------|---------|---------|-------|--------|
|      | ATOM | 3155 | N   | THR 437 | 20. 521 | 27. 821 | 63. 402 | 1. 00 | 41. 73 |
|      | ATOM | 3156 | CA  | THR 437 | 19. 724 | 26. 910 | 64. 218 | 1. 00 | 39. 10 |
|      | ATOM | 3157 | CB  | THR 437 | 18. 384 | 27. 553 | 64. 638 | 1. 00 | 37. 86 |
| 5    | ATOM | 3158 | OG1 | THR 437 | 18. 182 | 28. 763 | 63. 899 | 1. 00 | 37. 22 |
|      | ATOM | 3159 | CG2 | THR 437 | 18. 370 | 27. 856 | 66. 130 | 1. 00 | 37. 07 |
|      | ATOM | 3160 | C   | THR 437 | 19. 430 | 25. 672 | 63. 380 | 1. 00 | 38. 74 |
|      | ATOM | 3161 | O   | THR 437 | 18. 979 | 25. 784 | 62. 238 | 1. 00 | 39. 10 |
|      | ATOM | 3162 | N   | PHE 438 | 19. 696 | 24. 494 | 63. 936 | 1. 00 | 36. 24 |
| 10   | ATOM | 3163 | CA  | PHE 438 | 19. 449 | 23. 257 | 63. 210 | 1. 00 | 33. 18 |
|      | ATOM | 3164 | CB  | PHE 438 | 20. 556 | 22. 256 | 63. 491 | 1. 00 | 30. 88 |
|      | ATOM | 3165 | CG  | PHE 438 | 21. 905 | 22. 742 | 63. 093 | 1. 00 | 32. 48 |
|      | ATOM | 3166 | CD1 | PHE 438 | 22. 597 | 23. 652 | 63. 887 | 1. 00 | 31. 95 |
|      | ATOM | 3167 | CD2 | PHE 438 | 22. 489 | 22. 301 | 61. 913 | 1. 00 | 32. 85 |
| 15   | ATOM | 3168 | CE1 | PHE 438 | 23. 857 | 24. 118 | 63. 507 | 1. 00 | 31. 30 |
|      | ATOM | 3169 | CE2 | PHE 438 | 23. 745 | 22. 758 | 61. 522 | 1. 00 | 32. 28 |
|      | ATOM | 3170 | CZ  | PHE 438 | 24. 432 | 23. 668 | 62. 320 | 1. 00 | 31. 80 |
|      | ATOM | 3171 | C   | PHE 438 | 18. 102 | 22. 648 | 63. 563 | 1. 00 | 33. 15 |
|      | ATOM | 3172 | O   | PHE 438 | 17. 662 | 22. 729 | 64. 705 | 1. 00 | 34. 90 |
| 20   | ATOM | 3173 | N   | ILE 439 | 17. 450 | 22. 049 | 62. 570 | 1. 00 | 31. 06 |
|      | ATOM | 3174 | CA  | ILE 439 | 16. 150 | 21. 412 | 62. 738 | 1. 00 | 28. 59 |
|      | ATOM | 3175 | CB  | ILE 439 | 15. 010 | 22. 347 | 62. 321 | 1. 00 | 26. 74 |
|      | ATOM | 3176 | CG2 | ILE 439 | 15. 268 | 22. 879 | 60. 937 | 1. 00 | 27. 91 |
|      | ATOM | 3177 | CG1 | ILE 439 | 13. 683 | 21. 591 | 62. 312 | 1. 00 | 27. 91 |
| 25   | ATOM | 3178 | CD1 | ILE 439 | 12. 545 | 22. 406 | 61. 776 | 1. 00 | 26. 70 |
|      | ATOM | 3179 | C   | ILE 439 | 16. 113 | 20. 190 | 61. 837 | 1. 00 | 29. 76 |
|      | ATOM | 3180 | O   | ILE 439 | 16. 208 | 20. 310 | 60. 618 | 1. 00 | 29. 55 |
|      | ATOM | 3181 | N   | GLU 440 | 15. 977 | 19. 014 | 62. 434 | 1. 00 | 30. 76 |
|      | ATOM | 3182 | CA  | GLU 440 | 15. 934 | 17. 781 | 61. 666 | 1. 00 | 32. 34 |

- 254 -

|   | ATOM | 3183 | CB | GLU | 440 | 16.028 | 16.592 | 62.609 | 1.00 | 34.09 |
|---|------|------|----|-----|-----|--------|--------|--------|------|-------|
|   | ATOM | 3184 | CG | GLU | 440 | 17.272 | 16.583 | 63.458 | 1.00 | 38.93 |
|   | ATOM | 3185 | CD | GLU | 440 | 17.339 | 15.367 | 64.353 | 1.00 | 43.10 |
|   | ATOM | 3186 | OE1 | GLU | 440 | 16.378 | 15.162 | 65.131 | 1.00 | 44.22 |
| 5 | ATOM | 3187 | OE2 | GLU | 440 | 18.346 | 14.623 | 64.277 | 1.00 | 44.99 |
|   | ATOM | 3188 | C | GLU | 440 | 14.648 | 17.687 | 60.854 | 1.00 | 33.11 |
|   | ATOM | 3189 | O | GLU | 440 | 13.703 | 18.445 | 61.086 | 1.00 | 31.25 |
|   | ATOM | 3190 | N | SER | 441 | 14.613 | 16.764 | 59.896 | 1.00 | 34.70 |
|   | ATOM | 3191 | CA | SER | 441 | 13.416 | 16.587 | 59.086 | 1.00 | 37.07 |
| 10 | ATOM | 3192 | CB | SER | 441 | 13.738 | 15.904 | 57.761 | 1.00 | 34.79 |
|   | ATOM | 3193 | OG | SER | 441 | 14.159 | 14.579 | 57.988 | 1.00 | 34.61 |
|   | ATOM | 3194 | C | SER | 441 | 12.452 | 15.724 | 59.889 | 1.00 | 40.43 |
|   | ATOM | 3195 | O | SER | 441 | 12.866 | 14.964 | 60.773 | 1.00 | 38.99 |
|   | ATOM | 3196 | N | GLU | 442 | 11.168 | 15.855 | 59.571 | 1.00 | 43.31 |
| 15 | ATOM | 3197 | CA | GLU | 442 | 10.099 | 15.135 | 60.254 | 1.00 | 45.59 |
|   | ATOM | 3198 | CB | GLU | 442 | 8.764 | 15.638 | 59.724 | 1.00 | 46.37 |
|   | ATOM | 3199 | CG | GLU | 442 | 7.575 | 15.244 | 60.549 | 1.00 | 49.47 |
|   | ATOM | 3200 | CD | GLU | 442 | 6.653 | 16.421 | 60.794 | 1.00 | 52.25 |
|   | ATOM | 3201 | OE1 | GLU | 442 | 5.425 | 16.199 | 60.895 | 1.00 | 52.44 |
| 20 | ATOM | 3202 | OE2 | GLU | 442 | 7.160 | 17.568 | 60.894 | 1.00 | 53.16 |
|   | ATOM | 3203 | C | GLU | 442 | 10.165 | 13.607 | 60.174 | 1.00 | 47.69 |
|   | ATOM | 3204 | O | GLU | 442 | 10.828 | 13.035 | 59.314 | 1.00 | 47.21 |
|   | ATOM | 3205 | N | GLU | 443 | 9.435 | 12.964 | 61.076 | 1.00 | 50.15 |
|   | ATOM | 3206 | CA | GLU | 443 | 9.382 | 11.508 | 61.210 | 1.00 | 52.79 |
| 25 | ATOM | 3207 | CB | GLU | 443 | 8.911 | 11.204 | 62.623 | 1.00 | 55.86 |
|   | ATOM | 3208 | CG | GLU | 443 | 9.468 | 12.183 | 63.635 | 1.00 | 61.71 |
|   | ATOM | 3209 | CD | GLU | 443 | 10.948 | 11.962 | 63.877 | 1.00 | 66.19 |
|   | ATOM | 3210 | OE1 | GLU | 443 | 11.689 | 11.746 | 62.886 | 1.00 | 68.22 |
|   | ATOM | 3211 | OE2 | GLU | 443 | 11.365 | 12.006 | 65.058 | 1.00 | 67.57 |

- 255 -

|  | ATOM | 3212 | C | GLU | 443 | 8.521 | 10.711 | 60.218 | 1.00 | 53.03 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 3213 | O | GLU | 443 | 7.344 | 10.999 | 60.025 | 1.00 | 54.82 |
|  | ATOM | 3214 | N | GLY | 444 | 9.116 | 9.702 | 59.593 | 1.00 | 52.26 |
|  | ATOM | 3215 | CA | GLY | 444 | 8.373 | 8.861 | 58.667 | 1.00 | 52.32 |
| 5 | ATOM | 3216 | C | GLY | 444 | 7.966 | 9.389 | 57.302 | 1.00 | 53.07 |
|  | ATOM | 3217 | O | GLY | 444 | 6.767 | 9.460 | 57.003 | 1.00 | 52.97 |
|  | ATOM | 3218 | N | SER | 445 | 8.961 | 9.750 | 56.483 | 1.00 | 52.71 |
|  | ATOM | 3219 | CA | SER | 445 | 8.760 | 10.239 | 55.104 | 1.00 | 50.05 |
|  | ATOM | 3220 | CB | SER | 445 | 7.836 | 11.464 | 55.084 | 1.00 | 51.01 |
| 10 | ATOM | 3221 | OG | SER | 445 | 6.487 | 11.084 | 55.318 | 1.00 | 46.84 |
|  | ATOM | 3222 | C | SER | 445 | 10.076 | 10.545 | 54.356 | 1.00 | 46.51 |
|  | ATOM | 3223 | O | SER | 445 | 11.123 | 10.710 | 54.976 | 1.00 | 45.30 |
|  | ATOM | 3224 | N | GLY | 446 | 10.013 | 10.603 | 53.026 | 1.00 | 43.17 |
|  | ATOM | 3225 | CA | GLY | 446 | 11.207 | 10.842 | 52.235 | 1.00 | 40.08 |
| 15 | ATOM | 3226 | C | GLY | 446 | 11.199 | 12.057 | 51.330 | 1.00 | 39.05 |
|  | ATOM | 3227 | O | GLY | 446 | 11.414 | 13.164 | 51.803 | 1.00 | 42.74 |
|  | ATOM | 3228 | N | ARG | 447 | 10.940 | 11.873 | 50.039 | 1.00 | 37.60 |
|  | ATOM | 3229 | CA | ARG | 447 | 10.956 | 13.000 | 49.098 | 1.00 | 37.46 |
|  | ATOM | 3230 | CB | ARG | 447 | 11.549 | 12.546 | 47.747 | 1.00 | 45.51 |
| 20 | ATOM | 3231 | CG | ARG | 447 | 10.793 | 11.401 | 47.014 | 1.00 | 53.91 |
|  | ATOM | 3232 | CD | ARG | 447 | 11.521 | 10.902 | 45.743 | 1.00 | 58.18 |
|  | ATOM | 3233 | NE | ARG | 447 | 12.939 | 10.598 | 45.975 | 1.00 | 63.62 |
|  | ATOM | 3234 | CZ | ARG | 447 | 13.399 | 9.623 | 46.769 | 1.00 | 66.02 |
|  | ATOM | 3235 | NH1 | ARG | 447 | 12.560 | 8.825 | 47.425 | 1.00 | 67.97 |
| 25 | ATOM | 3236 | NH2 | ARG | 447 | 14.711 | 9.447 | 46.924 | 1.00 | 69.08 |
|  | ATOM | 3237 | C | ARG | 447 | 9.642 | 13.737 | 48.848 | 1.00 | 32.93 |
|  | ATOM | 3238 | O | ARG | 447 | 9.122 | 14.416 | 49.741 | 1.00 | 29.46 |
|  | ATOM | 3239 | N | GLY | 448 | 9.150 | 13.625 | 47.607 | 1.00 | 30.52 |
|  | ATOM | 3240 | CA | GLY | 448 | 7.902 | 14.245 | 47.202 | 1.00 | 26.03 |

- 256 -

|  | ATOM | 3241 | C | GLY | 448 | 6.845 | 13.828 | 48.200 | 1.00 | 25.25 |
|---|---|---|---|---|---|---|---|---|---|---|
|  | ATOM | 3242 | O | GLY | 448 | 5.752 | 14.378 | 48.244 | 1.00 | 24.59 |
|  | ATOM | 3243 | N | ALA | 449 | 7.186 | 12.840 | 49.018 | 1.00 | 23.74 |
|  | ATOM | 3244 | CA | ALA | 449 | 6.282 | 12.362 | 50.035 | 1.00 | 20.54 |
| 5 | ATOM | 3245 | CB | ALA | 449 | 6.611 | 10.917 | 50.410 | 1.00 | 18.12 |
|  | ATOM | 3246 | C | ALA | 449 | 6.340 | 13.251 | 51.282 | 1.00 | 22.37 |
|  | ATOM | 3247 | O | ALA | 449 | 5.307 | 13.782 | 51.693 | 1.00 | 22.56 |
|  | ATOM | 3248 | N | ALA | 450 | 7.524 | 13.443 | 51.881 | 1.00 | 22.28 |
|  | ATOM | 3249 | CA | ALA | 450 | 7.605 | 14.261 | 53.088 | 1.00 | 20.98 |
| 10 | ATOM | 3250 | CB | ALA | 450 | 9.056 | 14.432 | 53.535 | 1.00 | 9.63 |
|  | ATOM | 3251 | C | ALA | 450 | 6.937 | 15.594 | 52.872 | 1.00 | 20.66 |
|  | ATOM | 3252 | O | ALA | 450 | 6.417 | 16.168 | 53.826 | 1.00 | 19.81 |
|  | ATOM | 3253 | N | LEU | 451 | 6.943 | 16.109 | 51.702 | 1.00 | 19.91 |
|  | ATOM | 3254 | CA | LEU | 451 | 6.279 | 17.379 | 51.602 | 1.00 | 22.22 |
| 15 | ATOM | 3255 | CB | LEU | 451 | 6.586 | 18.056 | 50.279 | 1.00 | 26.74 |
|  | ATOM | 3256 | CG | LEU | 451 | 6.089 | 19.496 | 50.144 | 1.00 | 34.07 |
|  | ATOM | 3257 | CD1 | LEU | 451 | 6.894 | 20.425 | 51.040 | 1.00 | 37.55 |
|  | ATOM | 3258 | CD2 | LEU | 451 | 6.160 | 19.955 | 48.696 | 1.00 | 36.19 |
|  | ATOM | 3259 | C | LEU | 451 | 4.774 | 17.157 | 51.686 | 1.00 | 23.24 |
| 20 | ATOM | 3260 | O | LEU | 451 | 4.136 | 17.474 | 52.699 | 1.00 | 21.18 |
|  | ATOM | 3261 | N | VAL | 452 | 4.212 | 16.613 | 50.608 | 1.00 | 26.44 |
|  | ATOM | 3262 | CA | VAL | 452 | 2.798 | 16.405 | 50.557 | 1.00 | 26.90 |
|  | ATOM | 3263 | CB | VAL | 452 | 2.454 | 15.179 | 49.666 | 1.00 | 28.65 |
|  | ATOM | 3264 | CG1 | VAL | 452 | 3.082 | 15.353 | 48.300 | 1.00 | 26.01 |
| 25 | ATOM | 3265 | CG2 | VAL | 452 | 2.933 | 13.886 | 50.313 | 1.00 | 31.22 |
|  | ATOM | 3266 | C | VAL | 452 | 2.217 | 16.308 | 51.935 | 1.00 | 26.69 |
|  | ATOM | 3267 | O | VAL | 452 | 1.181 | 16.878 | 52.234 | 1.00 | 24.86 |
|  | ATOM | 3268 | N | SER | 453 | 2.880 | 15.579 | 52.769 | 1.00 | 26.07 |
|  | ATOM | 3269 | CA | SER | 453 | 2.377 | 15.346 | 54.125 | 1.00 | 26.79 |

- 257 -

| | ATOM | 3270 | CB | SER 453 | 3.058 | 14.127 | 54.756 | 1.00 | 28.88 |
|---|---|---|---|---|---|---|---|---|---|
| | ATOM | 3271 | OG | SER 453 | 2.553 | 13.881 | 56.057 | 1.00 | 37.16 |
| | ATOM | 3272 | C | SER 453 | 2.571 | 16.558 | 55.028 | 1.00 | 26.82 |
| | ATOM | 3273 | O | SER 453 | 1.658 | 17.301 | 55.377 | 1.00 | 26.28 |
| 5 | ATOM | 3274 | N | ALA 454 | 3.831 | 16.701 | 55.389 | 1.00 | 26.83 |
| | ATOM | 3275 | CA | ALA 454 | 4.250 | 17.807 | 56.177 | 1.00 | 23.37 |
| | ATOM | 3276 | CB | ALA 454 | 5.719 | 18.128 | 55.937 | 1.00 | 17.54 |
| | ATOM | 3277 | C | ALA 454 | 3.381 | 19.002 | 55.866 | 1.00 | 21.80 |
| | ATOM | 3278 | O | ALA 454 | 3.194 | 19.883 | 56.714 | 1.00 | 21.02 |
| 10 | ATOM | 3279 | N | VAL 455 | 2.848 | 19.044 | 54.656 | 1.00 | 21.59 |
| | ATOM | 3280 | CA | VAL 455 | 2.020 | 20.156 | 54.281 | 1.00 | 25.32 |
| | ATOM | 3281 | CB | VAL 455 | 2.313 | 20.557 | 52.841 | 1.00 | 28.03 |
| | ATOM | 3282 | CG1 | VAL 455 | 1.676 | 19.583 | 51.871 | 1.00 | 29.06 |
| | ATOM | 3283 | CG2 | VAL 455 | 1.813 | 21.961 | 52.577 | 1.00 | 29.98 |
| 15 | ATOM | 3284 | C | VAL 455 | 0.528 | 19.890 | 54.469 | 1.00 | 27.69 |
| | ATOM | 3285 | O | VAL 455 | -0.202 | 20.783 | 54.911 | 1.00 | 28.10 |
| | ATOM | 3286 | N | ALA 456 | 0.061 | 18.681 | 54.142 | 1.00 | 30.51 |
| | ATOM | 3287 | CA | ALA 456 | -1.367 | 18.349 | 54.318 | 1.00 | 31.54 |
| | ATOM | 3288 | CB | ALA 456 | -1.666 | 16.937 | 53.836 | 1.00 | 25.20 |
| 20 | ATOM | 3289 | C | ALA 456 | -1.702 | 18.505 | 55.797 | 1.00 | 31.77 |
| | ATOM | 3290 | O | ALA 456 | -2.853 | 18.713 | 56.176 | 1.00 | 33.11 |
| | ATOM | 3291 | N | CYS 457 | -0.673 | 18.384 | 56.625 | 1.00 | 31.33 |
| | ATOM | 3292 | CA | CYS 457 | -0.843 | 18.538 | 58.049 | 1.00 | 33.33 |
| | ATOM | 3293 | CB | CYS 457 | 0.262 | 17.815 | 58.811 | 1.00 | 36.53 |
| 25 | ATOM | 3294 | SG | CYS 457 | 1.040 | 16.448 | 57.890 | 1.00 | 44.65 |
| | ATOM | 3295 | C | CYS 457 | -0.903 | 19.990 | 58.438 | 1.00 | 34.59 |
| | ATOM | 3296 | O | CYS 457 | -1.745 | 20.391 | 59.237 | 1.00 | 34.67 |
| | ATOM | 3297 | N | LYS 458 | 0.005 | 20.779 | 57.881 | 1.00 | 37.14 |
| | ATOM | 3298 | CA | LYS 458 | 0.060 | 22.199 | 58.190 | 1.00 | 38.61 |

- 258 -

| ATOM | 3299 | CB | LYS | 458 | 1.363 | 22.799 | 57.669 | 1.00 | 37.21 |
|------|------|-----|-----|-----|-------|--------|--------|------|-------|
| ATOM | 3300 | CG | LYS | 458 | 2.573 | 22.474 | 58.538 | 1.00 | 37.81 |
| ATOM | 3301 | CD | LYS | 458 | 2.501 | 23.206 | 59.874 | 1.00 | 38.84 |
| ATOM | 3302 | CE | LYS | 458 | 3.820 | 23.143 | 60.639 | 1.00 | 38.18 |
| ATOM | 3303 | NZ | LYS | 458 | 3.812 | 24.023 | 61.851 | 1.00 | 36.51 |
| ATOM | 3304 | C | LYS | 458 | -1.128 | 22.920 | 57.596 | 1.00 | 40.24 |
| ATOM | 3305 | O | LYS | 458 | -1.377 | 24.079 | 57.898 | 1.00 | 39.64 |
| ATOM | 3306 | N | LYS | 459 | -1.869 | 22.223 | 56.752 | 1.00 | 43.69 |
| ATOM | 3307 | CA | LYS | 459 | -3.036 | 22.820 | 56.147 | 1.00 | 50.66 |
| ATOM | 3308 | CB | LYS | 459 | -3.242 | 22.248 | 54.747 | 1.00 | 55.88 |
| ATOM | 3309 | CG | LYS | 459 | -4.657 | 22.405 | 54.183 | 1.00 | 63.64 |
| ATOM | 3310 | CD | LYS | 459 | -5.037 | 23.850 | 53.856 | 1.00 | 66.97 |
| ATOM | 3311 | CE | LYS | 459 | -6.431 | 23.941 | 53.226 | 1.00 | 68.86 |
| ATOM | 3312 | NZ | LYS | 459 | -7.531 | 23.519 | 54.152 | 1.00 | 71.25 |
| ATOM | 3313 | C | LYS | 459 | -4.262 | 22.562 | 57.018 | 1.00 | 52.41 |
| ATOM | 3314 | O | LYS | 459 | -5.132 | 23.425 | 57.132 | 1.00 | 51.90 |
| ATOM | 3315 | N | ALA | 460 | -4.322 | 21.380 | 57.634 | 1.00 | 54.96 |
| ATOM | 3316 | CA | ALA | 460 | -5.449 | 20.997 | 58.495 | 1.00 | 57.72 |
| ATOM | 3317 | CB | ALA | 460 | -5.201 | 19.620 | 59.111 | 1.00 | 54.90 |
| ATOM | 3318 | C | ALA | 460 | -5.736 | 22.018 | 59.596 | 1.00 | 60.41 |
| ATOM | 3319 | O | ALA | 460 | -6.773 | 21.950 | 60.261 | 1.00 | 60.54 |
| ATOM | 3320 | N | CYS | 461 | -4.815 | 22.965 | 59.776 | 1.00 | 63.50 |
| ATOM | 3321 | CA | CYS | 461 | -4.961 | 24.022 | 60.776 | 1.00 | 66.18 |
| ATOM | 3322 | CB | CYS | 461 | -3.580 | 24.489 | 61.252 | 1.00 | 67.98 |
| ATOM | 3323 | SG | CYS | 461 | -3.604 | 26.041 | 62.185 | 1.00 | 75.61 |
| ATOM | 3324 | C | CYS | 461 | -5.727 | 25.217 | 60.200 | 1.00 | 65.92 |
| ATOM | 3325 | O | CYS | 461 | -6.940 | 25.348 | 60.490 | 1.00 | 65.70 |
| ATOM | 3326 | OXT | CYS | 461 | -5.099 | 26.001 | 59.454 | 1.00 | 65.20 |
| ATOM | 3327 | S | SO4 | 600 | 20.241 | 7.477 | 54.655 | 1.00 | 35.04 |

- 259 -

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3328 | O1 | SO4 | 600 | 19.370 | 7.951 | 53.566 | 1.00 | 33.14 |
| ATOM | 3329 | O2 | SO4 | 600 | 20.343 | 8.532 | 55.683 | 1.00 | 32.80 |
| ATOM | 3330 | O3 | SO4 | 600 | 19.690 | 6.249 | 55.260 | 1.00 | 33.32 |
| ATOM | 3331 | O4 | SO4 | 600 | 21.572 | 7.178 | 54.108 | 1.00 | 33.97 |
| ATOM | 3332 | S | SO4 | 601 | 22.953 | 22.471 | 69.199 | 1.00 | 77.32 |
| ATOM | 3333 | O1 | SO4 | 601 | 21.971 | 21.759 | 68.356 | 1.00 | 76.19 |
| ATOM | 3334 | O2 | SO4 | 601 | 22.411 | 23.803 | 69.553 | 1.00 | 77.48 |
| ATOM | 3335 | O3 | SO4 | 601 | 23.205 | 21.698 | 70.433 | 1.00 | 77.23 |
| ATOM | 3336 | O4 | SO4 | 601 | 24.224 | 22.628 | 68.461 | 1.00 | 77.19 |
| ATOM | 3337 | NA+1 | NA1 | 602 | 17.158 | 10.244 | 54.280 | 1.00 | 10.17 |
| ATOM | 3338 | OH2 | HOH | 603 | 19.770 | 14.543 | 47.159 | 1.00 | 1.00 |
| ATOM | 3340 | OH2 | HOH | 604 | 20.723 | 24.387 | 67.178 | 1.00 | 17.94 |
| ATOM | 3341 | OH2 | HOH | 605 | 10.880 | 33.802 | 37.628 | 1.00 | 1.00 |
| ATOM | 3342 | OH2 | HOH | 606 | 22.743 | 28.762 | 37.147 | 1.00 | 31.78 |
| ATOM | 3343 | OH2 | HOH | 607 | 38.906 | 1.328 | 74.611 | 1.00 | 37.76 |
| ATOM | 3344 | OH2 | HOH | 608 | 1.237 | 30.510 | 46.162 | 1.00 | 32.40 |
| ATOM | 3345 | OH2 | HOH | 609 | 34.702 | -1.731 | 56.455 | 1.00 | 62.03 |
| END | | | | | | | | | |

　　なお、表2は、当業者によって慣用されているプロテイン・データ・バンク
の表記方法に準拠して作成されている。表2中、HOHは水分子を表す。

　　本発明においては、配列番号5、及び／又は配列番号8と実質的に同一のア
ミノ酸配列を有し、グルコキナーゼ活性を有するタンパク質の結晶は本発明の
範囲内である。そのような結晶としては、例えば、表1、及び／又は表2に記
載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座
標データにおいて、表1、及び／又は表2に記載の三次元構造座標データで示
されるアミノ酸の主鎖の原子（Ｃα原子）と、該Ｃα原子と対応する前記変
更した三次元構造座標データで示されるＣα原子との平均二乗偏差が、０．

- 260 -

6オングストローム以下である結晶が挙げられる。原子の位置を表す座標の数値が異なっても、構造座標に含まれる対応する原子の位置を重ね合わせることができる二つの構造座標は、同一の三次元構造を表すものである。

5　　なお、表１、及び／又は表２に記載のＧＫタンパク質の三次元構造座標は、ドラッグデザインのための重要な情報であり、必要に応じて、コンピュータ読み取り可能な記憶媒体に保存され、コンピュータでこの情報を処理してドラッグデザインを行う。したがって、本発明の別の態様によれば、コンピュータを、表１、及び／又は表２に記載のアミノ酸残基の三次元座標を記憶する三次元座

10　標記憶手段として機能させるためのプログラムを記録したコンピュータ読み取り可能な記録媒体が提供される。

　　また、本発明の別の態様によれば、コンピュータを、表１、及び／又は表２に記載のアミノ酸残基の三次元座標に関する情報を記憶した三次元座標記憶手段と、前記三次元座標記憶手段に記憶された表１、及び／又は表２に記載のア

15　ミノ酸残基の三次元座標を用いて配列番号５、及び／又は配列番号８で表されるアミノ酸配列を有するタンパク質の化合物結合部位を推測する結合部位推測手段と、タンパク質と結合する化合物の種類と、当該化合物の三次元構造に関する情報を記憶した結合化合物記憶手段と、少なくとも、前記結合部位推測手段によって推測された配列番号５、及び／又は配列番号８で表されるアミノ酸

20　配列を有するタンパク質の化合物結合部位の三次元構造に関する情報と、前記結合化合物記憶手段に記憶された化合物の三次元構造に関する情報とを用いて前記配列表の配列番号１で表されるアミノ酸配列を有するタンパク質の化合物結合部位に適合する化合物の候補を選択する結合化合物候補選択手段、として機能させるプログラムを記録したコンピュータ読み取り可能な記録媒体が提供

25　される。さらに、本発明の別の態様によれば、上記各手段を備えるコンピュータも提供される。

（ＧＫタンパク質とそれに結合する化合物との複合体の結晶）
　　次に、本発明の別の態様によれば、配列番号５、又は配列番号８に記載のア

- 261 -

ミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含むタンパ
ク質と該タンパク質に結合可能な化合物との複合体を含む結晶及びその製造方
法が提供される。

　　GKタンパク質と結合する化合物が得られた場合は、まず、GKタンパク質
5　とその化合物を、例えば、水溶液中で混合し、複合体を形成する。このような
複合体の結晶は、共結晶法、ソーキング法などの公知の共結晶の製造方法が用
いられる。結晶化条件、結晶化方法については、上述した方法が参照される。

　　GKタンパク質と結合する化合物は、例えば、上記式（I）で表される化合
物群から選択される。

10　　ここで、上記式（I）のハロゲン原子としては、フッ素原子、塩素原子、臭
素原子、ヨウ素原子などが例示され、これらの中でも塩素原子が好ましい。

　　また、上記式（I）のA、B及び式（II）のヘテロアリール基における置
換基としては、アミノ基、カルバモイル基、カルバモイルアミノ基、カルバモ
イルオキシ基、カルボキシル基、シアノ基、スルファモイル基、トリフルオロ
15　メチル基、ハロゲン原子、ヒドロキシ基、ホルミル基、直鎖の$C_1-C_6$アルキ
ル基、環状の$C_3-C_6$炭化水素基、アラルキル基、N－アラルキルアミノ基、
N，N－ジアラルキルアミノ基、アラルキルオキシ基、アラルキルカルボニル
基、N－アラルキルカルバモイル基、アリール基、アリールチオ基、N－アリ
ールアミノ基、アリールオキシ基、アリールスルホニル基、アリールスルホニ
20　ルオキシ基、N－アリールスルホニルアミノ基、アリールスルファモイル基、
N－アリールカルバモイル基、アロイル基、アロキシ基、$C_2-C_6$アルカノイ
ル基、N－$C_2-C_6$アルカノイルアミノ基、$C_1-C_6$アルキルチオ基、N－$C_1$
－$C_6$アルキルスルファモイル基、N，N－ジ－$C_1-C_6$アルキルスルファモ
イル基、$C_1-C_6$アルキルスルフィニル基、$C_1-C_6$アルキルスルホニル基、
25　N－$C_1-C_6$アルキルスルホニルアミノ基、$C_1-C_6$アルコキシ基、$C_1-C_6$
アルコキシカルボニル基又は$C_1-C_6$アルキルアミノ基を示す）などが挙げら
れる。ここで用いられる好ましい置換基は、アミノ基、カルバモイル基、カル
バモイルアミノ基、カルバモイルオキシ基、カルボキシル基、シアノ基、スル
ファモイル基、トリフルオロメチル基、ハロゲン原子、ヒドロキシ基、ホルミ

- 262 -

ル基、直鎖のC$_1$－C$_6$アルキル基などが例示される。

　ここで、「炭化水素基」は、炭素数１乃至６の直鎖のアルキル基を示すか、又は該アルキル基を構成する炭素原子のうち、１又は２の、好ましくは１の炭素原子が窒素原子、硫黄原子又は酸素原子で置き換わっていてもよいか、及び／又は該炭素数１乃至６の直鎖のアルキル基中の炭素原子同士が二重結合又は三重結合で結合されていてもよい基である。該二重結合又は三重結合の数は、１又は２であることが好ましく、１であることがより好ましい。

　該炭化水素基としては、具体的には、メチル基、エチル基、プロピル基若しくはイソプロピル基、ブチル基又は下記式
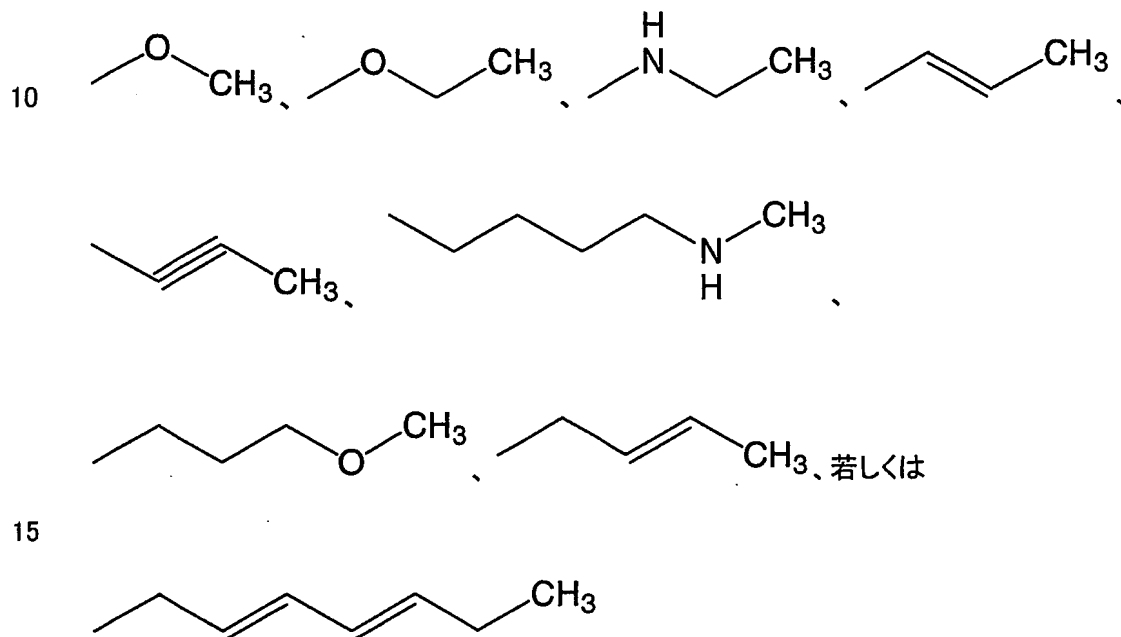


で表される基であることが好ましい。より好ましい炭化水素基は、メチル基、エチル基、プロピル基、イソプロピル基又は下記式
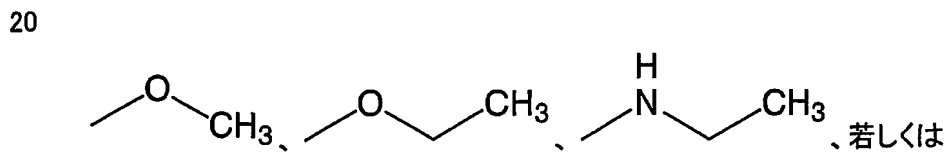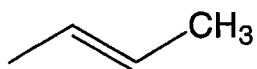
で表される基である。

　好ましいAとしては（p=0 の場合）、例えば、次の基が挙げられる。

5
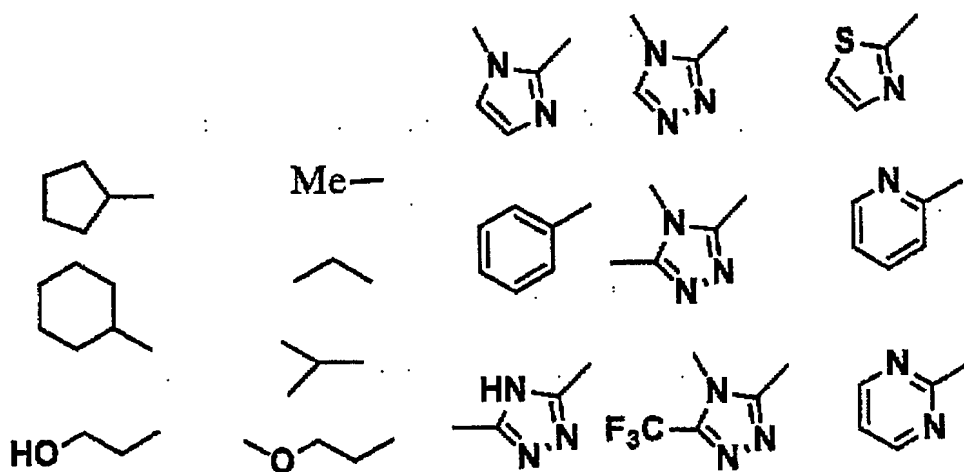


　好ましいBとしては、例えば、次の基が挙げられる。

10
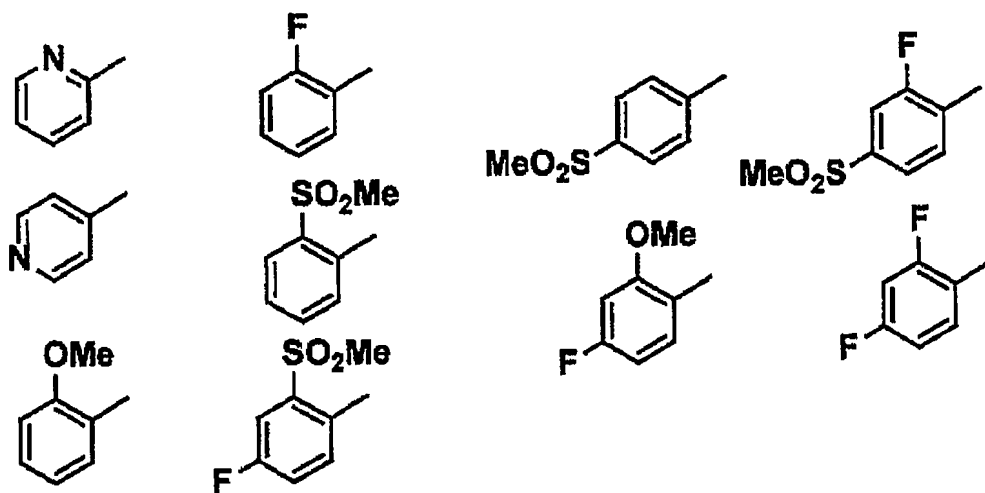
式（ＩＩ）で示されるヘテロアリール基としては、例えば，次の複素環基が
5　　挙げられる。
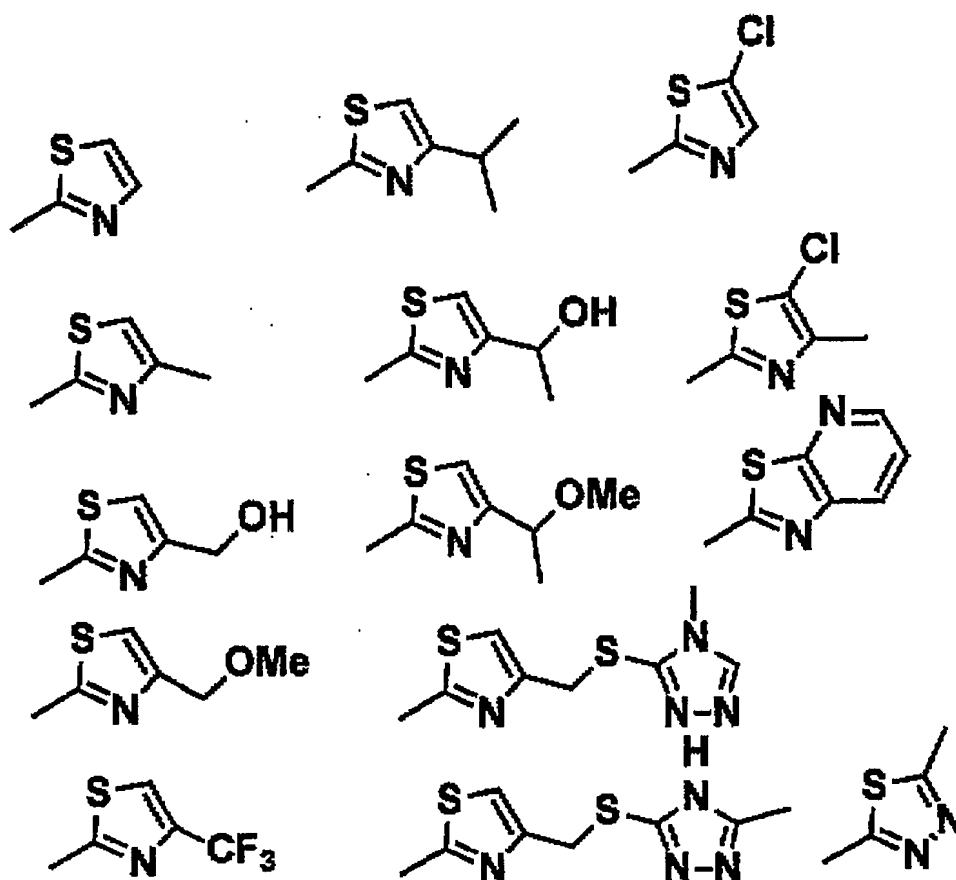
　なお、特に好ましい化合物は、上述した式（IIIa)〜式（IIIｃ）で表される
いずれかの化合物である。

　本発明の化合物（Ｉ）は、公知の反応手段を用いるか、或いは公知の方法に
従って容易に製造することができる。なお、本発明の一般式（Ｉ）の化合物は、
通常の液相における合成のみならず、近年発達の目覚しい例えばコンビナトリ
アル合成法やパラレル合成法等の固相を用いた合成によっても製造することが
できる。好ましくは例えば以下の方法により製造することができる。

- 266 -
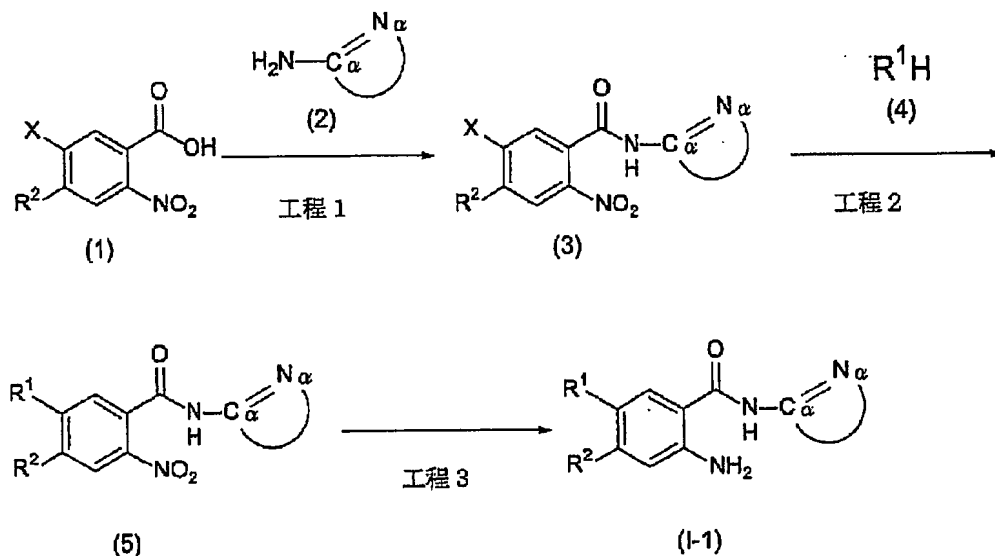


［式中、各記号は前記定義に同じ］

（工程1）

本工程は、カルボン酸化合物（1）又はその反応性誘導体と前記式（2）で表される置換されていてもよい単環の、又は双環のヘテロアリール基を有するアミノ化合物又はその塩とを反応させて、化合物（3）を製造する方法である。本反応は文献記載の方法（例えば、ペプチド合成の基礎と実験、泉屋信夫他、丸善、1983年、コンプリヘンシブ　オーガニック　シンセシス（Comprehensive　Organic　Synthesis）、第6巻、Pergamon　Press社、1991年、等）、それに準じた方法又はこれらと常法とを組み合わせることにより、通常のアミド形成反応を行えばよく、即ち、当業者に周知の縮合剤を用いて行うか、或いは、当業者に利用可能なエステル活性化方法、混合酸無水物法、酸クロリド法、カルボジイミド法等により行うことができる。このようなアミド形成試薬としては、例えば塩化チオニル、N，N－ジシクロヘキシルカルボジイミド、1－メチル－2－ブロモピリジニウムアイオダイド、N，N'－カルボニルジイミダゾール、ジフェニルフォスフォリルクロリド、ジフェニルフォスフォリルアジド、N，N'－ジスク

- 267 -

シニミジルカルボネート、 N，N'－ジスクシニミジルオキザレート、１－
エチル－３－（３－ジメチルアミノプロピル）カルボジイミド塩酸塩、クロロ
ギ酸エチル、クロロギ酸イソブチル又はベンゾトリアゾー１－リルーオキシー
トリス（ジメチルアミノ）フォスフォニウムヘキサフルオロフォスフェイト等
が挙げられ、中でも例えば塩化チオニル、N，N－ジシクロヘキシルカルボジ
イミド又はベンゾトリアゾー１－リルーオキシートリス（ジメチルアミノ）フ
ォスフォニウムヘキサフルオロフォスフェイト等が好適である。またアミド形
成反応においては、上記アミド形成試薬と共に塩基、縮合補助剤を用いてもよ
い。

用いられる塩基としては、例えばトリメチルアミン、トリエチルアミン、N，
N－ジイソプロピルエチルアミン、N－メチルモルホリン、N－メチルピロリ
ジン、N－メチルピペリジン、N，N－ジメチルアニリン、１，８－ジアザビ
シクロ［５．４．０］ウンデカ－７－エン（DBU）、１，５－アザビシクロ
［４．３．０］ノナ－５－エン（DBN）等の第３級脂肪族アミン；例えばピ
リジン、４－ジメチルアミノピリジン、ピコリン、ルチジン、キノリン又はイ
ソキノリン等の芳香族アミン等が挙げられ、中でも例えば第３級脂肪族アミン
等が好ましく、特に例えばトリエチルアミン又はN，N－ジイソプロピルエチ
ルアミン等が好適である。

用いられる縮合補助剤としては、例えばN－ヒドロキシベンゾトリアゾール
水和物、N－ヒドロキシスクシンイミド、N－ヒドロキシ－５－ノルボルネン
－２，３－ジカルボキシイミド又は３－ヒドロキシ－３，４－ジヒドロ－４－
オキソ－１，２，３－ベンゾトリアゾール等が挙げられ、中でも例えばN－ヒ
ドロキシベンゾトリアゾール等が好適である。

用いられるアミノ化合物（２）の量は、用いられる化合物及び溶媒の種類そ
の他の反応条件により異なるが、通常カルボン酸化合物（１）又はその反応性
誘導体１当量に対して、０．０２乃至５０当量、好ましくは０．２乃至２当量
である。ここにおいて、反応性誘導体としては、通常有機化学の分野において
用いられる、例えば活性エステル誘導体、活性アミド誘導体等が挙げられる。

用いられるアミド形成試薬の量は、用いられる化合物及び溶媒の種類その他

- 268 -

の反応条件により異なるが、通常カルボン酸化合物（１）又はその反応性誘導
体１当量に対して、１乃至５０当量、好ましくは１乃至５当量である。

用いられる縮合補助剤の量は、用いられる化合物及び溶媒の種類その他の反
応条件により異なるが、通常カルボン酸化合物（１）又はその反応性誘導体１
当量に対して、１乃至５０当量、好ましくは１乃至５当量である。

用いられる塩基の量は、用いられる化合物及び溶媒の種類その他の反応条件
により異なるが、通常１乃至５０当量、好ましくは３乃至５当量である。

本工程において用いられる反応溶媒としては、例えば不活性有機溶媒であり、
反応に支障のない限り、特に限定されないが、具体的には、例えば塩化メチレ
ン、クロロホルム、１，２－ジクロロエタン、トリクロロエタン、Ｎ，Ｎ－ジ
メチルホルムアミド、酢酸エチルエステル、酢酸メチルエステル、アセトニト
リル、ベンゼン、キシレン、トルエン、１，４－ジオキサン、テトラヒドロフ
ラン、ジメトキシエタン又はそれらの混合溶媒が挙げられるが、好適な反応温
度確保の点から、特に例えば塩化メチレン、クロロホルム、１，２－ジクロロ
エタン、アセトニトリル又はＮ，Ｎ－ジメチルホルムアミド等が好適である。

反応温度は、－１００℃乃至溶媒の沸点温度、好ましくは０乃至３０℃であ
る。

反応時間は、０．５乃至９６時間、好ましくは３乃至２４時間である。

本工程１で用いられる塩基、アミド形成試薬、縮合補助剤は、一種又はそれ
以上組み合わせて使用することができる。

化合物（３）が保護基を有している場合には、適宜当該保護基を除去するこ
とが可能である。当該補助基の除去は、文献記載の方法（プロテクティブ　グ
ループス　イン　オーガニック　シンセシス（Ｐｒｏｔｅｃｔｉｖｅ　Ｇｒｏ
ｕｐｓｉｎ　Ｏｒｇａｎｉｃ　Ｓｙｎｔｈｅｓｉｓ）、Ｔ．Ｗ．Ｇｒｅｅｎ著、
第２版、Ｊｏｈｎ　Ｗｉｌｅｙ＆Ｓｏｎｓ社、１９９１年、等）、それに準じ
た方法又はこれらと常法とを組み合わせることにより行うことができる。

このようにして得られる化合物（３）は、公知の分離精製手段、例えば濃縮、
減圧濃縮、結晶化、溶媒抽出、再沈殿、クロマトグラフィー等により単離精製
するか又は単離精製することなく次工程に付すことができる。

（工程２）

　本工程は、上記工程１で得られたアミド化合物（３）と化合物（４）とを反応させることにより化合物（５）を製造する方法である。

5　　本反応においては、反応系中に必要に応じて塩基を加えてもよい。用いられる化合物（４）としては、好ましくはフェノール誘導体又はチオール誘導体が好ましい。該フェノール誘導体又はチオール誘導体としては、例えばフェノール、チオフェノール、チオイミダゾール、チオトリアゾール等が挙げられる。用いられる化合物（４）の量は、用いられる化合物及び溶媒の種類その他の反応条件により異なるが、通常アミノ誘導体（３）１当量に対して、２乃至５０

10　当量、好ましくは２乃至５当量である。用いられる塩基としては、例えばトリメチルアミン、トリエチルアミン、Ｎ，Ｎ－ジイソプロピルエチルアミン、Ｎ－メチルモルホリン、Ｎ－メチルピロリジン、Ｎ－メチルピペリジン、Ｎ，Ｎ－ジメチルアニリン、１，８－ジアザビシクロ［５．４．０］ウンデカー７－

15　エン（ＤＢＵ）、１，５－アザビシクロ［４．３．０］ノナー５－エン（ＤＢＮ）等の第３級脂肪族アミン；例えばピリジン、４－ジメチルアミノピリジン、ピコリン、ルチジン、キノリン又はイソキノリン等の芳香族アミン；例えば金属カリウム、金属ナトリウム、金属リチウム等のアルカリ金属；例えば水素化ナトリウム、水素化カリウム等のアルカリ金属水素化物；例えばブチルリチウ

20　ム等のアルカリ金属アルキル化物；例えばカリウム－ｔｅｒｔ－ブチラート、ナトリウムエチラート又はナトリウムメチラート等のアルカリ金属アルコキシド；例えば水酸化カリウム、水酸化ナトリウム等のアルカリ金属水酸化物；例えば炭酸カリウム等のアルカリ金属炭酸塩等が挙げられ、中でも例えば第３級脂肪族アミン、アルカリ金属水素化物又はアルカリ金属炭酸塩が好ましく、特

25　に例えばトリエチルアミン、Ｎ，Ｎ－ジイソプロピルエチルアミン、水素化ナトリウム又は炭酸カリウムが好適である。

　用いられる当該塩基の量は、用いられる化合物及び溶媒の種類その他の反応条件により異なるが、アミド化合物（３）１当量に対して通常０乃至５０当量、好ましくは２乃至１０当量である。該塩基は、必要に応じて一種又は２種以上

- 270 -

用いることができる。

　用いられる不活性有機溶媒としては、反応に支障のないものであれば、特に限定されないが、具体的には、例えば塩化メチレン、クロロホルム、１，２－ジクロロエタン、トリクロロエタン、Ｎ，Ｎ－ジメチルホルムアミド、Ｎ，Ｎ－ジメチルアセトアミド、酢酸エチルエステル、酢酸メチルエステル、アセトニトリル、ベンゼン、キシレン、水、トルエン、１，４－ジオキサン、テトラヒドロフラン又はこれらの混合溶媒等が挙げられる。

　このようにして得られる化合物（５）は、公知の分離精製手段、例えば濃縮、減圧濃縮、結晶化、溶媒抽出、再沈殿、クロマトグラフィー等により単離精製することができる。


　（工程３）

　本工程は化合物（５）を還元して、本発明で用いる化合物（Ｉ）を製造する方法である。本工程において用いられる還元反応は、当業者に周知の方法が用いられる。本工程においてもちいられる還元反応としては、具体的には、例えば（１）水素、蟻酸、蟻酸アンモニウム、ヒドラジン水和物とパラジウム、白金、ニッケル触媒を用いる接触還元法、（２）塩酸、塩化アンモニウムと鉄を用いる還元法、（３）メタノールと塩化スズを用いる還元法等が挙げられる。

　上記還元反応において用いられる還元剤の量は、用いられる化合物及び溶媒の種類その他の反応条件により異なるが、化合物（５）１当量に対して通常１乃至５０当量、好ましくは２乃至２０当量である。

　用いられる反応溶媒としては、反応に支障のない限り、特に限定されないが、例えばジクロロメタン、クロロホルム等のハロゲン化炭化水素類、例えばジエチルエーテル、ｔｅｒｔ－ブチルメチルエーテル、　テトラヒドロフラン等のエーテル類、例えばＮ，Ｎ－ジメチルホルムアミド、Ｎ，Ｎ－ジメチルアセトアミド等のアミド類、例えばジメチルスルホキシド等のスルホキシド類、例えばアセトニトリル等のニトリル類、例えばメタノール、エタノール、プロパノール等のアルコール類、例えばベンゼン、トルエン、キシレン等の芳香族炭化水素類、水或いはこれらの混合溶媒を用いることができる。

　反応温度及び反応時間は特に限定されないが、－１０乃至１００℃程度、好ましくは０乃至５０℃程度の反応温度で１乃至２０時間程度、好ましくは１乃至５時間程度反応を行う。

　このようにして得られる本発明で用いる化合物（Ｉ）は、公知の分離精製手段、例えば濃縮、減圧濃縮、結晶化、溶媒抽出、再沈殿、クロマトグラフィー等により単離精製するか又は単離精製することなく、次工程に付すことができる。

　上記各工程の化合物は、各置換基上に保護基を有していてもよい。当該保護基は、各工程において適宜、公知の方法これに準じた方法、又はこれらと常法とを組み合わせた方法により除去することができる。除去の態様は、化合物、反応の種類その他の反応条件により、適宜の除去反応が可能であるが、個別に各保護基を除去する場合、各保護基を同時に除去する場合等が考えられ、当業者が適宜選択可能である。当該保護基としては、例えばヒドロキシ基の保護基、アミノ基の保護基、カルボキシル基の保護基、アルデヒドの保護基、ケト基の保護基等が挙げられる。また、当該保護基の除去順序は、特に限定されるものではない。

　ヒドロキシ基の保護基としては、例えばｔｅｒｔ－ブチルジメチルシリル基、ｔｅｒｔ－ブチルジフェニルシリル基等の低級アルキルシリル基、例えばメトキシメチル基、２－メトキシエトキシメチル基等の低級アルコキシメチル基、例えばベンジル基、ｐ－メトキシベンジル基等のアラルキル基、例えばホルミル基、アセチル基等のアシル基等が挙げられ、これらのうち、特にｔｅｒｔ－ブチルジメチルシリル基、アセチル基等が好ましい。

　アミノ基の保護基としては、例えばベンジル基、ｐ－ニトロベンジル基等のアラルキル基、例えばホルミル基、アセチル基等のアシル基、例えばエトキシカルボニル基、ｔｅｒｔ－ブトキシカルボニル基等の低級アルコキシカルボニル基、例えばベンジルオキシカルボニル基、ｐ－ニトロベンジルオキシカルボニル基等のアラルキルオキシカルボニル基等が挙げられ、これらのうち、特にニトロベンジル基、ｔｅｒｔ－ブトキシカルボニル基、ベンジルオキシカルボニル基等が好ましい。

- 272 -

　カルボキシル基の保護基としては、例えばメチル基、エチル基、tert－ブチル基等の低級アルキル基、例えばベンジル基、p－メトキシベンジル基等のアラルキル基等が挙げられ、これらのうち、特にメチル基、エチル基、tert－ブチル基、ベンジル基等が好ましい。

5　　ケト基の保護基としては、例えばジメチルケタール基、1，3－ジオキシラン基、1，3－ジオキソラン基、1，3－ジチアン基、1，3－ジチオラン基等が挙げられ、これらのうち、ジメチルケタール基、1，3－ジオキソラン基等がより好ましい。

　アルデヒド基の保護基としては、例えば、ジメチルアセタール基、1，3－ジオキシラン基、1，3－ジオキソラン基、1，3－ジチアン基、1，3－ジ
10　チオラン基等が挙げられ、これらのうちジメチルアセタール基、1，3－ジオキソラン基等がより好ましい。

　本発明で用いる化合物を製造するに当たっては、反応を効率よく進行させるために、官能基に保護基を導入する場合もある。これらの保護基の導入は、当業者に適宜選択可能であり、当該保護基の除去は、前記記載のプロテクティブ
15　グループス　イン　オーガニックシンセシス等の方法、これに準じた方法又はこれらと常法とを組み合わせることにより行うことができる。なお、保護基の除去の順序についても、当業者が適宜選択可能である。

　このようにして得られる化合物（Ｉ）は、公知の分離精製手段、例えば濃縮、
20　減圧濃縮、結晶化、再沈殿、溶媒抽出、クロマトグラフィー等により単離精製するか又は単離精製することなく次工程に付すことができる。

　また、本発明で用いる化合物である（Ｉ）は、下記の工程によっても製造することができる。
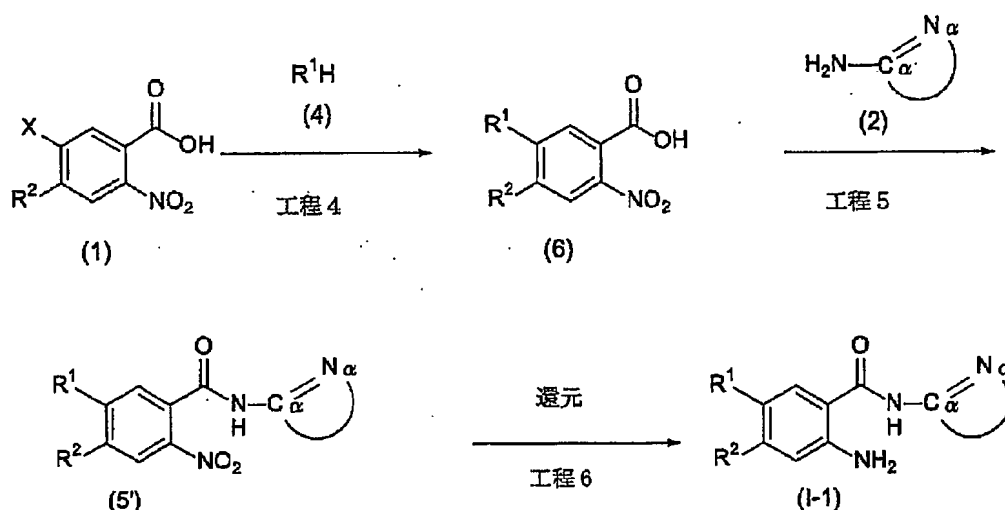
[式中各記号は前記定義に同じ]

　　　上記工程４、工程５及び工程６については、試薬の量、反応溶媒、反応温度
5　等その他の反応条件は、前記工程２、工程１及び工程３と同様にして行うこと
ができる。

　　　$R^2$に保護基が必要な場合には、前記記載のプロテクティブグループ　イ
ンオーガニックシンセシス等の方法、それに準じた方法又はこれらと常法とを
組み合わせることにより、当業者が保護基を適宜選択することによって行うこ
10　とができる。

　　　このようにして得られる化合物（６）、（５’）は、公知の分離精製手段、
例えば濃縮、減圧濃縮、結晶化、再沈殿、溶媒抽出等により単離精製するか、
又は単離精製することなく次工程に付すことができる。

　　　本発明で用いる化合物（Ｉ）は、公知の分離精製手段、例えば濃縮、減圧濃
15　縮、結晶化、再沈殿、溶媒抽出等により単離精製することができる。

　　　上記工程１乃至６において、保護基の除去は、当該保護基の種類及び化合物
の安定性により異なるが、前記記載のプロテクティブ　グループス　イン　オ
ーガニック　シンセシス（（Ｐｒｏｔｅｃｔｉｖｅ　Ｇｒｏｕｐｓ　ｉｎ　Ｏ

- 274 -

ｒｇａｎｉｃ　Ｓｙｎｔｈｅｓｉｓ）、Ｔ．Ｗ．Ｇｒｅｅｎ著　第２版、Ｊｏ
ｈｎ　Ｗｉｌｅｙ＆Ｓｏｎｓ社、１９９１年、等）、それに準じた方法又はこ
れらと常法とを組み合わせることにより行うことができる。例えば酸又は塩基
を用いる加溶媒分解、水素化金属錯体等を用いる化学的還元又はパラジウム炭
5　素触媒、ラネーニッケル等を用いる接触還元等により行うことができる。

　　本発明によって提供されるベンズアミド化合物は、薬学的に許容される塩と
して存在することができる。当該塩は、常法に従って製造することができる。
具体的には、上記化合物（Ｉ）が、当該分子内に例えばアミノ基、ピリジル基
等に由来する塩基性基を有している場合には、当該化合物を酸で処理すること
10　により、相当する薬学的に許容される塩に変換することができる。

　　当該酸付加塩としては、例えば塩酸塩、フッ化水素酸塩、臭化水素酸塩、ヨ
ウ化水素酸塩等のハロゲン化水素酸塩；硝酸塩、過塩素酸塩、硫酸塩、燐酸塩、
炭酸塩等の無機酸塩；メタンスルホン酸塩、トリフルオロメタンスルホン酸塩、
エタンスルホン酸塩等の低級アルキルスルホン酸塩；ベンゼンスルホン酸塩、
15　ｐ－トルエンスルホン酸塩等のアリールスルホン酸塩；フマル酸塩、コハク酸
塩、クエン酸塩、酒石酸塩、シュウ酸塩、マレイン酸塩等の有機酸塩；及びグ
ルタミン酸塩、アスパラギン酸塩等のアミノ酸等の有機酸である酸付加塩を挙
げることができる。また、本発明の化合物が酸性基を当該基内に有している場
合、例えばカルボキシル基等を有している場合には、当該化合物を塩基で処理
20　することによっても、相当する薬学的に許容される塩に変換することができる。
当該塩基付加塩としては、例えば例えばナトリウム、カリウム等のアルカリ金
属塩、カルシウム、マグネシウム等のアルカリ土類金属塩、アンモニウム塩、
グアニジン、トリエチルアミン、ジシクロヘキシルアミン等の有機塩基による
塩が挙げられる。さらに本発明の化合物は、遊離化合物又はその塩の任意の水
25　和物又は溶媒和物として存在してもよい。

　　本発明においては、実施例の記載にて詳述するように、配列番号５に示すア
ミノ酸配列を有するＧＫタンパク質と上記式(IIIa)～式（IIIｃ）との化合物
の複合体の結晶が得られている。これらの、結晶の３次元構造座標を解析する
ことによって、配列番号５で示すＧＫタンパク質においては、化合物結合部位

- 275 -

が、チロシン６１～セリン６９、グルタミン酸９６～グルタミン９８、イソロ
イシン１５９、メチオニン２１０～チロシン２１５、ヒスチジン２１８～グル
タミン酸２２１、メチオニン２３５、アルギニン２５０、ロイシン４５１～リ
ジン４５９のアミノ酸残基から構成されることが解明されている。

5

　なお、本発明の別の態様によれば、配列番号２に記載のアミノ酸配列を有す
るタンパク質から、上述のようにＮ末端側、および／またはＣ末端側の所定の
数のアミノ酸残基を欠損したアミノ酸配列を有するタンパク質を製造するタン
パク質製造工程と、前記タンパク質製造工程で得られたタンパク質と結合する

10　化合物と、前記タンパク質製造工程で得られたタンパク質とを反応させる工程
とを含む、タンパク質及びそのタンパク質と結合する化合物の複合体を含む結
晶を製造する方法が提供される。
　上記タンパク質製造工程において製造されるタンパク質としては、結晶内で
隣接するＧＫタンパク質との間で立体的な障害がなくなる範囲であればその数

15　は限定されない。具体的には、例えば、配列番号２で表されるアミノ酸配列に
おいて、Ｎ末端側の１～５０個、好ましくは３～３０個、より好ましくは５～
２５個、さらに好ましくは８～１８個、特に好ましくは１１～１５個のアミノ
酸残基を欠失させたアミノ酸配列などが挙げられる。また、Ｃ末端側の１～８
個、好ましくは１～７個、より好ましくは２～６個のアミノ酸残基を欠失させ

20　たアミノ酸配列などが挙げられる。


（３次元構造座標を用いるドラッグデザイン方法）
　上記のようにして得られる本発明のＧＫタンパク質の３次元構造は、ＣＡＲ
ＤＤ (Computer Aided Rational Drug Design) による創薬システムのための重

25　要な情報である。このＧＫタンパク質の活性中心、及びアロステリック部位を
明らかにし、その部位に適合し、ＧＫタンパク質と相互作用することにより、
ＧＫタンパク質を阻害、または活性化する物質を検索することは、ＧＫタンパ
ク質をターゲットとする創薬開発の重要なステップである。
　すなわち、本発明の別の態様によれば、タンパク質の立体構造情報に基づい

- 276 -

て該タンパク質に結合する化合物の構造をデザインするドラッグデザイン方法
であって、該タンパク質の立体構造情報が、上述のようにして得られる結晶を
解析することによって得られる情報であることを特徴とする、ドラッグデザイ
ン方法が提供される。このようなドラッグデザイン方法としては、エネルギー
5　計算、若しくはこれに類似する活性予測値、又はファルマコフォアを用いてド
ラッグデザインする手法と、コンピュータグラフィックスの技術を用いて視覚
的にドラッグデザインをする手法がある。

　エネルギー計算、若しくはこれに類する活性予測値、又はファルマコフォア
を用いる手法による方法としては、（1）上述したようにして得られる立体構
10　造情報に基づいて、上記タンパク質の化合物結合部位を推測する結合部位推測
工程と、前記結合部位推測工程で推測された化合物結合部位に適合する化合物
を、化合物ライブラリより選択する選択工程とを含むことを特徴とするドラッ
グデザイン方法、（2）前記立体構造情報に基づいて、前記タンパク質の化合
物結合部位を推測する結合部位推測工程と、前記結合部位推測工程で推測され
15　た化合物結合部位に適合する化合物の構造を構築する化合物構造構築工程とを
含むことを特徴とする、ドラッグデザイン方法などが例示される。

　上記タンパク質の化合物結合部位を推測する方法としては、例えば、化合物
との共結晶においてリガンドが結合している部位をコンピュータのディスプレ
イ上で目視で確認して特定する方法の他、リガンドが結合していない状態で解
20　かれたタンパク質結晶構造に対してリガンドが結合しそうな部位を推定して特
定する方法が挙げられる。いずれの方法においても公知の方法や市販のコンピ
ュータソフトウエアを用いることができる。前者の方法においては、例えば、
InsightII (Accelrys Inc. )、SYBYL (Tripos Inc.)、MOE (Chemical
Computing Group) 等のソフトウエアを用いることができる。一方、後者の方法
25　においては、例えば、Cavity search: an algorithm for the isolation and
display of cavity-like binding regions. (Journal of Computer-Aided
Molecular Design. 4(4):337-54, 1990) 等の公知の手法を用いることができ、
SiteID (Tripos Inc.)等のソフトウエアを用いて実施することができる。

　タンパク質における化合物との結合部位が推測できたら、その推測された結

- 277 -

合部位に適合し得る化合物を選択する。この化合物候補を選択する方法として
は、既存の化合物ライブラリからの化合物の構造情報を入手して、そのライブ
ラリ中の化合物の構造情報と上記のようにして推測された結合部位の構造情報
とを比較することによって、結合可能化合物候補を選択する。

5    より具体的には、配列番号5に示すアミノ酸配列のアミノ酸残基（チロシン
61～セリン69、グルタミン酸96～グルタミン98、イソロイシン159、メチオ
ニン210～チロシン215、ヒスチジン218～グルタミン酸221、メチオニン235、
アルギニン250、ロイシン451～リジン459）から1つないしは2つ以上
の残基もしくは複合体中のリガンドの官能基から形成される水素結合性または
10   疎水性などのファルマコフォアと、蛋白構造またはその一部の側鎖の配向を改
変させた構造から作成される蛋白表面を検索条件として、化合物ライブラリよ
り各化合物の配座、配向を網羅的に探索しながら条件を満たすかどうかを判断
して選択する。

　　他の代替方法として、化合物ライブラリより各化合物の配座、配向を網羅的
15   に探索しながら、アミノ酸残基（チロシン61～セリン69、グルタミン酸96～
グルタミン98、イソロイシン159、メチオニン210～チロシン215、ヒスチジ
ン218～グルタミン酸221、メチオニン235、アルギニン250、ロイシン451
～リジン459）から構成されるリガンド結合部位の構造またはその一部の側
鎖の配向を改変させた構造に対して候補化合物をバーチャルでドッキングさせ、
20   アミノ酸残基（チロシン61～セリン69、グルタミン酸96～グルタミン98、イ
ソロイシン159、メチオニン210～チロシン215、ヒスチジン218～グルタミン
酸221、メチオニン235、アルギニン250、ロイシン451～リジン459）
から1つないしは2つ以上の残基と4オングストローム以下で近接した相互作
用を形成したものを選択したり、エネルギー評価関数を用いた選択を行う。

25   一方、候補化合物は、上記のようにして推測された結合部位の構造情報に基
づいて結合可能化合物を設計することによっても選択することができる。より
具体的には、配列番号5に示すアミノ酸配列のアミノ酸残基（チロシン61～
セリン69、グルタミン酸96～グルタミン98、イソロイシン159、メチオニン
210～チロシン215、ヒスチジン218～グルタミン酸221、メチオニン235、ア

- 278 -

ルギニン 250、ロイシン４５１～リジン４５９）から構成される化合物結合部

位の構造またはその一部の側鎖の配向を改変させた構造に対して、１つないし

は２つ以上の残基と相互作用するように各種原子種、官能基を種々つなぎ合わ

せて化合物構造を構築する。この方法としては、メチル、エチル等の化学基を

5　活性部位に並べて適合する化合物を探す方法と、原子を活性部位にコンピュー

タプログラムを用いて結合させていく方法とが知られている。

　なお、コンピュータによるエネルギー評価による方法では、例えば分子力場

計算を用いて化合物と、ＧＫタンパク質との結合のエネルギーを求める方法が

挙げられる。その計算をデータベースの中の各化合物に適用し、安定に結合で

10　きる化合物候補を、ライブラリ化合物の中から求める。Ｉｎｓｉｇｈｔ ＩＩ

のＬｕｄｉなどコンピュータプログラムによっては、蛋白質分子において相互

作用するアミノ酸残基の３次元構造座標を与えると、自動的に結合可能な化合

物の候補を選択し出力するものもあり、好適に利用することができる。

　また、分子の３次元構造に基づくドラッグデザインについては、医薬品の開

15　発・第７巻「分子設計」（廣川書店）をはじめとして数多くの文献が知られて

いる。具体的には、第一にFlexiDock、FlexX等のフレキシブルリガンドバイ

ンディングシミュレーションソフトウエアを用いて、低分子（分子量 1000 以

下）化合物のライブラリ（たとえば約 150000 種）をコンピュータでスクリー

ニングすることができる。このライブラリ内の化学物質は CONCORD 等のプログ

20　ラムで３次元構造を構築し、活性部位に適合する化合物を選択することができ

る。

　一方、目視的によりドラッグデザインする方法としては、前記立体構造情報

に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

前記結合部位推測工程で推測された化合物結合部位と該化合物結合部位に適合

25　する化合物とが相互作用するように化合物の構造を目視によりデザインするデ

ザイン工程とを含むことを特徴とする、ドラッグデザイン方法が挙げられる。

例えば、配列番号５に示すアミノ酸配列のアミノ酸残基（チロシン 61～セリ

ン 69、グルタミン酸 96～グルタミン 98、イソロイシン 159、メチオニン 210

～チロシン 215、ヒスチジン 218～グルタミン酸 221、メチオニン 235、アルギ

- 279 -

ニン 250、ロイシン４５１〜リジン４５９）から構成されるリガンド結合部位
の構造またはその一部の側鎖の配向を改変させた構造に対して、これらの残基
のうち１つないしは２つ以上の残基と相互作用するように目視による構造構築、
もしくは構造改変を行う。

　　具体的には、視覚的方法では、まずコンピュータの画面上にＧＫタンパク質
とそれに結合する化合物との複合体の結晶の構造を、得られた構造座標に従っ
て表示する。そして、コンピュータ上で化学的相互作用を考慮しながら、ライ
ブラリ中にある化合物とＧＫタンパク質との結合可能性を順次検討する。ここ
で考慮すべき化学的相互作用は静電相互作用、疎水性相互作用、水素結合、フ
ァンデルワールス相互作用などである。すなわち、該化合物の３次元空間での
構造が、その官能基群においてカルボキシル基、ニトロ基、ハロゲン基などの
陰性電荷を帯びやすい基が、ＧＫタンパク質のリジン、アルギニン、ヒスチジ
ンといった正電荷を持つアミノ酸残基に相互作用するように、アミノ基、イミ
ノ基、グアニジル基などの陽性電荷を帯びやすい基が、ＧＫタンパク質のグル
タミン酸、アスパラギン酸といった負電荷を持つアミノ酸残基に相互作用する
ように、脂肪族基や芳香族基といった疎水性の官能基が、アラニン、ロイシン、
イソロイシン、バリン、プロリン、フェニルアラニン、トリプトファン及びメ
チオニンといった疎水性のアミノ酸残基と相互作用するように、水酸基、アミ
ド基などの水素結合に関与する基が、ＧＫタンパク質の主鎖や側鎖部分と水素
結合ができるように、更には、該化合物とＧＫタンパク質の結合において立体
的な障害が生じないように、また、更には、空隙部分がなるべくできないよう
に空隙部分が充填され、ファンデルワールス相互作用が大きくなるようになど、
相互作用に好ましい構造になっているかを総合的に考慮する。このように、静
電相互作用、疎水性相互作用、ファンデルワールス相互作用、水素結合などの
因子を、コンピュータ画面上で視覚的に総合的に考慮して、最終的に候補化合
物がＧＫタンパク質に結合し得るか否かの判断を行う。

　　このように目視によって化合物候補を選択するプログラムとしては、
Insight II や MOE 等のシミュレーションプログラムが例示される。ＧＫタン
パク質と相互作用する化合物の有力候補を挙げるために、候補化合物とＧＫタ

- 280 -

ンパク質と接触させ、ＧＫタンパク質の活性を測定する。有力候補化合物を実

際にＧＫタンパク質と混合し、結晶化し適合するかどうかを検討する。更に適

合した複合物を有機合成を用いて修飾することにより、より望ましい構造とす

る。

5　　　なお、視覚的手法と、エネルギーを考慮した手法は、適宜組合わせて用いる

こともできる。そのようなコンピュータソフトウエアとしては、FlexiDock

（Tripos Inc.）、FlexX（Tripos Inc.）、SYBYL（Tripos Inc.）、Insight

II（Accelrys Inc.）、MOE（Chemical Computing Group Inc.）などが挙げら

れる。

10　　　なお、本発明においては、上述したドラッグデザイン方法によって選択され

た化合物を実際に合成し、これらの化合物群を化合物アレイ（又は化合物ライ

ブラリ）として提供することができる。このような化合物アレイを利用すれば、

ハイスループットスクリーニングの技術などを用いて、一度に大量の候補化合

物をアッセイすることができるので、グルコキナーゼの活性化剤又は阻害剤を

15　効率良くスクリーニングすることができる。


（本発明の方法によって得られる化合物及びそれを含む治療剤）

　　　上記のドラッグデザイン方法によって設計される化合物は、グルコキナーゼ

と結合する能力を有するので、グルコキナーゼの活性化化合物又はグルコキナ

20　ーゼ阻害化合物として用いることができる。また、このような化合物を含有す

る治療剤又は医薬組成物は、グルコキナーゼ活性が関与する疾患の治療剤（例

えば、糖尿病治療剤）として有効に用いることができる。

　　　上記医薬組成物は、本発明のグルコキナーゼと結合する化合物を有効成分と

して、その薬学的有効量を、適当な薬学的に許容される担体ないし希釈剤と共

25　に含有する。上記医薬組成物（医薬製剤）に利用できる薬学的に許容できる担

体としては、製剤の使用形態に応じて通常使用される、充填剤、増量剤、結合

剤、付湿剤、崩壊剤、表面活性剤、滑沢剤などの希釈剤或は賦形剤などが例示

される。これらの担体は、得られる製剤の投与単位形態に応じて適宜選択使用

される。

- 281 -

　本発明の医薬組成物の投与単位形態としては、各種の形態が治療目的に応じて選択でき、その代表的なものとしては、錠剤、丸剤、散剤、粉末剤、顆粒剤、カプセル剤などの固体投与形態や、溶液、懸濁剤、乳剤、シロップ、エリキシルなどの液剤投与形態が含まれ、これらは更に投与経路に応じて経口剤、非経口剤、経鼻剤、経膣剤、坐剤、舌下剤、軟膏剤などに分類され、それぞれ通常の方法に従い、調合、成形、調製することができる。例えば、錠剤の形態に成形するに際しては、上記製剤担体として例えば乳糖、白糖、塩化ナトリウム、ブドウ糖、尿素、デンプン、炭酸カルシウム、カオリン、結晶セルロース、ケイ酸、リン酸カリウムなどの賦形剤、水、エタノール、プロパノール、単シロップ、ブドウ糖液、デンプン液、ゼラチン溶液、カルボキシメチルセルロース、ヒドロキシプロピルセルロース、メチルセルロース、ポリビニルピロリドンなどの結合剤、カルボキシメチルセルロースナトリウム、カルボキシメチルセルロースカルシウム、低置換度ヒドロキシプロピルセルロース、乾燥デンプン、アルギン酸ナトリウム、カンテン末、ラミナラン末、炭酸水素ナトリウム、炭酸カルシウムなどの崩壊剤、ポリオキシエチレンソルビタン脂肪酸エステル類、ラウリル硫酸ナトリウム、ステアリン酸モノグリセリドなどの界面活性剤、白糖、ステアリン、カカオバター、水素添加油などの崩壊抑制剤、第４級アンモニウム塩基、ラウリル硫酸ナトリウムなどの吸収促進剤、グリセリン、デンプンなどの保湿剤、デンプン、乳糖、カオリン、ベントナイト、コロイド状ケイ酸などの吸着剤、精製タルク、ステアリン酸塩、ホウ酸末、ポリエチレングリコールなどの滑沢剤などを使用できる。更に錠剤は必要に応じ通常の剤皮を施した錠剤、例えば糖衣錠、ゼラチン被包錠、腸溶被錠、フィルムコーティング錠とすることができ、また二重錠ないしは多層錠とすることもできる。

　丸剤の形態に成形するに際しては、製剤担体として例えばブドウ糖、乳糖、デンプン、カカオ脂、硬化植物油、カオリン、タルクなどの賦形剤、アラビアゴム末、トラガント末、ゼラチン、エタノールなどの結合剤、ラミナラン、カンテンなどの崩壊剤などを使用できる。

　カプセル剤は、常法に従い通常本発明の有効成分を上記で例示した各種の製剤担体と混合して硬質ゼラチンカプセル、軟質カプセルなどに充填して調整さ

- 282 -

れる。

　経口投与用液体投与形態は、慣用される不活性希釈剤、例えば水、を含む医薬的に許容される溶液、エマルジョン、懸濁液、シロップ、エリキシルなどを包含し、更に湿潤剤、乳剤、懸濁剤などの助剤を含ませることができ、これらは常法に従い調製される。

　非経口投与用の液体投与形態、例えば滅菌水性乃至非水性溶液、エマルジョン、懸濁液などへの調製に際しては、希釈剤として例えば水、エチルアルコール、プロピレングリコール、ポリエチレングリコール、エトキシ化イソステアリルアルコール、ポリオキシ化イソステアリルアルコール、ポリオキシエチレンソルビタン脂肪酸エステル及びオリーブ油などの植物油などを使用でき、また注入可能な有機エステル類、例えばオレイン酸エチルなどを配合できる。これらには更に通常の溶解補助剤、緩衝剤、湿潤剤、乳化剤、懸濁剤、保存剤、分散剤などを添加することもできる。　滅菌は、例えばバクテリア保留フィルターを通過させる濾過操作、殺菌剤の配合、照射処理及び加熱処理などにより実施できる。また、これらは使用直前に滅菌水や適当な滅菌可能媒体に溶解することのできる滅菌固体組成物形態に調製することもできる。

　坐剤や膣投与用製剤の形態に成形するに際しては、製剤担体として、例えばポリエチレングリコール、カカオ脂、高級アルコール、高級アルコールのエステル類、ゼラチン及び半合成グリセライドなどを使用できる。

　ペースト、クリーム、ゲルなどの軟膏剤の形態に成形するに際しては、希釈剤として、例えば白色ワセリン、パラフィン、グリセリン、セルロース誘導体、プロピレングリコール、ポリエチレングリコール、シリコン、ベントナイト及びオリーブ油などの植物油などを使用できる。

　経鼻又は舌下投与用組成物は、周知の標準賦形剤を用いて、常法に従い調製することができる。

　尚、本発明薬剤中には、必要に応じて着色剤、保存剤、香料、風味剤、甘味剤などや他の医薬品などを含有させることもできる。

　上記医薬製剤中に含有されるべき有効成分の量及びその投与量は、特に限定されず、所望の治療効果、投与法、治療期間、患者の年齢、性別その他の条件

- 283 -

などに応じて広範囲より適宜選択される。一般的には、投与量は、通常、１日
当り体重６０ｋｇ当り、約０．０１ｍｇ～１０００ｍｇ、好ましくは約１ｍｇ
～１００ｍｇとするのがよく、１日に１～数回に分けて投与することができる。

5　　本明細書の配列表の配列番号は、以下の配列を示す。

〔配列番号：１〕

ヒト由来肝臓型グルコキナーゼをコードするＤＮＡの塩基配列を示す。

〔配列番号：２〕

ヒト由来肝臓型グルコキナーゼのアミノ酸配列を示す。

10　　〔配列番号：３〕

ヒト由来 β 細胞グルコキナーゼのアミノ酸配列を示す。

〔配列番号：４〕

ヒト由来肝臓型グルコキナーゼのＮ末端側のアミノ酸残基１１個を欠失させ
たタンパク質をコードするＤＮＡの塩基配列を示す。

15　　〔配列番号：５〕

ヒト由来肝臓型グルコキナーゼのＮ末端側のアミノ酸残基１１個を欠失させ
たタンパク質のアミノ酸配列を示す。

〔配列番号：６〕

以下の実施例１におけるＰＣＲ反応で使用した、プライマー１の塩基配列を
20　示す。

〔配列番号：７〕

以下の実施例１におけるＰＣＲ反応で使用した、プライマー２の塩基配列を
示す。

〔配列番号：８〕

25　　ヒト由来肝臓型グルコキナーゼのＮ末端側のアミノ酸残基１５個を欠失させ
たタンパク質のアミノ酸配列を示す。

〔配列番号：９〕

以下の実施例６におけるＰＣＲ反応で使用した、プライマーの塩基配列を示
す。

- 284 -

〔配列番号：１０〕

以下の実施例６におけるＰＣＲ反応で使用した、プライマーの塩基配列を示す。


5　　（実施例）

以下、本発明を、実施例を用いて具体的に説明する。

（変異型酵素の精製方法）

　Human グルコキナーゼには、プロモーターの違いよって肝臓型と膵臓型が存在し、Ｎ末端の 15 残基が異なる。三次元構造解析を目的に結晶化を行うた

10　めに、この部分の一部あるいはすべてを欠損した変異型酵素を以下の方法で作成した。

　pCR2.1(INTROGEN 社製)上にクローニングされた Human 肝臓型グルコキナーゼの cDNA と２種のプライマーセット

　　5' - gtcacaaggagccagaagcttatggccttgactctggtag- 3'（配列番号６）　及び

15　　5' -gaagccccacgacattgttcccttctgc - 3　（配列番号７）の組み合わせ、ならびに、

　　5' - ccaggcccagacagccaagcttatggtagagcagatcc- 3'、　（配列番号９）及び

　　5' -gaagccccacgacattgttcccttctgc　3'　（配列番号１０）

を用いて PCR 反応を行った。得られた PCR 産物の Hind III、ClaI 断片を

20　pFLAG・CTC ベクター (Eastman Kodak) の Hind III, Eco RI 部位にクローニングされていた肝臓型 GK の Hind III - Cla Ｉ領域と置換することで、肝臓型 GK の 1～11 残基を欠損する変異型 GK（Δ１－１１）、及び 1～15 残基を欠損する変異型 GK（Δ１－１５）をコードする cDNA を得た。得られた cDNA の配列を確認した後、これらのベクターを発現ベクターとし、大腸菌 DH5α株（宝

25　酒造社製）を形質変換した。

　形質変換体を LB 培地で 600nm の吸収が 0.8 になるまで 37℃で培養した後、終濃度が 0.4mM になるようにイソプロピル－１－チオ－β－Ｄ－ガラクシド（和光純薬社製）を加え、25℃で 16 時間、タンパク質の生産誘導を行った。

- 285 -

培養された大腸菌を遠心機で収集し、以下の成分を含む緩衝液（50 mM リン酸カリ（Potassium Phosphate） pH7.5, 50mM NaCl, 2 mM DTT, 0.5 mM Pefabloc SC（関東化学社製）、a proteinase inhibitor mixture（Roche 社製））に懸濁した。

5    収集した大腸菌は、超音波破砕法によって破砕し、可溶化画分を上記の緩衝液に対して透析した後、HiTrapQ カラム（アマシャム社製）により精製した。HiTrap Q カラムより塩化カリウムのグラジエントにより溶出された GK 画分を希釈により塩濃度 50mM に希釈した。

希釈された GK 画分を論文（Preparative Biochemistry, 20(2), 163-

10   178(1990)）に示されている方法で作製した Glucosamin Sepharose カラムにより精製した。GK 画分を Glucosamin Sepharose カラムに吸着させ 100mM 塩化ナトリウムで不純物を除いた後、1M のグルコースにより溶出させた。

溶出された GK 画分は、MonoQ10/10 カラムにより精製した。MonoQ10/10 カラム（アマシャム社製）より塩化ナトリウムのグラジエントにより溶出された

15   GK 画分を、移動層として 50mM Tris-Cl pH7.2, 50mM NaCl 緩衝液を用いて、Superdex200 カラム（アマシャム社製）により精製した。


（結晶化方法）

（変異型 GK（Δ1－11）／グルコース／化合物複合体の結晶）

20   変異型 GK（Δ1－11）／グルコース／化合物複合体の結晶は、以下に示す蒸気拡散の手法を用いて得た。なお、変異型 GK（Δ1－11）は、配列番号5で表されるアミノ酸配列を有するグルコキナーゼを意味する。

すなわち、高純度に精製された変異型 GK を濃縮し、最終的に 10mg/ml 程度の変異型 GK の溶液（25 mM Tris-Cl, 50 mM NaCl, 5 mM TCEP）とした。これ

25   に最終濃度 20mM のグルコース、及び最終濃度 0.3 mM の GK を活性化する下記化合物1（式 IIIa の化合物）を加え、結晶化に用いた。タンパク質溶液 1～5 μl に結晶化溶液として 28～30% PEG 1500、0.1 M Hepes - NaOH（pH6.6）を等量加えて混合した溶液を 0.5～1ml の結晶化溶液を入れた密閉容器に、両溶液が触れ合わないように収め、20℃で静置した。およそ3日～1ヶ月の静置の

- 286 -

後に、試料溶液中に最大 0.4 mm×0.4 mm×0.7 mm 程度の結晶が得られた（実

施例１）。

　さらに上記の方法で得られた結晶を下記化合物２（式IIIbで表される化合

物）が0.3 mMの濃度で含まれるようにして、28～30% PEG 1500、0.1 M Hepes

5　 - NaOH（pH6.6)溶液に３～７日程度浸透することによって、下記化合物２と上

記変異型GKの複合体結晶を得た（実施例２）。

化合物１



(IIIa)

10　化合物２



(IIIb)
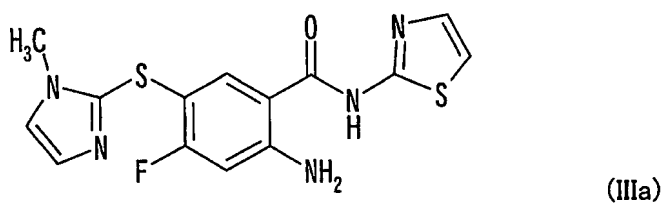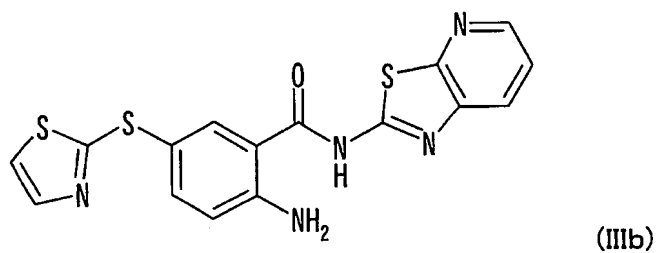
　また、前記化合物１に代えて化合物３（式 IIIc で表される化合物）を用い

た以外は、実施例１と同様にして結晶化を試みた結果、それぞれ実施例１と同

15　様な結晶が得られた（実施例３）。

化合物３

(IIIc)
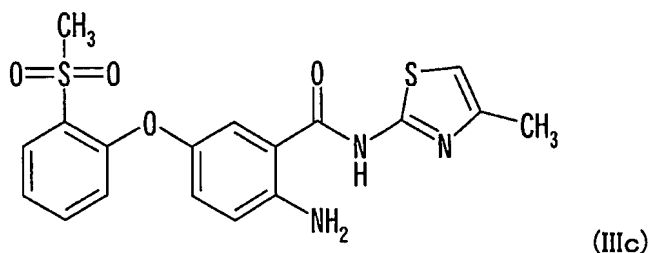
　　　得られた結晶を１０％のグリセロールを加えた結晶化溶液に浸し、続いて液
　　体窒素中で急速に凍結した。シンクロトロン施設 KEK−PF の BL6B において振
5　動法により、凍結した結晶のＸ線回折データを 100K 窒素気流中で収集した。
　　得られた回折像から、DENZO/SCALEPACK（HKL 社製）を用いて回折強度を数値
　　化し、結晶構造因子を求めた。この段階で結晶は六方晶系で空間群は $P6_522$ あ
　　るいは $P6_122$ を有し、結晶の単位格子は、a = b = 79.9 オングストローム，c
　　= 322.2 オングストローム， α= β = 90°， γ = 120° であるとわかった。
10　　得られた構造因子と Human ヘキソキナーゼ　タイプ１の３次元構造座標を
　　用いて分子置換法を行い構造を解析した。計算には８オングストロームから４
　　オングストロームの分解能のデータを用い、CCP4 (Council for the Central
　　laboratory of the Research Councils) の Amore プログラムにより行った。
　　計算により得られた構造のＲ因子は、53.7％であり、結晶の空間群は $P6_522$ で
15　非対称単位に変異型 GK 一分子を含むことが分かった。この構造と構造因子か
　　ら電子密度マップを得て、プログラム O（Dat-ONO 社製）を用いて変異型グル
　　コキナーゼの構造を決定した。
　　　次に CNX（Accelrys Inc.）を用いてアミノ酸の位置の精密化を行い、プロ
　　グラム O を用いてアミノ酸残基の同定を行った。この操作を繰り返し行い、変
20　異型グルコキナーゼのスレオニン 14 からシステイン 461 までの 448 アミノ酸
　　残基の構造座標、１分子のグルコース分子、１分子の化合物 A、１個のナトリウ
　　ムイオン、及び 149 個の水分子を同定し構造座標を決定した。最終的に決定さ
　　れた構造の正確さの指標とされるＲ因子は、30 オングストロームから 2.3 オ
　　ングストロームの分解能のデータに対して R=23.2％であり、構造の精密化の
25　段階で計算に用いなかったデータに対するＲ因子（Rfree）は 27.4％であった。

- 288 -

ラマチャンドラン・プロットで確認したところ許容されない構造を持ったアミ
ノ酸残基はなかった。

　決定された変異型グルコキナーゼの構造は、アイソザイムであるヘキソキナ
ーゼの構造と似たものであったが、グルコキナーゼを活性化する化合物１（式
5　IIIaの化合物）の結合している部位の構造は異なっていた。この構造の相違
は、現在の計算化学の能力で予想できうるものでなく、今回の構造解析により、
この部位がアクティベーターの結合部位であること、そしてその詳細な立体構
造が初めて明らかとなった。図１ａは、ここで解明されたグルコキナーゼの三
次元構造を示すリボン図である。図１ａに示されるように、新規に見つかった
10　アクティベーター結合部位は、ラージドメインとスモールドメインの間に位置
しており、基質であるグルコースが結合しているグルコキナーゼの活性中心か
ら、約20オングストローム離れていた。アクティベーター結合部位を構成し
ているグルコキナーゼのアミノ酸残基は以下のとおりであった。チロシン61
〜セリン69、グルタミン酸96〜グルタミン98、イソロイシン159、メチオニ
15　ン210〜チロシン215、ヒスチジン218〜グルタミン酸221、メチオニン235、
アルギニン250、ロイシン４５１〜リジン４５９。

　また、この結合部位に対する化合物１（式IIIaの化合物）の結合様式を図
２に、グルコキナーゼの結合部位の構造を図３に示す。チアゾール環は、バリ
ン62、バリン452、バリン455のそれぞれのアミノ酸側鎖の分子とファンデル
20　ワールス接触をしており、またチアゾール環上の窒素原子がアルギニン63の
主鎖の窒素原子と水素結合をしていた。化合物１上のアミドの窒素原子は、ア
ルギニン63の主鎖の酸素原子と水素結合をしていた。化合物１のベンゼン環
部分はイソロイシン211とファンデルワールス接触をしており、ベンゼン環に
置換したフッ素原子はチロシン214の側鎖とファンデルワールス接触をしてい
25　た。化合物１のアニリン構造は、チロシン215の側鎖の酸素原子と水素結合を
形成していた。硫黄を介してベンゼン環と結合しているイミダゾール環部分は、
メチオニン210、メチオニン235、チロシン214のアミノ酸側鎖部分とファン
デルワールス接触をしていた。ラージドメインとスモールドメインを結んでい
る、セリン64〜セリン69の部分は、溶液に露出した構造をしており、化合物

- 289 -

1は、この部分が形作るアーチ状構造の下部に結合していた（図3）。


（実施例4：ドラッグデザインの実施例）

　ソフトウエア UNITY（トライポス社製）を用い、Arg63 の主鎖 NH, CO からそ
5　れぞれ発生させた水素結合アクセプター、水素結合ドナーのファルマコフォア
と、複合体を形成するリガンドのアニリン部分のフェニル基に相当する空間に
形成された疎水性のファルマコフォア、および蛋白の構造を元に作成した蛋白
表面を検索条件としてライブラリ化合物をスクリーニングし、下記化合物4、
及び化合物5が得られ、アッセイを行ったところ、それぞれ７８０％、および
10　５６０％の活性が認められた。なお活性が７８０％とは、グルコキナーゼの活
性をコントロールを１００％としたときに、これらの化合物によって７８０％
まで増強されたことを示す（グルコース 2.5M 及びリガンド 10μM を使用）。


化合物4



15　　　　　　　　　　　　　　　　　　　活性：７８０％


化合物5



　　　　　　　　　　　　　　　　　　　　　活性：５６０％


20　　（実施例5）

　　（変異型 GK（Δ1−15）の結晶）
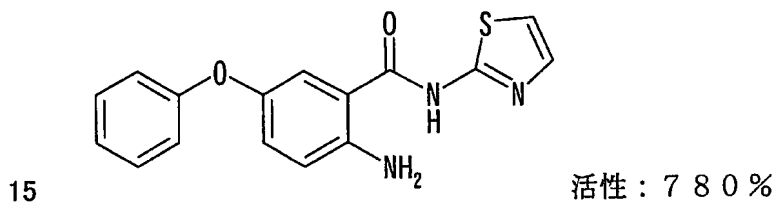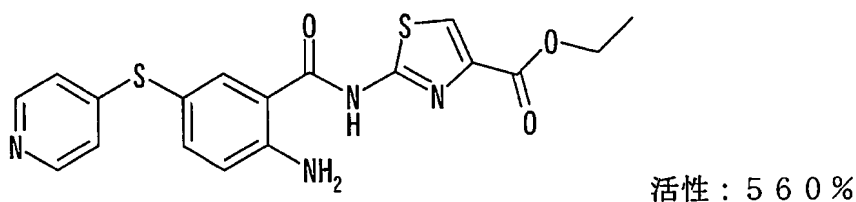
　　変異型 GK（Δ1−15）（配列番号8で表されるアミノ酸配列を有するグ
ルコキナーゼ）の単体の結晶は、以下に示す蒸気拡散の手法を用いて得た。

- 290 -

　　すなわち、高純度に精製された変異型GKを濃縮し、最終的に 10mg／ml 程度
の変異型 GK の溶液（25 mM Tris-Cl pH7.2, 50 mM NaCl, 5 mM TCEP）とした。
タンパク質溶液 1～5μl に結晶化溶液（1.5 ～ 1.6 M 硫酸アンモニウム、
50mM NaCl、0.1 M Bicine NaOH(pH8.7)）を等量加えて混合した溶液を 0.5～

5　1ml の結晶化溶液が入った密閉容器に、両溶液が触れ合わないように収め、
20℃で静置した。およそ 3 日～1ヶ月の静置の後に、試料溶液中に最大 0.07mm
×0.07mm×0.5mm 程度の大きさの結晶が得られた。

　　得られた結晶を 20％のグリセロールを加えた結晶化溶液に浸し、続いて液
体窒素中で急速に凍結した。シンクロトロン施設 Spring-8 の BL32B2 において、

10　振動法により、凍結した結晶の X 線回折データを 100K 窒素気流中で収集した。
得られた回折像から、Mosflm を用いて回折強度を数値化し、結晶構造因子を
求めた。この段階で結晶は六方晶系であり、空間群は P6$_5$22 あるいは P6$_1$22 を
有し、結晶の単位格子は、a = b = 103.2 Å, c = 281.0Å, α= β = 90°,
γ = 120° であることが明らかとなった。

15　　次に、得られた構造因子をもちいて分子置換法を行い、構造を解析した。立
体構造のモデルとして、変異型 GK（Δ1－11）／グルコース／化合物複合
体結晶により決定されたグルコキナーゼの各ドメインの 3 次元構造座標をそれ
ぞれ別々に用いた。計算は、8～4 オングストロームの分解能のデータを用い
て、CCP4(Council for the Central laboratory of the Research Councils)

20　の Amore プログラムにより行った。結晶の空間群は P6$_5$22 であり、非対称単位
に変異型 GK（Δ1－15）一分子を含むことが分かった。この構造と構造因
子から電子密度マップを得て、プログラム O（Dat-ONO 社製）を用いて変異型
GK（Δ1－15）単体の構造を決定した。

　　次に、CNX（モレキュラーシミュレーション社製）を用いてアミノ酸の位置

25　の精密化を行い、プログラム O を用いてアミノ酸残基の同定を行った。この操
作を繰り返し行い、変異型グルコキナーゼのメチオニン 15 からヒスチジン
156 とアスパラギン 180 からシステイン 461 までの 424 アミノ酸残基の構造座
標、2 分子の硫酸イオン、1 個のナトリウムイオン、及び 7 個の水分子を同定
し構造座標を決定した。最終的に決定された構造の正確さの指標とされる R 因

- 291 -

子は、50〜3．4オングストロームの分解能のデータに対してR=23．8％であり、構造の精密化の段階で計算に用いなかったデータに対するR因子（Rfree）は30．6％であった。ラマチャンドラン・プロットで確認したところ、許容されない構造を持ったアミノ酸残基はなかった。

5　　図1a及び図1bに、それぞれグルコキナーゼ（Δ1－11）／グルコース／化合物1の構造を示すリボン図、及びグルコキナーゼ（Δ1－15）単体の構造を示すリボン図を示す。なお、右図は、左図を回転した図である。決定された変異型GK（Δ1－15）単体の構造においてラージドメイン及びスモールドメインの主要部分の構造は、変異型GK（Δ1－11）／グルコース／化合物複
10　合体結晶により決定されたグルコキナーゼにおけるそれぞれの構造と似たものであったが、2つのドメインの相対位置が大きく異なっていた。変異型GK（Δ1－15）単体構造においてスモールドメインの主要部分は、変異型GK（Δ1－11）／グルコース／化合物複合体構造におけるスモールドメインの位置からおよそ99度回転していた。また、グルコキナーゼのC末端領域に位置し
15　変異型GK（Δ1－11）／グルコース／化合物複合体構造においてはスモールドメインを構成していたα13ヘリックスは、変異型GK（Δ1－15）単体構造においてはもはやスモールドメインを構成せず、両ドメイン間に位置していた。さらに、変異型GK（Δ1－11）／グルコース／化合物複合体構造における基質グルコースの結合部位及び活性化剤結合部位はどちらも2つのド
20　メイン間に存在していたため、新たに決定した構造ではそれらの部位の構造は大きく変化していた。変異型GK（Δ1－15）単体構造では酵素活性に重要な役割を果たすアミノ酸残基が活性部位を形成しておらず、今回解析した変異型GK（Δ1－15）単体の構造は、グルコキナーゼの不活性状態の構造であった。また、変異型GK（Δ1－15）単体の構造において活性化剤結合部位
25　は、完全に消失していた。変異型GK（Δ1－11）／グルコース／化合物複合体構造および変異型GK（Δ1－15）単体構造により観測されたグルコキナーゼの構造変化（約99度のドメインの回転）は、今まで知られていたヘキソキナーゼの構造変化（約12度のドメインの回転）と比較してはるかに大きな

- 292 -

ものであり、現在の計算化学の能力で予想でき得るものではなく、今回の構造解析により初めて明らかとなったものである。

　また、不活性型である変異型GK（Δ1－15）単体構造への構造変化を阻害する目的として、変異型GK（Δ1－11）／グルコース／化合物複合体構造で示された化合物結合部位に結合する化合物を設計することにより、グルコキナーゼの活性化剤を設計できることが明らかとなった。


産業上の利用可能性

　以上説明したように、本発明によれば、従来は結晶化が困難であったグルコキナーゼタンパク質の結晶を得ることができた。この結晶の構造を解析することによって得られる三次元構造座標は、グルコキナーゼに結合する化合物を設計するために好適に用いることができる。また、このようにして設計される化合物は、グルコキナーゼに結合するので、グルコキナーゼ活性化剤又は阻害剤として、グルコキナーゼ活性が関与する疾患の治療剤（例えば、糖尿病治療剤）として用いることができる。

- 293 -
請求の範囲


1．　結晶化に用いることを特徴とする、グルコキナーゼタンパク質。

2．　配列番号５に記載のアミノ酸配列からなることを特徴とする、請求項１
に記載のタンパク質。

3．　配列番号５に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一
のアミノ酸配列からなることを特徴とするタンパク質の結晶。

4．　前記タンパク質がグルコキナーゼタンパク質である、請求項３に記載の
結晶。

5．　配列番号５に記載のアミノ酸配列を有するタンパク質の結晶である、請
求項３に記載の結晶。

6．　格子定数が、下記式（１）～（４）：

　　a=b=79.9±4オングストローム　…（１）

　　c=322.2±15オングストローム　…（２）

　　$\alpha = \beta = 90°$　…（３）

　　$\gamma = 120°$　…（４）

を満たす、請求項３に記載の結晶。

7．　空間群が$P6_5 22$である、請求項６に記載の結晶。

8．　表１に記載の三次元構造座標データによって特定されるタンパク質の結
晶。

9．　表１に記載の三次元構造座標データの少なくとも一つのデータを変更し
た三次元構造座標データにおいて、表１に記載の三次元構造座標データで示さ
れるアミノ酸の主鎖の原子（Ｃα原子）と、該Ｃα原子と対応する前記変更し
た三次元構造座標データで示されるＣα原子との平均二乗偏差が、０．６オン
グストローム以下である結晶。

１０．　化合物結合部位が、配列番号５に示すアミノ酸配列における、チロシ
ン６１～セリン６９、グルタミン酸９６～グルタミン９８、イソロイシン１５
９、メチオニン２１０～チロシン２１５、ヒスチジン２１８～グルタミン酸２
２１、メチオニン２３５、アルギニン２５０、ロイシン４５１～リジン４５９

のアミノ酸残基の少なくともひとつによって構成されている、請求項３～９の
いずれかに記載の結晶。

１１．　配列番号５に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同
一のアミノ酸配列からなるタンパク質と該タンパク質に結合可能な化合物との
複合体を含む結晶。

１２．　前記化合物が、式（Ｉ）で表される、請求項１１に記載の結晶。
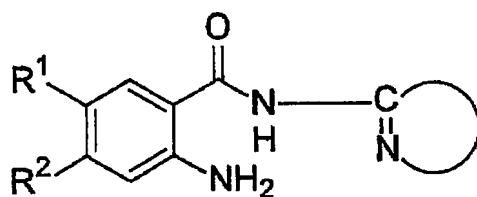


(I)

[式中、$R^1$は、ハロゲン原子、－Ｓ－(O)p－Ａ、－Ｓ－(O)q－Ｂ又は－Ｏ
－Ｂを示し（ここで、ｐ及びｑは同一又は異なって、０～２の整数を示し、Ａ
は置換されていてもよい直鎖の$C_1$－$C_6$アルキル基を示し、Ｂは置換されてい
てもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、
$R^2$は水素原子又はハロゲン原子を示し、



(II)
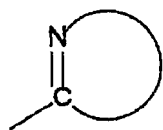
は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていても
よい単環の又は双環のヘテロアリール基を示す）

１３．　前記化合物が、式(IIIa)～式（IIIc）で表されるいずれかの化合物
である請求項１２に記載の結晶。

(IIIa)

(IIIb)

5

(IIIc)
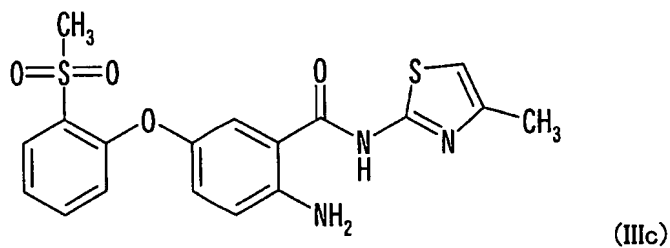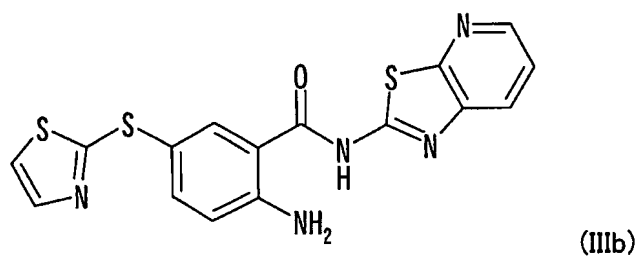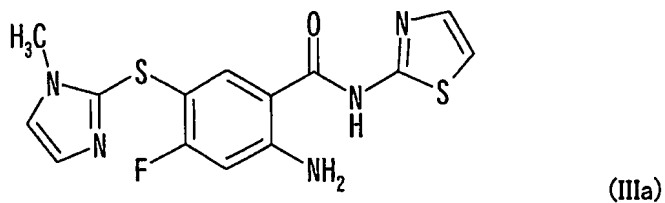
１４．　配列番号８に記載のアミノ酸配列からなることを特徴とする、請求項
１に記載のタンパク質。

１５．　配列番号８に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同
10　一のアミノ酸配列からなることを特徴とするタンパク質の結晶。

１６．　前記タンパク質がグルコキナーゼタンパク質である、請求項１５に記
載の結晶。

１７．　配列番号８に記載のアミノ酸配列を有するタンパク質の結晶である、
請求項１５に記載の結晶。

15　１８．　格子定数が、下記式

$$a=b=103.2\pm5 \text{ オングストローム } \cdots (5)$$

$$c=281.0\pm7 \text{ オングストローム } \cdots (6)$$

$$\alpha=\beta=90° \quad \cdots (7)$$

- 296 -

$\gamma = 120°$ … (8)

を満たす、請求項１５に記載の結晶。

１９．　空間群が $P6_522$ である、請求項１８に記載の結晶。

２０．　表２に記載の三次元構造座標データによって特定されるタンパク質の結晶。

２１．　表２に記載の三次元構造座標データの少なくとも一つのデータを変更した三次元構造座標データにおいて、表２に記載の三次元構造座標データで示されるアミノ酸の主鎖の原子（Ｃα原子）と、該Ｃα原子と対応する前記変更した三次元構造座標データで示されるＣα原子との平均二乗偏差が、０．６オングストローム以下である結晶。

２２．　配列番号２に記載のアミノ酸配列を有するタンパク質のＮ末端、Ｃ末端のいずれかまたは両方から、１〜５０個のアミノ酸残基を欠損したアミノ酸配列を有するタンパク質を製造するタンパク質製造工程と、

　前記タンパク質製造工程で得られたタンパク質と結合する化合物と、前記タンパク質製造工程で得られたタンパク質とを反応させるタンパク質反応工程とを含む、

　タンパク質及びそのタンパク質と結合する化合物の複合体を含む結晶の製造方法。

２３．　タンパク質の結晶を製造する方法であって、

　配列番号５に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミノ酸配列を含みグルコキナーゼ活性を有するタンパク質、及び該タンパク質に結合可能な化合物を用いることを特徴とする、結晶の製造方法。

２４．　前記タンパク質に結合可能な化合物が、式（Ｉ）で表される化合物であることを特徴とする、請求項２３に記載のタンパク質の結晶の製造方法。

- 297 -
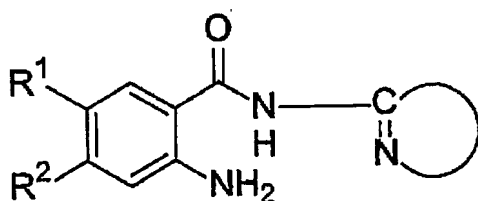


(I)

[式中、$R^1$は、ハロゲン原子、－S－(O)p－A、－S－(O)q－B又は－O
－Bを示し（ここで、p及びqは同一又は異なって、0〜2の整数を示し、A
は置換されていてもよい直鎖の$C_1$－$C_6$アルキル基を示し、Bは置換されてい
てもよい五員環又は六員環のアリール基又はヘテロアリール基を示し、
$R^2$は水素原子又はハロゲン原子を示し、



(II)
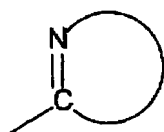
は、アミド基に結合した炭素原子の隣に窒素原子を有する、置換されていても
よい単環の又は双環のヘテロアリール基を示す）

　２５．　共結晶法又はソーキング法による、請求項２３、又は請求項２４に記
載の結晶の製造方法。

　２６．　タンパク質の立体構造情報に基づいて該タンパク質に結合する化合物
の構造をデザインするドラッグデザイン方法であって、

　該タンパク質の立体構造情報が、請求項３〜１３、請求項１５〜２１のうちの
いずれか一項に記載の結晶を解析することによって得られる情報であることを
特徴とする、ドラッグデザイン方法。

　２７．　前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推
測する結合部位推測工程と、

　前記結合部位推測工程で推測された化合物結合部位に適合する化合物を、化合

- 298 -

物ライブラリより選択する選択工程と、

　を含むことを特徴とする、請求項２６に記載のドラッグデザイン方法。

　２８．　前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

5　前記結合部位推測工程で推測された化合物結合部位に適合する化合物の構造を構築する化合物構造構築工程と、

　を含むことを特徴とする、請求項２６に記載のドラッグデザイン方法。

　２９．　前記立体構造情報に基づいて、前記タンパク質の化合物結合部位を推測する結合部位推測工程と、

10　前記結合部位推測工程で推測された化合物結合部位と該化合物結合部位に適合する化合物とが相互作用するように化合物の構造を目視によりデザインするデザイン工程と、

　を含むことを特徴とする、請求項２６に記載のドラッグデザイン方法。

　３０．　前記化合物結合部位が、配列番号５に示すアミノ酸配列における、チ

15　ロシン６１～セリン６９、グルタミン酸９６～グルタミン９８、イソロイシン１５９、メチオニン２１０～チロシン２１５、ヒスチジン２１８～グルタミン酸２２１、メチオニン２３５、アルギニン２５０、ロイシン４５１～リジン４５９のアミノ酸残基の少なくともひとつによって構成されている、請求項２６～２９のうちのいずれか一項に記載のドラッグデザイン方法。

20　３１．　さらに、前記化合物結合部位に適合すると推定される候補化合物の生理活性を測定する工程を含む、請求項２６～３０のいずれか一項に記載のドラッグデザイン方法。

　３２．　さらに、前記化合物結合部位に適合すると推定される候補化合物と、配列番号５に記載のアミノ酸配列又はそのアミノ酸配列と実質的に同一のアミ

25　ノ酸配列を含むタンパク質とを接触させ、その候補化合物が該タンパク質に結合するか否か判定する結合判定工程を含む、請求項２６～３０のいずれか一項に記載のドラッグデザイン方法。

　３３．　請求項２６～３０のいずれか一項に記載のドラッグデザイン方法によって選択された化合物群を化合物アレイとして組み合わせることを含む化合物

- 299 -

アレイの製造方法。

5

図1

a



ラージドメイン

←グルコース　　グルコース→

化合物1→　　　　←化合物1

スモールドメイン

α 13ヘリックス

b



ラージドメイン

α 13ヘリックス

スモールドメイン

ディスオーダー領域

図2
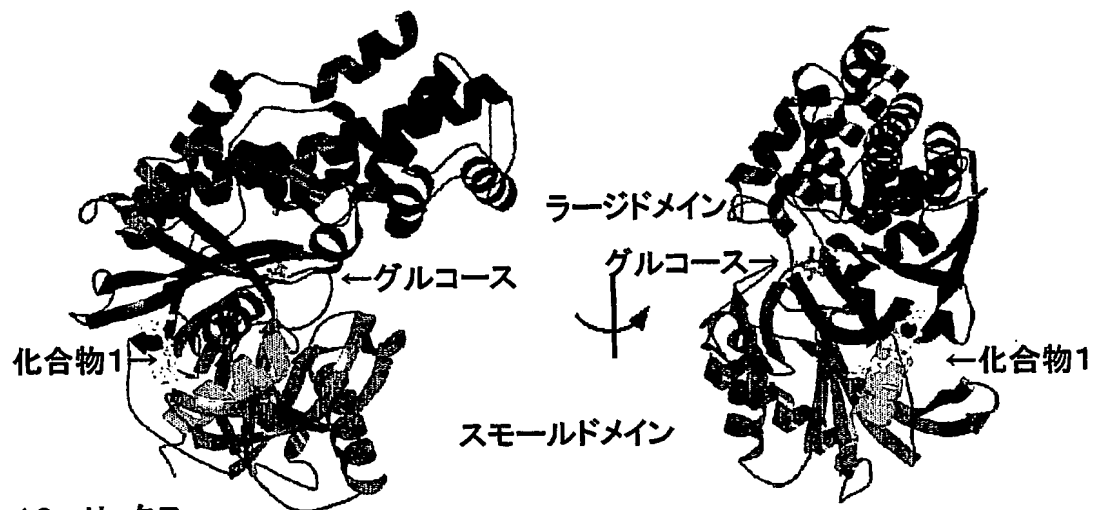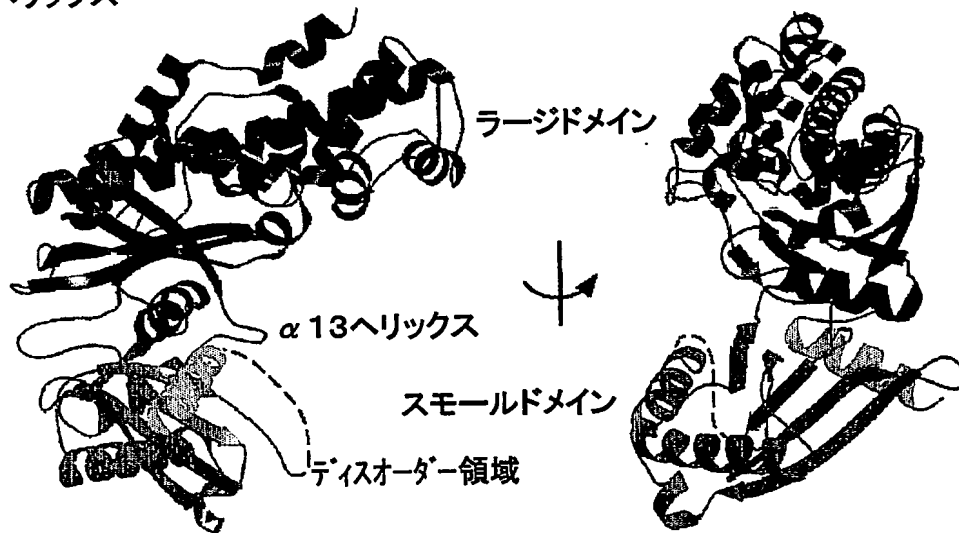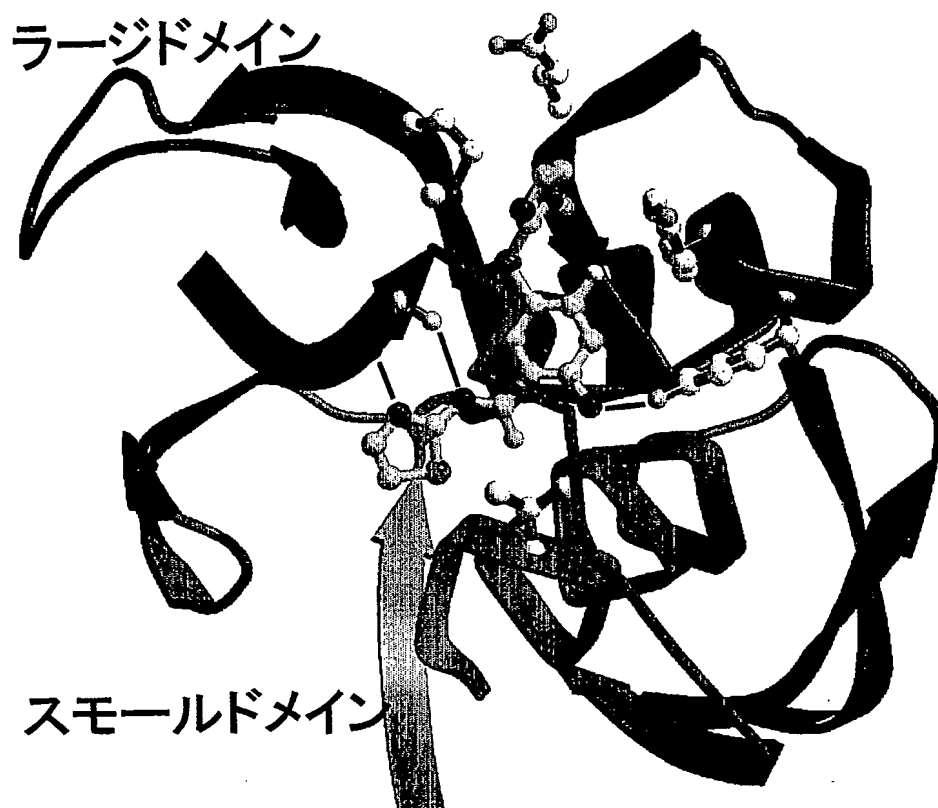
図3
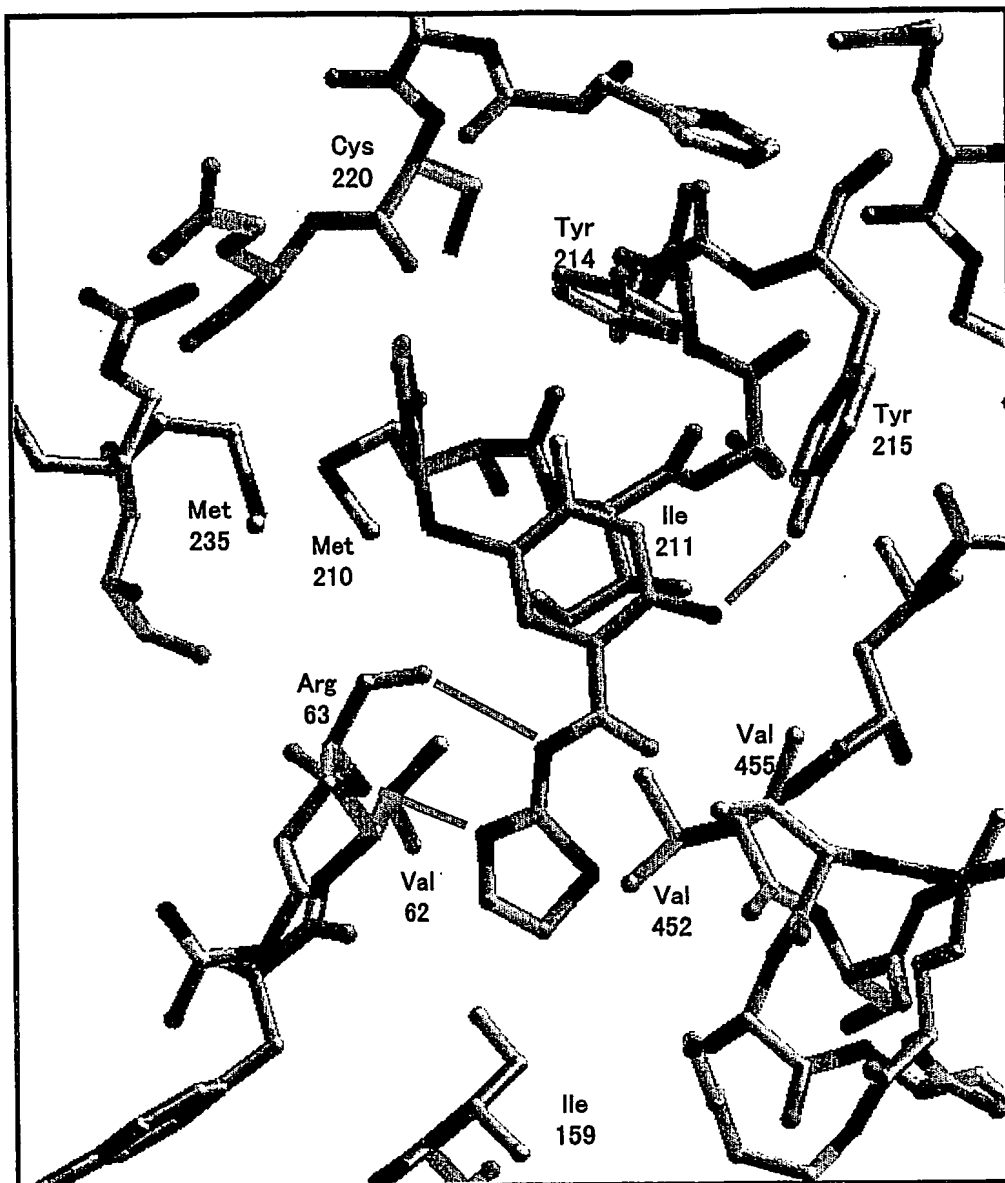
1/15
SEQUENCE LISTING

<110> Banyu Pharmaceutical Co., Ltd.

<120> Crystal of Glucokinase Protein and Drug Desing Method
      Using Thereof

<130> P03-0064PCT

<140>
<141>

<150> JP2002-142232
<151> 2002-05-16

<160> 10

<170> PatentIn Ver. 2.1

<210> 1
<211> 1401
<212> DNA
<213> Homo sapiens

<400> 1
atggcgatgg atgtcacaag gagccaggcc cagacagcct tgactctggt agagcagatc 60
ctggcagagt tccagctgca ggaggaggac ctgaagaagg tgatgagacg gatgcagaag 120
gagatggacc gcggcctgag gctggagacc catgaagagg ccagtgtgaa gatgctgccc 180
acctacgtgc gctccacccc agaaggctca gaagtcgggg acttcctctc cctggacctg 240
ggtggcacta acttcagggt gatgctggtg aaggtgggag aaggtgagga ggggcagtgg 300
agcgtgaaga ccaaacacca gatgtactcc atccccgagg acgccatgac cggcactgct 360
gagatgctct tcgactacat ctctgagtgc atctccgact tcctggacaa gcatcagatg 420
aaacacaaga agctgcccct gggcttcacc ttctcctttc ctgtgaggca cgaagacatc 480
gataagggca tccttctcaa ctggaccaag ggcttcaagg cctcaggagc agaagggaac 540
aatgtcgtgg ggcttctgcg agacgctatc aaacggagag gggactttga aatggatgtg 600
gtggcaatgg tgaatgacac ggtggccacg atgatctcct gctactacga agaccatcaɕ 660

```
tgcgaggtcg gcatgatcgt gggcacgggc tgcaatgcct gctacatgga ggagatgcag 720
aatgtggagc tggtggaggg ggacgagggc cgcatgtgcg tcaataccga gtggggcgcc 780
ttcggggact ccggcgagct ggacgagttc ctgctggagt atgaccgcct ggtggacgag 840
agctctgcaa accccggtca gcagctgtat gagaagctca taggtggcaa gtacatgggc 900
gagctggtgc ggcttgtgct gctcaggctc gtggacgaaa acctgctctt ccacggggag 960
gcctccgagc agctgcgcac acgcggagcc ttcgagacgc gcttcgtgtc gcaggtggag 1020
agcgacacgg gcgaccgcaa gcagatctac aacatcctga gcacgctggg gctgcgaccc 1080
tcgaccaccg actgcgacat cgtgcgccgc gcctgcgaga gcgtgtctac gcgcgctgcg 1140
cacatgtgct cggcgggggct ggcgggcgtc atcaaccgca tgcgcgagag ccgcagcgag 1200
gacgtaatgc gcatcactgt gggcgtggat ggctccgtgt acaagctgca ccccagcttc 1260
aaggagcggt tccatgccag cgtgcgcagg ctgacgccca gctgcgagat caccttcatc 1320
gagtcggagg agggcagtgg ccggggcgcg gccctggtct cggcggtggc ctgtaagaag 1380
gcctgtatgc tgggccagtg a                                         1401
```

<210> 2
<211> 466
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Ala Met Asp Val Thr Arg Ser Gln Ala Gln Thr Ala Leu Thr Leu
 1               5                  10                  15


Val Glu Gln Ile Leu Ala Glu Phe Gln Leu Gln Glu Glu Asp Leu Lys
             20                  25                  30


Lys Val Met Arg Arg Met Gln Lys Glu Met Asp Arg Gly Leu Arg Leu
         35                  40                  45


Glu Thr His Glu Glu Ala Ser Val Lys Met Leu Pro Thr Tyr Val Arg
     50                  55                  60


Ser Thr Pro Glu Gly Ser Glu Val Gly Asp Phe Leu Ser Leu Asp Leu
 65                  70                  75                  80
```

3/15

Gly Gly Thr Asn Phe Arg Val Met Leu Val Lys Val Gly Glu Gly Glu
                85                  90                  95

Glu Gly Gln Trp Ser Val Lys Thr Lys His Gln Met Tyr Ser Ile Pro
            100                 105                 110

Glu Asp Ala Met Thr Gly Thr Ala Glu Met Leu Phe Asp Tyr Ile Ser
        115                 120                 125

Glu Cys Ile Ser Asp Phe Leu Asp Lys His Gln Met Lys His Lys Lys
    130                 135                 140

Leu Pro Leu Gly Phe Thr Phe Ser Phe Pro Val Arg His Glu Asp Ile
145                 150                 155                 160

Asp Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly Phe Lys Ala Ser Gly
                165                 170                 175

Ala Glu Gly Asn Asn Val Val Gly Leu Leu Arg Asp Ala Ile Lys Arg
                180                 185                 190

Arg Gly Asp Phe Glu Met Asp Val Val Ala Met Val Asn Asp Thr Val
            195                 200                 205

Ala Thr Met Ile Ser Cys Tyr Tyr Glu Asp His Gln Cys Glu Val Gly
    210                 215                 220

Met Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr Met Glu Glu Met Gln
225                 230                 235                 240

Asn Val Glu Leu Val Glu Gly Asp Glu Gly Arg Met Cys Val Asn Thr
                245                 250                 255

Glu Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu Asp Glu Phe Leu Leu
            260                 265                 270

4/15

Glu Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala Asn Pro Gly Gln Gln
        275                 280             285

Leu Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met Gly Glu Leu Val Arg
        290                 295             300

Leu Val Leu Leu Arg Leu Val Asp Glu Asn Leu Leu Phe His Gly Glu
305             310             315             320

Ala Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe Glu Thr Arg Phe Val
                325             330             335

Ser Gln Val Glu Ser Asp Thr Gly Asp Arg Lys Gln Ile Tyr Asn Ile
            340             345             350

Leu Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr Asp Cys Asp Ile Val
        355             360             365

Arg Arg Ala Cys Glu Ser Val Ser Thr Arg Ala Ala His Met Cys Ser
    370             375             380

Ala Gly Leu Ala Gly Val Ile Asn Arg Met Arg Glu Ser Arg Ser Glu
385             390             395             400

Asp Val Met Arg Ile Thr Val Gly Val Asp Gly Ser Val Tyr Lys Leu
                405             410             415

His Pro Ser Phe Lys Glu Arg Phe His Ala Ser Val Arg Arg Leu Thr
            420             425             430

Pro Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu Glu Gly Ser Gly Arg
        435             440             445

Gly Ala Ala Leu Val Ser Ala Val Ala Cys Lys Lys Ala Cys Met Leu
    450             455             460

5/15

Gly Gln
465

```
<210> 3
<211> 465
<212> PRT
<213> Homo sapiens

<400> 3
Met Leu Asp Asp Arg Ala Arg Met Glu Ala Ala Lys Lys Glu Lys Val
 1               5                  10                  15

Glu Gln Ile Leu Ala Glu Phe Gln Leu Gln Glu Glu Asp Leu Lys Lys
             20                  25                  30

Val Met Arg Arg Met Gln Lys Glu Met Asp Arg Gly Leu Arg Leu Glu
         35                  40                  45

Thr His Glu Glu Ala Ser Val Lys Met Leu Pro Thr Tyr Val Arg Ser
     50                  55                  60

Thr Pro Glu Gly Ser Glu Val Gly Asp Phe Leu Ser Leu Asp Leu Gly
 65                  70                  75                  80

Gly Thr Asn Phe Arg Val Met Leu Val Lys Val Gly Glu Gly Glu Glu
                 85                  90                  95

Gly Gln Trp Ser Val Lys Thr Lys His Gln Met Tyr Ser Ile Pro Glu
             100                 105                 110

Asp Ala Met Thr Gly Thr Ala Glu Met Leu Phe Asp Tyr Ile Ser Glu
             115                 120                 125

Cys Ile Ser Asp Phe Leu Asp Lys His Gln Met Lys His Lys Lys Leu
     130                 135                 140
```

6/15

Pro Leu Gly Phe Thr Phe Ser Phe Pro Val Arg His Glu Asp Ile Asp
145　　　　　　　　150　　　　　　　155　　　　　　　160

Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly Phe Lys Ala Ser Gly Ala
　　　　　　165　　　　　　　170　　　　　　　175

Glu Gly Asn Asn Val Val Gly Leu Leu Arg Asp Ala Ile Lys Arg Arg
　　　　　180　　　　　　　185　　　　　　　190

Gly Asp Phe Glu Met Asp Val Val Ala Met Val Asn Asp Thr Val Ala
　　　　　195　　　　　　　200　　　　　　　205

Thr Met Ile Ser Cys Tyr Tyr Glu Asp His Gln Cys Glu Val Gly Met
　　　210　　　　　　　215　　　　　　　220

Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr Met Glu Glu Met Gln Asn
225　　　　　　　230　　　　　　　235　　　　　　　240

Val Glu Leu Val Glu Gly Asp Glu Gly Arg Met Cys Val Asn Thr Glu
　　　　　245　　　　　　　250　　　　　　　255

Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu Asp Glu Phe Leu Leu Glu
　　　　　260　　　　　　　265　　　　　　　270

Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala Asn Pro Gly Gln Gln Leu
　　　　275　　　　　　　280　　　　　　　285

Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met Gly Glu Leu Val Arg Leu
　　　290　　　　　　　295　　　　　　　300

Val Leu Leu Arg Leu Val Asp Glu Asn Leu Leu Phe His Gly Glu Ala
305　　　　　　　310　　　　　　　315　　　　　　　320

Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe Glu Thr Arg Phe Val Ser
　　　　325　　　　　　　330　　　　　　　335

Gln Val Glu Ser Asp Thr Gly Asp Arg Lys Gln Ile Tyr Asn Ile Leu
            340                 345                 350

Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr Asp Cys Asp Ile Val Arg
            355                 360                 365

Arg Ala Cys Glu Ser Val Ser Thr Arg Ala Ala His Met Cys Ser Ala
        370                 375                 380

Gly Leu Ala Gly Val Ile Asn Arg Met Arg Glu Ser Arg Ser Glu Asp
385                 390                 395                 400

Val Met Arg Ile Thr Val Gly Val Asp Gly Ser Val Tyr Lys Leu His
            405                 410                 415

Pro Ser Phe Lys Glu Arg Phe His Ala Ser Val Arg Arg Leu Thr Pro
            420                 425                 430

Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu Glu Gly Ser Gly Arg Gly
        435                 440                 445

Ala Ala Leu Val Ser Ala Val Ala Cys Lys Lys Ala Cys Met Leu Gly
        450                 455                 460

Gln
465


<210> 4
<211> 1368
<212> DNA
<213> Homo sapiens

<400> 4
atggccttga ctctggtaga gcagatcctg gcagagttcc agctgcagga ggaggacctg 60

8/15

```
aagaaggtga tgagacggat gcagaaggag atggaccgcg gcctgaggct ggagacccat 120
gaagaggcca gtgtgaagat gctgcccacc tacgtgcgct ccaccccaga aggctcagaa 180
gtcggggact tcctctccct ggacctgggt ggcactaact tcagggtgat gctggtgaag 240
gtgggagaag gtgaggaggg gcagtggagc gtgaagacca aacaccagat gtactccatc 300
cccgaggacg ccatgaccgg cactgctgag atgctcttcg actacatctc tgagtgcatc 360
tccgacttcc tggacaagca tcagatgaaa cacaagaagc tgcccctggg cttcaccttc 420
tcctttcctg tgaggcacga agacatcgat aagggcatcc ttctcaactg gaccaagggc 480
ttcaaggcct caggagcaga agggaacaat gtcgtggggc ttctgcgaga cgctatcaaa 540
cggagagggg actttgaaat ggatgtggtg gcaatggtga atgacacggt ggccacgatg 600
atctcctgct actacgaaga ccatcagtgc gaggtcggca tgatcgtggg cacgggctgc 660
aatgcctgct acatggagga gatgcagaat gtggagctgg tggaggggga cgagggccgc 720
atgtgcgtca ataccgagtg gggcgccttc ggggactccg gcgagctgga cgagttcctg 780
ctggagtatg accgcctggt ggacgagagc tctgcaaacc ccggtcagca gctgtatgag 840
aagctcatag gtggcaagta catgggcgag ctggtgcggc ttgtgctgct caggctcgtg 900
gacgaaaacc tgctcttcca cggggaggcc tccgagcagc tgcgcacacg cggagccttc 960
gagacgcgct tcgtgtcgca ggtggagagc gacacgggcg accgcaagca gatctacaac 1020
atcctgagca cgctggggct gcgaccctcg accaccgact gcgacatcgt gcgccgcgcc 1080
tgcgagagcg tgtctacgcg cgctgcgcac atgtgctcgg cggggctggc gggcgtcatc 1140
aaccgcatgc gcgagagccg cagcgaggac gtaatgcgca tcactgtggg cgtggatggc 1200
tccgtgtaca agctgcaccc cagcttcaag gagcggttcc atgccagcgt gcgcaggctg 1260
acgcccagct gcgagatcac cttcatcgag tcggaggagg cagtggccg gggcgcggcc 1320
ctggtctcgg cggtggcctg taagaaggcc tgtatgctgg gccagtga           1368
```

<210> 5
<211> 455
<212> PRT
<213> Homo sapiens

<400> 5

| Met | Ala | Leu | Thr | Leu | Val | Glu | Gln | Ile | Leu | Ala | Glu | Phe | Gln | Leu | Gln |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| Glu | Glu | Asp | Leu | Lys | Lys | Val | Met | Arg | Arg | Met | Gln | Lys | Glu | Met | Asp |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | 20 | | | | | 25 | | | | | 30 | | | |

9/15

```
Arg Gly Leu Arg Leu Glu Thr His Glu Glu Ala Ser Val Lys Met Leu
         35                  40                  45

Pro Thr Tyr Val Arg Ser Thr Pro Glu Gly Ser Glu Val Gly Asp Phe
     50                  55                  60

Leu Ser Leu Asp Leu Gly Gly Thr Asn Phe Arg Val Met Leu Val Lys
 65                  70                  75                  80

Val Gly Glu Gly Glu Glu Gly Gln Trp Ser Val Lys Thr Lys His Gln
             85                  90                  95

Met Tyr Ser Ile Pro Glu Asp Ala Met Thr Gly Thr Ala Glu Met Leu
         100                 105                 110

Phe Asp Tyr Ile Ser Glu Cys Ile Ser Asp Phe Leu Asp Lys His Gln
         115                 120                 125

Met Lys His Lys Lys Leu Pro Leu Gly Phe Thr Phe Ser Phe Pro Val
     130         ·           135                 140

Arg His Glu Asp Ile Asp Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly
145                 150                 155                 160

Phe Lys Ala Ser Gly Ala Glu Gly Asn Asn Val Val Gly Leu Leu Arg
             165                 170                 175

Asp Ala Ile Lys Arg Arg Gly Asp Phe Glu Met Asp Val Val Ala Met
         180                 185                 190

Val Asn Asp Thr Val Ala Thr Met Ile Ser Cys Tyr Tyr Glu Asp His
         195                 200                 205

Gln Cys Glu Val Gly Met Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr
     210                 215                 220
```

10/15

Met Glu Glu Met Gln Asn Val Glu Leu Val Glu Gly Asp Glu Gly Arg
225           230           235           240

Met Cys Val Asn Thr Glu Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu
          245           250           255

Asp Glu Phe Leu Leu Glu Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala
          260           265           270

Asn Pro Gly Gln Gln Leu Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met
          275           280           285

Gly Glu Leu Val Arg Leu Val Leu Leu Arg Leu Val Asp Glu Asn Leu
          290           295           300

Leu Phe His Gly Glu Ala Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe
305           310           315           320

Glu Thr Arg Phe Val Ser Gln Val Glu Ser Asp Thr Gly Asp Arg Lys
          325           330           335

Gln Ile Tyr Asn Ile Leu Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr
          340           345           350

Asp Cys Asp Ile Val Arg Arg Ala Cys Glu Ser Val Ser Thr Arg Ala
          355           360           365

Ala His Met Cys Ser Ala Gly Leu Ala Gly Val Ile Asn Arg Met Arg
          370           375           380

Glu Ser Arg Ser Glu Asp Val Met Arg Ile Thr Val Gly Val Asp Gly
385           390           395           400

Ser Val Tyr Lys Leu His Pro Ser Phe Lys Glu Arg Phe His Ala Ser
          405           410           415

11/15

Val Arg Arg Leu Thr Pro Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu
        420                     425                 430

Glu Gly Ser Gly Arg Gly Ala Ala Leu Val Ser Ala Val Ala Cys Lys
        435                     440                 445

Lys Ala Cys Met Leu Gly Gln
    450                 455


<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 6
gtcacaagga gccagaagct tatggcctga ctctggtag                              39


<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 7
gaagccccac gacattgttc ccttctgc                                         28


<210> 8
<211> 451

<212> PRT
<213> Homo sapiens

<400> 8
Met Val Glu Gln Ile Leu Ala Glu Phe Gln Leu Gln Glu Glu Asp Leu
 1               5                  10                  15

Lys Lys Val Met Arg Arg Met Gln Lys Glu Met Asp Arg Gly Leu Arg
                20                  25                  30

Leu Glu Thr His Glu Glu Ala Ser Val Lys Met Leu Pro Thr Tyr Val
            35                  40                  45

Arg Ser Thr Pro Glu Gly Ser Glu Val Gly Asp Phe Leu Ser Leu Asp
        50                  55                  60

Leu Gly Gly Thr Asn Phe Arg Val Met Leu Val Lys Val Gly Glu Gly
65                  70                  75                  80

Glu Glu Gly Gln Trp Ser Val Lys Thr Lys His Gln Met Tyr Ser Ile
                85                  90                  95

Pro Glu Asp Ala Met Thr Gly Thr Ala Glu Met Leu Phe Asp Tyr Ile
                100                 105                 110

Ser Glu Cys Ile Ser Asp Phe Leu Asp Lys His Gln Met Lys His Lys
            115                 120                 125

Lys Leu Pro Leu Gly Phe Thr Phe Ser Phe Pro Val Arg His Glu Asp
        130                 135                 140

Ile Asp Lys Gly Ile Leu Leu Asn Trp Thr Lys Gly Phe Lys Ala Ser
145                 150                 155                 160

Gly Ala Glu Gly Asn Asn Val Val Gly Leu Leu Arg Asp Ala Ile Lys
                165                 170                 175

Arg Arg Gly Asp Phe Glu Met Asp Val Val Ala Met Val Asn Asp Thr
        180            185            190

Val Ala Thr Met Ile Ser Cys Tyr Tyr Glu Asp His Gln Cys Glu Val
        195            200            205

Gly Met Ile Val Gly Thr Gly Cys Asn Ala Cys Tyr Met Glu Glu Met
        210            215            220

Gln Asn Val Glu Leu Val Glu Gly Asp Glu Gly Arg Met Cys Val Asn
225            230            235            240

Thr Glu Trp Gly Ala Phe Gly Asp Ser Gly Glu Leu Asp Glu Phe Leu
        245            250            255

Leu Glu Tyr Asp Arg Leu Val Asp Glu Ser Ser Ala Asn Pro Gly Gln
        260            265            270

Gln Leu Tyr Glu Lys Leu Ile Gly Gly Lys Tyr Met Gly Glu Leu Val
        275            280            285

Arg Leu Val Leu Leu Arg Leu Val Asp Glu Asn Leu Leu Phe His Gly
        290            295            300

Glu Ala Ser Glu Gln Leu Arg Thr Arg Gly Ala Phe Glu Thr Arg Phe
305            310            315            320

Val Ser Gln Val Glu Ser Asp Thr Gly Asp Arg Lys Gln Ile Tyr Asn
            325            330            335

Ile Leu Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr Asp Cys Asp Ile
        340            345            350

Val Arg Arg Ala Cys Glu Ser Val Ser Thr Arg Ala Ala His Met Cys
        355            360            365

14/15

Ser Ala Gly Leu Ala Gly Val Ile Asn Arg Met Arg Glu Ser Arg Ser
    370                 375                 380

Glu Asp Val Met Arg Ile Thr Val Gly Val Asp Gly Ser Val Tyr Lys
385                 390                 395                 400

Leu His Pro Ser Phe Lys Glu Arg Phe His Ala Ser Val Arg Arg Leu
                405                 410                 415

Thr Pro Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu Glu Gly Ser Gly
            420                 425                 430

Arg Gly Ala Ala Leu Val Ser Ala Val Ala Cys Lys Lys Ala Cys Met
        435                 440                 445

Leu Gly Gln
    450


<210> 9
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 9
ccaggcccag acagccaagc ttatggtaga gcagatcc                          38


<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 10
gaagccccac gacattgttc ccttctgc                                    28

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/06054

## A. CLASSIFICATION OF SUBJECT MATTER
Int.Cl⁷ C12N9/12, C12Q1/48

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
Int.Cl⁷ C12N9/12, C12Q1/48

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
CA(STN), BIOSIS(DIALOG), WPI(DIALOG),
SwissProt/PIR/Genbank/EMBL/DDBJ/GeneSeq

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X<br>A | TANIZAWA, Y. et al., Human Liver Glucokinase Gene: Cloning and Sequence Determination of Two Alternatively Spliced cDNAs, Proc.Natl.Acad.Sci. USA., 1991, Vol.88, pages 7294 to 7297 | 1<br>2-25 |
| A | MAHALINGAM B. et al., Structural model of human glucokinase in complex with glucose and ATP., Diabetes, 1999, Vol.48, pages 1698 to 1705 | 1-25 |
| A | WILLSON M. et al., Yeast hexokinase inhibitors designed from the 3-D enzyme structure reboiling. J. Enzyme Inhib., 1997, Vol.12, No.2, pages 101 to 121 | 1-25 |

☐ Further documents are listed in the continuation of Box C.  ☐ See patent family annex.

| | | | |
|---|---|---|---|
| * | Special categories of cited documents: | "T" | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| "A" | document defining the general state of the art which is not considered to be of particular relevance | | |
| "E" | earlier document but published on or after the international filing date | "X" | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| "L" | document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | "Y" | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| "O" | document referring to an oral disclosure, use, exhibition or other means | | |
| "P" | document published prior to the international filing date but later than the priority date claimed | "&" | document member of the same patent family |

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 12 June, 2003 (12.06.03) | 24 June, 2003 (24.06.03) |

| Name and mailing address of the ISA/ | Authorized officer |
|---|---|
| Japanese Patent Office | |
| Facsimile No. | Telephone No. |

Form PCT/ISA/210 (second sheet) (July 1998)

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP03/06054

---

**Box I    Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 26 to 33

   because they relate to subject matter not required to be searched by this Authority, namely:
   Inventions according to said claims relate to subject matters not required
   to be searched by this Authority in accordance with PCT Article 17 (2) (a)
   and PCT Rule 39.1. (see extra sheet for details)

2. ☐ Claims Nos.:

   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:

   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

---

**Box II    Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

**Remark on Protest**    ☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

---

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1998)

Continuation of Box No.I-1 of continuation of first sheet(1)

"Method for drug design" according to the present invention relates to the design of a compound to be bonded to a protein, on the basis of the information on the three-dimensional structure of the protein. The design according to the present invention involves the work of the inventor to estimate a suitable compound by his mental acts, and such work is considered to correspond to the performance of purely mental acts.

| A. | 発明の属する分野の分類（国際特許分類（ＩＰＣ）） |
|----|----|

Int. Cl⁷　C12N9/12, C12Q1/48

| B. | 調査を行った分野 |
|----|----|

調査を行った最小限資料（国際特許分類（ＩＰＣ））
Int. Cl⁷　C12N9/12, C12Q1/48

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用した電子データベース（データベースの名称、調査に使用した用語）
CA(STN), BIOSIS(DIALOG), WPI(DIALOG)
SwissProt/PIR/Genbank/EMBL/DDBJ/GeneSeq

| C. | 関連すると認められる文献 |
|----|----|

| 引用文献の<br>カテゴリー* | 引用文献名　及び一部の箇所が関連するときは、その関連する箇所の表示 | 関連する<br>請求の範囲の番号 |
|----|----|----|
| X<br>A | TANIZAWA Y. Tanizawa, et al., Human Liver Glucokinase Gene: Cloning and Sequence Determination of Two Alternatively Spliced cDNAs<br>Proc. Natl. Acad. Sci. USA., 1991, Vol.88, p.7294-7297 | 1<br>2-25 |
| A | MAHALINGAM B. et al., Structural model of human glucokinase in complex with glucose and ATP.<br>Diabetes, 1999, Vol.48, p1698-1705 | 1-25 |

☒　Ｃ欄の続きにも文献が列挙されている。　　　　☐　パテントファミリーに関する別紙を参照。

＊　引用文献のカテゴリー
「Ａ」特に関連のある文献ではなく、一般的技術水準を示すもの
「Ｅ」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの
「Ｌ」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献（理由を付す）
「Ｏ」口頭による開示、使用、展示等に言及する文献
「Ｐ」国際出願日前で、かつ優先権の主張の基礎となる出願

の日の後に公表された文献
「Ｔ」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの
「Ｘ」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの
「Ｙ」特に関連のある文献であって、当該文献と他の１以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの
「＆」同一パテントファミリー文献

| 国際調査を完了した日<br>　　12. 06. 03 | 国際調査報告の発送日　24.06.03 |
|----|----|
| 国際調査機関の名称及びあて先<br>　日本国特許庁（ＩＳＡ／ＪＰ）<br>　　郵便番号１００－８９１５<br>　　東京都千代田区霞が関三丁目４番３号 | 特許庁審査官（権限のある職員）　　　4B　3037<br>　鈴木　恵理子　　　　　　　印<br>電話番号　０３－３５８１－１１０１　内線　３４８８ |

様式ＰＣＴ／ＩＳＡ／２１０（第２ページ）（１９９８年７月）

| C（続き）. | 関連すると認められる文献 | |
|---|---|---|
| 引用文献の<br>カテゴリー＊ | 引用文献名　及び一部の箇所が関連するときは、その関連する箇所の表示 | 関連する<br>請求の範囲の番号 |
| A | WILLSON M. et al., Yeast hexokinase inhibitors designed from the 3-D enzyme structure reboilding.<br>J. Enzyme Inhib., 1997, Vol. 12, No. 2, p. 101-121 | 1-25 |

| 国際調査報告 | 国際出願番号　ＰＣＴ／ＪＰ０３／０６０５４ |
|---|---|

**第Ⅰ欄　請求の範囲の一部の調査ができないときの意見（第１ページの２の続き）**

法第８条第３項（ＰＣＴ１７条(2)(a)）の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. ☒　請求の範囲　　２６－３３　　　　　は、この国際調査機関が調査をすることを要しない対象に係るものである。
つまり、

　　当該請求の範囲に記載された発明は、ＰＣＴ１７条（２）（ａ）（ｉ）及びＰＣＴ規則３９．１（ｉｉｉ）の規定により、この国際調査機関が調査することを要しない対象に係るものである。
（詳細は「特別ページ」を参照されたい）

2. ☐　請求の範囲　　　　　　　　　　　は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、

3. ☐　請求の範囲　　　　　　　　　　　は、従属請求の範囲であってＰＣＴ規則6.4(a)の第２文及び第３文の規定に従って記載されていない。

**第Ⅱ欄　発明の単一性が欠如しているときの意見（第１ページの３の続き）**

　次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

1. ☐　出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。

2. ☐　追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。

3. ☐　出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったので、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。

4. ☐　出願人が必要な追加調査手数料を期間内に納付しなかったので、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

追加調査手数料の異議の申立てに関する注意
　　　☐　追加調査手数料の納付と共に出願人から異議申立てがあった。
　　　☐　追加調査手数料の納付と共に出願人から異議申立てがなかった。

様式ＰＣＴ／ＩＳＡ／２１０（第１ページの続葉（１））（１９９８年７月）

『第1ページの続葉（1）「第Ｉ欄1．」』の続き

　本願発明に係る「ドラッグデザイン方法」は、タンパク質の立体構造情報に基づいて該タンパク質に結合する化合物の構造をデザインすることであるが、発明者がその精神活動によって適切な化合物を推測する行為を包含しており、これは純粋に精神的な行為の遂行に相当すると認められる。

## Specification

Crystal of glucokinase protein and drug design method using crystal thereof.

## The Field of Technology

This invention relates to crystal of novel glucokinase protein (hereinafter it is called "GK protein") and the drug design method or the like employing three-dimensional structure coordinates obtained by using the crystal thereof.

## Background Technique

Glucokinase (ATP: D-hexose 6-phosphotransferaze, EC2.7.1.1) is one of four kinds of hexokinase isozymes of mammals (hexokinase IV). These isozymes catalyse the same reaction, however, differences exist in the Km value with respect to glucose. In other words, the Km value of hexokinase I, II and III being $10^{-6}$-$10^{-4}$ M, but on the other hand the Km value of hexokinase IV, called glucokinase with respect to glucose is much greater at about $10^{-2}$ M. Hexokinase is an enzyme participating in the initial stage of glycolytic pathway, and catalyses the reaction from the glucose to glucose-6-phosphate.

As for glucokinase, the expression is mainly localised in liver and pancreatic beta cell, and it plays an important role in glucose metabolism of the whole body by controlling the rate-determining step of glucose metabolism in these cells. As for the glucokinase of liver and pancreatic beta cell, the sequence of 15 amino acids at N terminal is respectively different due to splicing difference. However, the enzymatic characteristics are the same.

The hypothesis that glucokinase acts as glucose sensor of pancreatic beta cell and liver is proposed since approximately 10 years ago (Garfinkel D, et al: Am J Physiol 247 [3Pt2]: R527-536, 1984). In practice, it is becoming clear from results of recent glucokinase gene manipulation mouse, that the glucokinase plays an important role in glucose homeostasis of the whole body.

The mouse in which glucokinase gene is destroyed dies of diabetes mellitus soon after birth (Grupe A, et al: Cell 83: 69-78. 1995). On the other hand, as for the mouse which overexpressed glucokinase, the blood glucose level becomes low (Ferre T, et al: Proc Natl Acad Sci USA 93: 7225-7230. 1996). When glucokinase activity is increased by the rise in glucose concentration, although the reactions of

pancreatic beta cell and hepatocyte are different, in each case, it acts in the direction of lowering blood glucose. The pancreatic beta cell starts to secrete more insulin, the liver takes up sugar and stores as glycogen and at the same time lowers the sugar release.

In this way, the fluctuation of glucokinase enzyme activity plays an important role in glucose homeostasis of mammal through liver and pancreatic beta cell. Glucokinase gene mutation is discovered in the case that develops diabetes mellitus in youth known as MODY2 (maturity-onset diabetes of the young), and the lowering of glucokinase activity is said to be the cause of blood glucose rise (Vionnet N, et al.: Nature 356: 721-722, 1992). On the other hand, the lineage having mutation to increase glucokinase activity is also found, and such persons show hypoglycemic symptom (Glaser B, et al.: N Engl J Med 338: 226-230, 1998).

From the above, glucokinase also acts glucose sensor in human and plays an important role in glucose homeostasis. On the other hand, because the glucokinase of many type II diabetics is not mutated, the blood glucose control using glucokinase sensor system is considered possible. Because the glucokinase activator substance can be expected to have insulin secretion promotion action of pancreatic beta cell and sugar up take acceleration and sugar release suppression actions in liver, it is considered as useful therapeutic drug of type II diabetic patients.

Recently, a localised expression of pancreatic beta cell type glucokinase was found in rat brain, in particular in ventromedial hypothalamic nucleus (Ventromedial hypothalamus, VMH) which is the feeding centre. About 20 % of neurons of VMH was known as glucose responsive neuron, and it has been considered to play an important role in weight control in the past. When glucose is administered intracerebrally to rat, food consumption falls, whereas when the glucose metabolism is suppressed by administration of glucose analogue, glucosamine in brain, overeating occurs. From electrophysiological experiment, glucose responsive neurons are found to be activated in response to physiological glucose concentration changes (5-20 mM), however its activity is suppressed when the glucose metabolism is inhibited with glucosamine and the like. In glucose concentration sensing system of VMH, a mechanism through glucokinase the same as insulin secretion of pancreatic beta cells is assumed. Accordingly, there is a possibility that a substance that causes glucokinase activation of VHM in addition to liver, pancreatic beta cell is expected to correct problem of obesity which is a problem in many type II diabetic patients,

in addition to blood glucose correction effect.

On the other hand, it is described in DIABETES, vol. 48, 1698-1705, September 1999 that the stereostructure of glucokinase was predicted from hexokinase 1. However, in practice, crystallisation was not carried out, nor it was a practical one.

In accordance with the above, to elucidate three-dimensional stereostructure of glucokinase and to enable efficient discovery of a compound that interacts with glucokinase are thought to greatly contribute to the development of for example a therapeutic agent or preventative agent of diabetes, a therapeutic agent or preventative agent of chronic complication of diabetes mellitus such as retinopathy, nephropathy, neurosis, ischemic cardiac disease, arteriosclerosis or the like, a therapeutic agent or preventative agent of obesity.

Presently, CARDD (Computer Aided Rational Drug Design) using computer for the tasks such as analysis of active centre of a protein or a prediction of reaction mechanism has been employed at practical level.

In the drug creation system using CARDD, the structure of active site of protein is predicted based on the three-dimensional structure analysis data of the target protein. And information about candidate compounds which can bind to the structure of active site thereof is obtained from the compound database. Thereafter, on consideration of the three-dimensional structure and physical properties of the active site of the target protein and the candidate compound, candidate compounds which can bind to the target protein are selected. These steps are so-called in silico screening step.

Whether the compound selected by in silico screening step binds to the target protein and change the activity thereof or not, is examined by actual examination (wet experiment). And the compound that changes the activity of the target protein becomes the effective ingredient of a drug. Thereby a compound that interacts with the target protein can be efficiently screened without carrying out the procedure wherein innumerable compounds are acted on the target protein one by one and the interactions are confirmed.

In silico screening can be said as an effective means of pharmaceutical development because the

4

candidate compounds that bind to the target protein can be greatly narrowed down.

Three-dimensional structure analysis data by X-ray structure analysis of the target protein becomes an important information in drug creation system using CARDD. Crystal of target protein is required as analysis sample in three-dimensional structural analysis by X-ray structure analysis. Accordingly, in order to carry out development of drug creation related to GK based on the drug creation system using CARDD, the crystal of GK is required. However, as stated above, crystallisation of GK was difficult, and it could not provide information necessary for CARDD.

This invention was made on consideration of the problems of aforesaid technology of the prior art, and had objects to obtain crystal of glucokinase and to design compounds that bind to glucokinase based on the information obtained from aforesaid crystal.

Disclosure of the Invention
At least one of aforesaid objects is solved by the following invention.

[1] A glucokinase protein characterised in being used for crystallisation.

[2] A protein in accordance with aforesaid [1] comprising amino acid sequence in accordance with Sequence Number 5.

[3] A crystal of protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof.

[4] A crystal in accordance with aforesaid [3], wherein the said protein is glucokinase protein.

[5] A crystal in accordance with aforesaid [3] comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 5.

[6] A crystal in accordance with aforesaid [3], wherein the lattice constant satisfies the following equations (1)-(4)

5

a = b = 79.9 +/- 4 Å          (1)

c = 322.2 +/- 15 Å          (2)

alpha = beta = 90°          (3)

gamma = 120°          (4)


[7] A crystal in accordance with aforesaid [6], wherein the space group is $P6_522$.


[8] A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 1.


[9] A crystal wherein in three-dimensional structure coordinates data changed in at least one data of three-dimensional structure coordinates data in accordance with Table 1, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 1 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.


[10] A crystal in accordance with any of [3]-[9], wherein the compound binding site is constructed by at least one of amino acid residues of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.


[11] A crystal including a complex of the protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and a compound which can bind to the said protein.


[12] A crystal in accordance with aforesaid [11], wherein aforesaid compound is represented by formula (1).
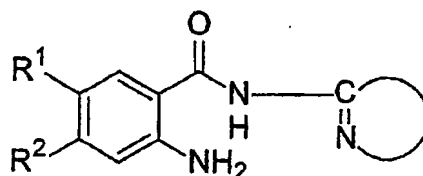
6



(I)

[wherein, R1 shows halogen atom, -S-(O)p-A, -S-(O)q-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and



(II)

denotes an optionally substituted monocyclic or bicyclic heteroaryl group having a nitrogen atom adjacent to the carbon atom bonded to amide group].

[13]. A crystal in accordance with aforesaid [12], wherein aforesaid compound is any of the compound represented by formula (IIIa)-(IIIc).
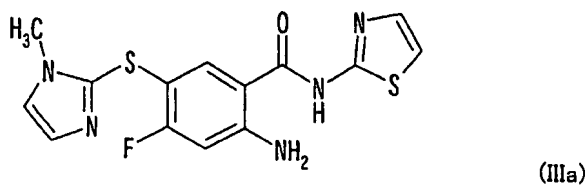


(IIIa)



(IIIb)

7

(IIIc)
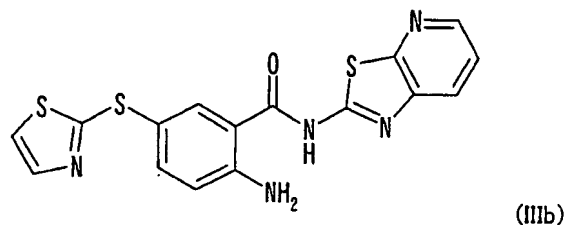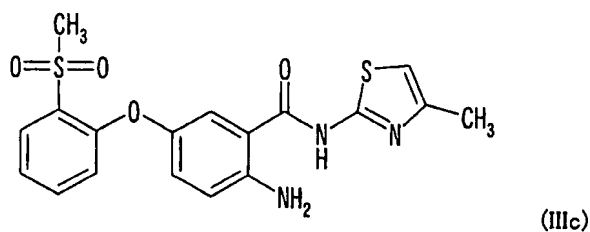
[14] A protein in accordance with aforesaid [1] comprising amino acid sequence in accordance with Sequence Number 8.

[15] A crystal of protein comprising amino acid sequence in accordance with Sequence Number 8 or amino acid sequence substantially the same amino acid sequence thereof.

[16] A crystal in accordance with aforesaid [15], wherein the said protein is glucokinase protein.

[17] A crystal in accordance with aforesaid [15] comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 8.

[18] A crystal in accordance with aforesaid [15], wherein the lattice constant satisfies the following equations

$a = b = 103.2 +/- 5$ Å            (5)

$c = 281.0 +/- 7$ Å            (6)

alpha = beta = 90°            (7)

gamma = 120°            (8)

[19] A crystal in accordance with aforesaid [18], wherein the space group is $P6_522$.

[20] A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 2.

[21] A crystal wherein in three-dimensional structure coordinates data changed at least one data of three-dimensional structure coordinates data in accordance with Table 2, the mean square error between atoms

8

of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 2 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.

[22] A process for the production of crystal containing a complex of protein and a compound that binds to the protein thereof, including

a protein production step wherein a protein containing the amino acid sequence having deletion of 1-50 amino acid residues from either or both of N terminal and C terminal of the protein containing amino acid sequence in accordance with Sequence Number 2 is produced, and

a protein reaction step wherein a compound that binds to the protein obtained in the said protein production step and the protein obtained in the said protein production step are reacted.

[23] A process to produce crystal of the kind wherein a crystal of a protein is produced, characterised in that a protein including amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and having glucokinase activity and a compound which can bind to the said protein are used.

[24] A process for the production of crystalline protein in accordance with aforesaid [23], wherein the compound which can bind to said protein is a compound represented by formula (1).



(I)

[wherein, R1 shows halogen atom, -S-(O)p-A, -S-(O)q-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and

**(II)**

denotes an optionally substituted monocyclic or bicyclic heteroaryl group containing nitrogen atom adjacent to the carbon atom bonded to amide group].

[25]. A process for the production of crystal in accordance with aforesaid [23] or [24] using co-crystallisation or soaking method

[26] A drug design method of the kind wherein based on stereostructural information of a protein, the structure of compound that binds to said protein is designed, characterised in that the stereostructure information of said protein is the information obtained by analysing crystal in accordance with any one of aforesaid [3]-[13] or [15]-[21].

[27] A drug design method in accordance with aforesaid [26] characterised in that
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and
a selection step wherein a compound compatible to the compound binding site deduced in aforesaid binding site deduction step is selected from compound library,
are included.

[28] A drug design method in accordance with aforesaid [26] characterised in that
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and
a compound structure assembly step wherein the structure of compound compatible to compound binding site deduced in aforesaid binding site deduction step is constructed,
are included.

[29] A drug design method in accordance with aforesaid [26] characterised in that

a binding site deduction step wherein the compound binding site of said protein is deduced on aforesaid stereostructure information, and

a design step wherein the structure of compound is designed by visual observation so that the compound binding site deduced in aforesaid binding site deduction step and a compound compatible to said compound binding site interact,

are included.

[30] A drug design method in accordance with any of aforesaid [26]-[29], wherein aforesaid compound binding site is constituted by at least one of amino acid residue of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.

[31] A drug design method in accordance with any of aforesaid [26]-[30] further including a step to measure physiological activity of the candidate compound predicted to be compatible to aforesaid compound binding site.

[32] A drug design method in accordance with any of aforesaid [26]-[30] further including a binding determination step wherein the candidate compound predicted to be compatible to aforesaid compound binding site and a protein including amino acid sequence in accordance with and Sequence Number 5 or amino acid sequence which is substantially the same amino acid sequence thereof are contacted, and whether the candidate compound binds to the said protein or not is assessed.

[33] A process for the production of compound array including the compound group selected by drug design method in accordance with any of aforesaid [26]-[30] is combined as compound array.

Brief Description of the Figures

Figure 1 is a ribbon diagram showing three-dimensional structure of glucokinase.

(Figure 1a is a ribbon diagram showing the structure of glucokinase (Δ1-11)/glucose/compound 1 (compound of formula IIIa). Moreover, the figure on the right is a rotated figure of the figure on the left.)

(Figure 1b is a ribbon diagram showing the simple substance of glucokinase [ΔI-15]. Moreover, the figure on the right is a rotated figure of the figure on the left.)

Figure 2 is a figure showing coupling scheme of compound 1 (compound of formula IIIa) with respect to the binding site of glucokinase (ΔI-11)

Figure 3 is a figure showing the structure of binding site of glucokinase (ΔI-11).

Ideal form for Carrying Out the Invention

In this specification, amino acids, peptides and proteins are represented using abbreviations adopted from the IUPAC-IUB biochemistry designation committee (CBN) shown below. Moreover, the sequence of amino acid residues of peptide and protein are represented so that the N terminal to C terminal comprises from the left end to the right end and moreover the N terminal comprises the first.

Hereinafter, each embodiment of this invention is described in greater detail.

(Glucokinase protein).

Firstly, this invention puts forward glucokinase protein characterised in being used for crystallisation. Glucokinase protein (GK protein) is involved in extremely important sugar metabolism in vivo as described above. Accordingly, by solving the three-dimensional structure of GK protein and by elucidating active site of GK protein, it is possible to search compounds that bind to GK protein (activator or inhibitor). Therefore it is important to clarify the three-dimensional structure of GK protein.

As technique to clarify the three-dimensional structure of protein, X-ray crystal structure analysis is well known. In other words, protein is crystallised, mono-chromatised X-ray is irradiated to the crystal thereof, and three-dimensional structure of said protein is elucidated on the basis of the obtained X-ray diffraction pattern (Blundell, T.L. and Johnson, L.N, PROTEIN CRYSTALLOGRAPHY, pp. 1-565, (1976) Academic Press, New York). First GK protein needs to be crystallised in order to provide for the x-ray crystal structure analysis of GK protein.

Wherein, the "GK protein" of this invention refers to human derived liver type glucokinase having amino acid sequence shown in sequence Number 2 and a protein containing amino acid sequence which is substantially the same as Sequence Number 2. Wherein, as aforesaid protein containing amino acid sequence which is substantially the same, a species having glucokinase activity is preferable. Accordingly, in this specification, the GK protein includes not only the human derived liver type glucokinase, however also human derived pancreas type glucokinase, and non-human derived GK proteins such as mouse, rat, monkey and the like. In this invention human liver type glucokinase is preferably used. In glucokinase derived from human, 15 amino acid residues at N terminal differ in the liver type and the pancreas type. Wherein, "glucokinase activity" refers to an activity to catalyse reaction from glucose to glucose-6-phosphate.

It is generally well known that the crystallisation of protein is difficult, and the GK protein was not able to be crystallised without treatment. These inventors carried out various investigations with trial and error, as a result succeeded in crystallisation of GK protein for the first time by deletion of 11 or 15 amino acids at the N terminal side of GK protein. It was thought that the deleted region protruded from the globular GK protein molecule when the crystallisation was attempted, as a result, caused steric hindrance between adjacent GK protein molecules, and prevented the crystallisation of the GK protein. In other words, in this invention, the crystal of GK protein was obtained by using a GK protein in which 11 amino acid residues at N terminal side is deleted (Sequence Number 5) or a GK protein in which 15 amino acid residues at N terminal side is deleted (Sequence Number 8) in the glucokinase in which amino acids sequence had been known however the crystallisation had been unsuccessful. Wherein the number of amino acids is not restricted as long as it is within a range that the steric hindrance disappears between adjacent crystals. In an embodiment for example, in amino acid sequence represented by Sequence Number 2, amino acids sequence or the like in which amino acid residues of 1-50, preferably 3-30, more preferably 5-25, more preferably still 8-18, most preferably 11-15 at N terminal side are deleted, can be used in this invention. Moreover, the amino acid sequence or the like in which amino acid residues of 1-8, preferably 1-7, more preferably 2-6 at C terminal side are deleted, is used in this invention.

(Crystal of glucokinase protein and a process for the production thereof).

Next, in this invention, crystals including protein containing amino acids sequence in accordance with Sequence Number 5, and Sequence Number 8 or amino acids sequence which is substantially the same as

amino acid sequence thereof are put forward.

As described earlier, as GK protein used in crystallisation, proteins containing amino acids sequence in accordance with Sequence Number 5, and/or Sequence Number 8 or amino acids sequence which is substantially the same as amino acid sequence thereof, or the like are used.

The proteins containing amino acids sequence in accordance with Sequence Number 5, and/or Sequence Number 8 or amino acids sequence which is substantially the same as the amino acid sequence thereof (hereinafter it may be abbreviated as "GK protein" together with proteins containing amino acids sequence in accordance with Sequence Number 2 or amino acids sequence which is substantially the same as the amino acid sequence thereof) can be any as long as crystallisation is possible, and the amino acid sequence thereof is not restricted in particular. Wherein, the proteins containing amino acids sequence which is substantially the same as the amino acid sequence in accordance with Sequence Number 5, and/or Sequence Number 8 does not necessarily have glucokinase activity, and may be an inactive mutant (for example, a mutant inactivated by the presence of mutation at ATP binding site) as long as it has a crystal structure from which the information necessary for drug design can be obtained. Wherein, as proteins containing amino acids sequence which is substantially the same as the amino acid sequence in accordance with Sequence Number 2 or Sequence Number 5, amino acids sequences having about 60 % or more, preferably about 70% or more, more preferably about 80% or more, in particular preferably about 90% or more, and most preferably about 95% or more homology to the amino acids sequence in accordance with Sequence Number 2 or Sequence Number 5, or the like are nominated. Moreover, as proteins containing amino acids sequence which is substantially the same as the amino acids sequence in accordance with Sequence Number 2 or Sequence Number 5, for example, amino acids sequences in which amino acid residues of 1-10, preferably 1-5, more preferably 1-3 more preferably still 1-2 are substituted, deleted, added and/or inserted in the amino acids sequence in accordance with Sequence Number 2 or Sequence Number 5 are exemplified.

Three-dimensional structural analysis of GK protein is carried out for example as follows. Firstly, the protein is purified. And a series of steps such as crystallisation, X-ray diffraction intensity data collection, phase determination of each diffraction spot, electron density calculation, molecular model construction, refinement of structure or the like is carried out. As main equipment for performing

protein structure analysis, incubator for crystallisation, binocular microscope, X-ray diffractometer, three dimensional computer graphics apparatus or the like are used. The actual experimental process to produce protein crystals is divided into step to purify protein in large amount (several mg or more is preferred), a step to widely search conditions for obtaining crystal and a step to obtain high quality crystal suitable for X-ray analysis. Hereinafter, each step is described in concrete terms.

For crystallisation, GK protein is purified to high purity. As process for purification, well known processes can be used, and for example, column chromatography, salt precipitation, centrifugation or the like are used.

Purified GK protein is crystallised and provided as a sample for X-ray crystal structure analysis. Crystallisation is performed based on well known method such as vapor diffusion method, dialysis or the like. When obtaining protein crystals, many elements such as purity / concentration of protein, temperature, pH, concentration of the precipitant used need to be examined. Investigation of crystallisation conditions can be carried out over a wide range using commercial screening reagent, and it is preferably screened using 1-2 μl of protein solution in protein concentration of 1-2 % per condition. In this way when microcrystals or the like are obtained, it is preferred to further refined the conditions.

Moreover, extremely many conditions must be searched in order to obtain crystal of GK protein. Accordingly, a large quantity expression system of the protein is preferably constructed also for the investigation of crystallisation condition. Generally, among proteins, many of the crystallising species are monodispersed in solution state, and polydispersed species do not crystallise in most cases. Therefore, N terminal of GK protein is successively removed, monodispersion properties of protein solution are assessed for the obtained protein using light scattering apparatus, and whether sample is suitable for crystallisation or not may be examined.

Next, using the obtained crystal of GK protein, X-ray diffraction intensity measurement is carried out. Recently, a method wherein the crystal is scooped with a ring of narrow thread or the like, is rapidly cooled to liquid nitrogen temperature, and is measured at low temperature as it is, may also be used. Usually, the intensity measurement of diffracted x-ray is performed by two-dimensional detector such as image plate or the like. Many diffraction lines generated by rotating crystal while irradiating the X-ray

are recorded on image plate, and the recorded diffraction intensities are read by shining a laser.

Next, it is preferred to prepare heavy atom iso-form replacement bodies by heavy atom soaking method or co-crystallisation method. Using this, the phase of the protein crystal can be determined by multiple isomorphous replacement method (MIR method). Instead of introducing heavy atom, the phase is also determined by multiwavelength anomalous scattering method (MAD method) based on the diffraction intensity data using complex X-rays. Molecular replacement method (MR method) in which, when a structure of molecule containing analogous structure has been already solved, the initial structure can be obtained by applying the molecular structure thereof in the crystal, Furrier synthesis diagram is drawn on the basis of this, and the structure of remaining part is elucidated, and the total structure is determined, is known as well.

Once the phase was determined by aforesaid process, electron density is determined from this. The precision of this depends on the number of reflection (resolution) and the precision of the reflection used. The resolution is expressed with the minimum plane spacing of the reflection used. Molecular model is constructed from this electron density diagram. When the molecular model is constructed, the atomic coordinates are obtained, therefore, the calculated value of structure factor is determined from this, and refinement of atomic parameters is carried out by the least-square method to approximate this size to the observed value. In this way, the most reasonable structural information is obtained.

In accordance with this invention, the crystal of GK protein shown in sequence Number 5 has been successfully prepared (cf. later described Example). The obtained crystal of GK protein had lattice constant which satisfied the following equations (1)-(4).

$a = b = 79.9 +/- 4$ Å $\qquad$ (1)

$c = 322.2 +/- 15$ Å $\qquad$ (2)

alpha = beta = 90° $\qquad$ (3)

gamma = 120° $\qquad$ (4)

Moreover, this crystal was elucidated to have space group $P6_522$. Wherein, aforesaid $a = b$ is preferably 79.9 +/- 3 Å, more preferably 79.9 +/- 2 Å and even more preferably 79.9 +/- 1 Å. Moreover, aforesaid c is preferably 322.2 +/- 10 Å, more preferably 322.2 +/- 8 Å, and even more preferably 322.2 +/- 5 Å.

The three-dimensional structural coordinates of the GK protein crystal obtained in this way are shown in Table 1.

**Table 1**

Moreover, Table 1 is constructed in accordance with representation method of protein data bank generally used by a person skilled in the art. The GLC in Table 1 denotes glucose molecule, and CP1 denotes the compound represented by formula IIIa, and HOH denotes water molecule.

Moreover, in this invention, the crystal of GK protein shown in sequence Number 8 has been successfully prepared (cf. later described Example). The obtained crystal of GK protein had lattice constant which satisfied the following equations (5)-(8).

$a = b = 103.2 +/- 5$ Å      (5)

$c = 281.0 +/- 7$ Å      (6)

$alpha = beta = 90°$      (7)

$gamma = 120°$      (8)

Moreover, this crystal was elucidated to have space group $P6_522$. Wherein, aforesaid a = b is preferably 103.2 +/- 3 Å, more preferably 103.2 +/- 2 , and even more preferably 103.2 +/- 1 Å. Moreover, aforesaid c is preferably 281.0 +/- 6 Å, more preferably 281.0 +/- 4 Å, and even more preferably 281.0 +/- 2 Å.

The three-dimensional structural coordinates of the GK protein crystal obtained in this way are shown in Table 2.

**Table 2**

Moreover, Table 2 is constructed in accordance with representation method of protein data bank generally used by a person skilled in the art. The HOH in Table 2 denotes water molecule.

In this invention, crystals of the protein having amino acids sequence which is substantially the same as Sequence Number 5 and/or Sequence Number 8 and having glucokinase activity are within the range of

this invention. As such crystals, for example, crystals wherein in three-dimensional structure coordinates data changed at least one data of three-dimensional structure coordinates data in accordance with Table 1 and/or 2, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 1 and/or 2 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less, are nominated. Even if the numerical values of coordinates representing the position of atoms differ, two structural coordinates which can superimpose corresponding atoms contained in the structural coordinates on top of one another show the same three-dimensional structure.

Moreover, the three-dimensional structural coordinates of GK protein in accordance with Table 1 and/or Table 2 are important information for drug design, and stored in a storage medium that can be read by computer in accordance with requirements, this information is processed with computer, and drug design is carried out. Accordingly, in another embodiment of this invention, a computer readable recording medium which recorded a program to function a computer as three dimensional coordinate memory means that memorises three-dimensional coordinates of amino acid residue in accordance with Table 1 and/or 2 is put forward.

Moreover, according to another embodiment of this invention, a computer readable recording medium that recorded a program which functions using computer as three dimensional coordinates memory means that memorised the three-dimensional coordinates of amino acid residue in accordance with Table 1 and/or 2, as binding site deduction means that deduces compound binding site of a protein having amino acid sequence represented by Sequence Number 8 and/or Sequence Number 5 using three dimensional coordinates of amino acid residue in accordance with Table 1 and/or 2 memorised in aforesaid three-dimensional coordinates memory measure, as binding compound memory means which memorised information about the type of compounds that bind to the protein and three-dimensional structure of aforesaid compounds, and as binding compound candidate selection means for selecting candidate compounds which are compatible to the compound binding site of the protein having amino acid sequence represented by Sequence Number 1 at least using the information about the three-dimensional structure of compound binding site of protein containing amino acid sequence represented by Sequence Number 8 and/or inferred Sequence Number 5 deduced by aforesaid binding site deduction means and the

information about three-dimensional structure of compound memorised in aforesaid binding compounds memory means, is put forward. Moreover, according to another embodiment of this invention, a computer equipped with aforesaid each means, is also put forward.

<u>(Crystal of complex of GK protein with compound that binds to this).</u>
Next, according to another embodiment of this invention, a crystal containing a complex of protein including amino acid sequence in accordance with Sequence Number 5 or Sequence Number 8 or amino acid sequence which is substantially the same amino acid sequence thereof with the compound which can bind to the said protein and a process for the production thereof are put forward.

When a compound which binds to GK protein is obtained, firstly, the GK protein and the compound thereof are mixed for example in an aqueous solution, and a complex is formed. As for the crystal of such complex, well known processes for the production of co-crystals such as co-crystallisation, soaking method or the like are used. As for the crystallisation condition and crystallisation process, refer to aforesaid processes.

For example, a compound that binds to GK protein is selected from the compound group represented by aforesaid formula (I).

Wherein, as halogen atom of aforesaid formula (1), fluorine atom, chlorine atom, bromine atom, iodine atom or the like are exemplified, and among these, chlorine atom is preferred.

Moreover, as far as substituents in heteroaryl group of A, B of aforesaid formula (1) and formula (II) are concerned, amino group, carbamoyl group, carbamoyl amino group, carbamoyloxy group, carboxyl group, cyano group, sulphamoyl group, trifluoromethyl group, halogen atom, hydroxy group, formyl group, straight chained C1-C6 alkyl group, cyclic C3-C6 hydrocarbon group, aralkyl group, N-aralkyl amino group, N,N-diaralkyl amino group, aralkyloxy group, aralkyl carbonyl group, N-aralkyl carbamoyl group, aryl group, arylthio group, N-arylamino group, aryloxy group, aryl sulphonyl group, aryl sulphonyloxy group, N-arylsulfonylamino group, aryl sulphamoyl group, N-aryl carbamoyl group, aroyl group, aroxy group, C2-C6 alkanoyl group, N-C2-C6 alkanoyl amino group, C1-C6 alkylthio group, N-C1-C6 alkyl sulphamoyl group, N,N-di-C1-C6 alkyl sulphamoyl group, C1-C6 alkyl sulfinyl group, C1-

C6 alkylsulfonyl group, N-C1-C6 alkylsulfonyl amino group, C1-C6 alkoxy group, C1-C6 alkoxycarbonyl group or C1-C6 alkylamino group are denoted), or the like is nominated. Wherein, as for the preferably used substituent, amino group, carbamoyl group, carbamoyl amino group, carbamoyloxy group, carboxyl group, cyano group, sulphamoyl group, trifluoromethyl group, halogen atom, hydroxy group, formyl group, straight chained C1-C6 alkyl group or the like are exemplified.

Wherein, "hydrocarbon group" denotes 1-6 C straight chained alkyl group, or, among carbon atom constituting said alkyl group, a group in which 1 or 2, preferably 1 carbon atom may be substituted with nitrogen atom, sulfur atom or oxygen atom and/or carbon atom themselves in the said 1-6 C straight chain alkyl group may be bonded with double bond or triple bond. Number of said double bond or triple bond is preferably 1 or 2 and 1 is more preferred.

As said hydrocarbon group, in an embodiment, it is preferred to be methyl group, ethyl group, propyl group or isopropyl group, butyl group or a group represented by following formulae
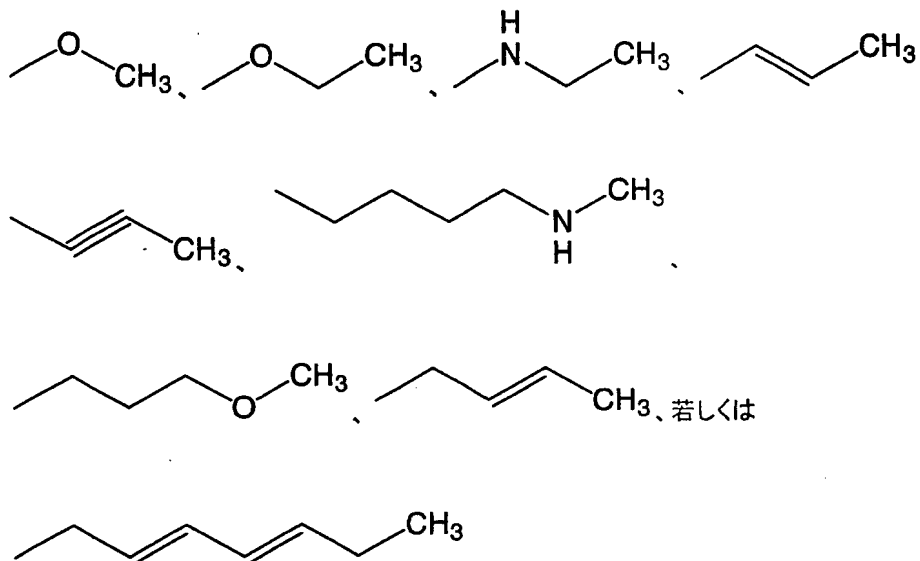


More preferred hydrocarbon group is methyl group, ethyl group, propyl group, isopropyl group or a group represented by following formulae



、若しくは

or
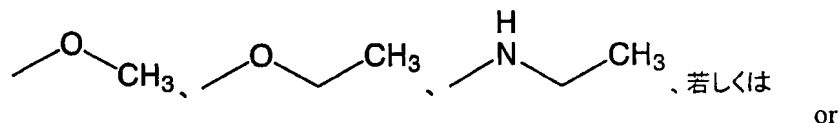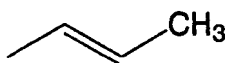
For example, as preferred A (in case of p = 0), the following groups are nominated.
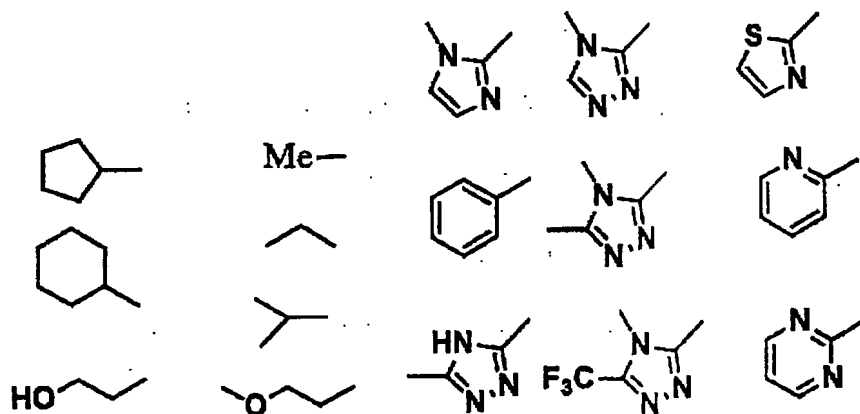


As preferred B, for example, the following groups are nominated.
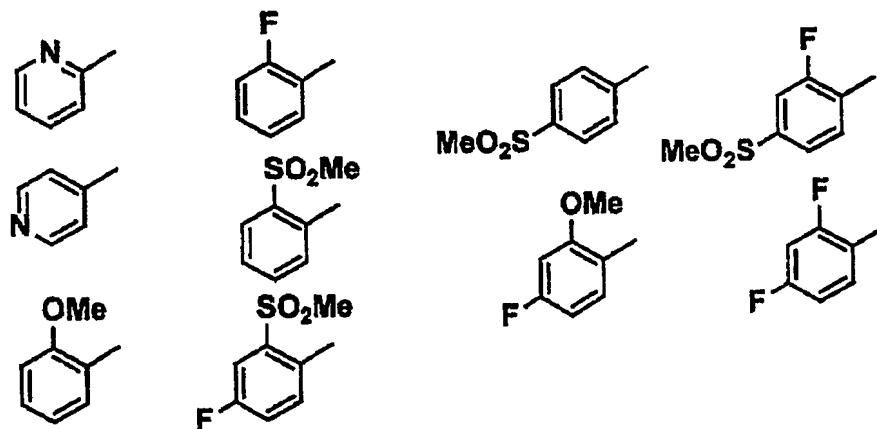


As heteroaryl group represented by formula (II), for example following heterocyclic groups are nominated.
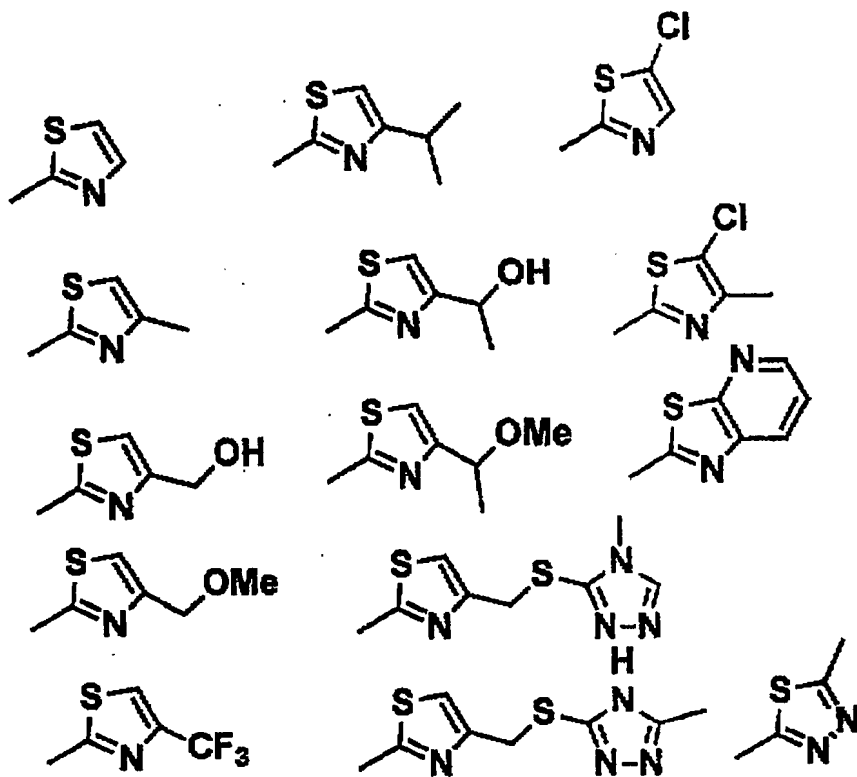
Moreover, particularly preferred compounds are any of the compound represented by aforesaid formulae (IIIa)-(IIIc).

The compound of this invention (1) can be readily produced by using well known reaction means or according to well known method. Moreover, the compound of general formula (I) of this invention can be produced not only by synthesis in ordinary liquid phase, but also by synthesis using solid phase developed remarkably in recent years such as combinatorial synthesis method, parallel synthesis method or the like. Preferably, it can be produced for example using the following process.

Step 1 to Step 2 to Step 3
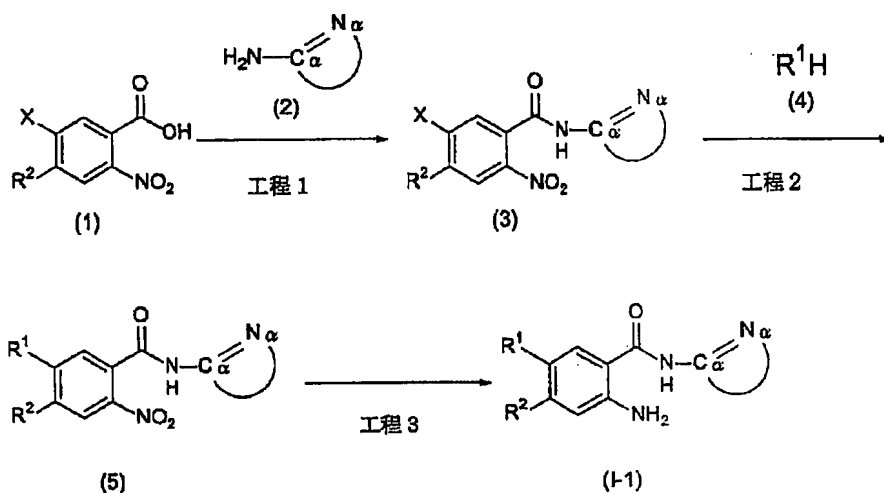
(wherein, each symbol is the same as in the aforesaid definition)

Step 1

This step is a process to produce compound (3) by reacting carboxylic acid compound (1) or reactive derivative thereof and amino compound containing optionally substituted monocyclic or bicyclic heteroaryl group represented by aforesaid formula (2) or salts thereof. In this reaction, ordinary amide formation reaction may be carried out by a method described in literature (for example Base and experiment of peptide synthesis, Shinya Izumiya et al., Maruzen, 1983, Comprehensive Organic Synthesis, vol 6, Pergamon Press Co. 1991 and the like) or in accordance with these, or by combining these and conventional method, in other word, it can be carried out by using condensing agent well-known for a person skilled in the art or by ester activation method, mixed acid anhydride method, acid chloride method, carbodiimide method and the like which can be used by a person skilled in the art. As such amide forming reagent, for example thionyl chloride, N,N-dicyclohexylcarbodiimide, 1-methyl-2-bromo pyridinium iodide, N,N'-carbonyldiimidazole, diphenyl phosphoryl chloride, diphenyl phosphoryl azide, N,N'-disuccinimidyl carbonate, N,N'-disuccinimidyl oxalato, 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride, ethylchloroformate, chloro formic acid isobutyl ester or benzo triazol-1-yl-oxy-tris (dimethylamino) phosphonium hexafluoro phosphate and the like are proposed, and wherein, for example thionyl chloride, N,N-dicyclohexylcarbodiimide or benzo triazol-1-yl-oxy-tris (dimethylamino) phosphonium hexafluoro phosphate and the like are suitable. Moreover, in amide forming reaction, a base, a condensation assistant may be used with the aforesaid amide forming reagent.

As base used, for example tertiary aliphatic amine such as trimethylamine, triethylamine, N,N-diisopropyl ethylamine, N-methylmorpholine, N-methylpyrrolidine, N-methylpiperidine, N,N-dimethylaniline, 1,8-diazabicyclo[5.4.0] undec-7-ene (DBU), 1,5-azabicyclo[4.3.0] non-5-ene (DBN) or the like, for example aromatic amine such as pyridine, 4-dimethylaminopyridine, picoline, lutidine, quinoline, isoquinoline and the like are proposed, and wherein, for example tertiary aliphatic amine and the like is preferred, and in particular, for example triethylamine or N,N-diisopropyl ethylamine and the like is suitable.

As condensation assistant used, for example N-hydroxybenzotriazole hydrate, N-hydroxy succinimide, N-hydroxy-5-norbornene-2,3-dicarboximide or 3-hydroxy-3,4-dihydro-4-oxo-1,2,3-benzotriazole and the like are proposed, and among these, for example N-hydroxybenzotriazole and the like are suitable.

The amount of amino compound (2) used differs depending on the kind of compound and solvent used and other reaction conditions, however, usually, 0.02 to 50 equivalents, preferably 0.2 to 2 equivalents with respect to 1 equivalent of carboxylic acid compound (1) or reactive derivative thereof. Herein, as reactive derivative, for example active ester derivative, active amide derivative and the like which are used in the sphere of usual organic chemistry are nominated.

The amount of used amide forming reagent differs depending on the kind of compound and solvent used and other reaction conditions, however, usually 1-50 equivalents, preferably 1-5 equivalents with respect to 1 equivalent of carboxylic acid compound (1) or reactive derivative thereof.

The amount of used condensation assistant differs depending on the kind of compound and solvent used and other reaction conditions, however, usually it is 1-50 equivalents, preferably 1-5 equivalents with respect to 1 equivalent of carboxylic acid compound (1) or reactive derivative thereof.

The amount of used base differs depending on the kind of compound and solvent used and other reaction conditions, however, usually 1 to 50 equivalents, preferably 3 to 5 equivalents.

The reaction solvent used in this step, is for example insert organic solvent, and it is not restricted in

particular so long as it does not hinder the reaction. However, in an embodiment, for example methylene chloride, chloroform, 1,2-dichloroethane, trichloroethane, N,N-dimethylformamide, acetic acid ethylester, acetic acid methylester, acetonitrile, benzene, xylene, toluene, 1,4-dioxane, tetrahydrofuran, dimethoxyethane or a mixed solvent thereof are proposed, however, in particular for example methylene chloride, chloroform, 1,2-dichloroethane, acetonitrile, N,N-dimethylformamide or the like are suitable in term of securing a suitable reaction temperature.

The reaction temperature is -100°C to boiling point of solvent, preferably 0 to 30°C.

The reaction time is 0.5 to 96 hours, preferably 3 to 24 hours.

The base, amide formation reagent, condensation assistant used in this step 1 can be used as a single species or in combination of two or more.

When the compound (3) contains protecting group, said protecting group can be suitably eliminated. Elimination of aforesaid protecting group can be carried out by method described in literature (Protective Groups in Organic Synthesis, written by T.W. Green, the second edition, John Wiley & Sons Co, 1991, or the like) or method in accordance with this or by combining these and conventional method.

Compound (3) obtained in this way can be provided for the next step by isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like or without isolating and purifying.

Step 2

This step comprises a process to produce compound (5) by reacting amide compound (3) obtained in aforesaid step 1 and compound (4).

In this reaction, a base may be added to the reaction system in accordance with requirements. As used compound (4), preferably phenol derivative or thiol derivative is preferred. As said phenol derivative or thiol derivative, for example phenol, thiophenol, thio imidazole, thio triazole and the like are

nominated. The amount of compound (4) used differs depending on the kind of compound and solvent used or other reaction conditions, however, usually it is 2-50 equivalents, preferably 2-5 equivalents with respect to 1 equivalent of amino derivative (3). As used base, for example tertiary aliphatic amine such as trimethylamine, triethylamine, N,N-diisopropyl ethylamine, N-methylmorpholine, N-methylpyrrolidine, N-methylpiperidine, N,N-dimethylaniline, 1,8-diazabicyclo[5.4.0] undec-7-ene (DBU), 1,5-azabicyclo[4.3.0] non-5-ene (DBN) or the like, for example aromatic amine such as pyridine, 4-dimethylaminopyridine, picoline, lutidine, quinoline, isoquinoline and the like, alkali metal such as metallic potassium, metallic sodium, metallic lithium and the like, alkali metal hydride such as sodium hydride, potassium hydride and the like, alkali metal alkylate such as butyl lithium and the like, alkali metal alkoxide such as potassium-tert-butyrate, sodium ethylate or sodium methylate and the like, alkali metal hydroxide such as potassium hydroxide, sodium hydroxide and the like, alkali metal carbonate such as potassium carbonate and the like are nominated, among these for example tertiary aliphatic amine, alkali metal hydride or alkali metal carbonate are preferred, and in particular, for example triethylamine, N,N-diisopropyl ethylamine, sodium hydride or potassium carbonate are suitable.

The amount of aforesaid base used differs depending on the kind of compound and solvent used and other reaction conditions, however, it is usually 0 to 50 equivalents, preferably 2-10 equivalents with respect to 1 equivalent of amide compound (3). Said base can be used as a single species or two or more species in accordance with requirements.

As used insert organic solvent, there are no restrictions in particular so long as the reaction is not hindered. However, in an embodiment, for example methylene chloride, chloroform, 1,2-dichloroethane, trichloroethane, N,N-dimethylformamide, N,N-dimethyl acetamide, acetic acid ethylester, acetic acid methylester, acetonitrile, benzene, xylene, water, toluene, 1,4-dioxane, tetrahydrofuran, or a mixed solvent thereof are proposed.

Compound (5) obtained in this way can be and isolated and purified with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like.

Step 3

This step is a process to produce compound (1) used in this invention by reduction of compound (5). As for reductive reaction used in this step, well-known processes to a person skilled in the art are used. As the reductive reaction used in this step, in an embodiment, for example (1) catalytic reduction method using hydrogen, formic acid, ammonium formate, hydrazine hydrate and palladium, platinum, nickel catalyst, (2) reduction method using hydrochloric acid, ammonium chloride and iron, (3) reduction method using methanol and tin chloride are nominated.

The amount of reducing agent used in the aforesaid reductive reaction differs depending on the kind of compound and solvent to be used and other reaction conditions, however, it is usually 1-50 equivalents, preferably 2-20 equivalents with respect to 1 equivalent of compound (5).

The reaction solvent used is not restricted in particular so long as the reaction is not hindered. However, for example halogenated hydrocarbons such as dichloromethane, chloroform and the like, ethers such as diethyl ether, tert-butyl methyl ether, tetrahydrofuran and the like, amides such as N,N-dimethylformamide, N,N-dimethylacetamide and the like, sulphoxides such as dimethylsulfoxide and the like, nitriles such as acetonitrile and the like, an alcohol such as methanol, ethanol, propanol and the like, aromatic hydrocarbons such as benzene, toluene, xylene and the like, water or mixed solvent thereof can be used.

Reaction temperature and the reaction time are not restricted in particular. However, the reaction is carried out for 1-20 hours approx. and preferably 1 to 5 hours approx. at a reaction temperature of -10 to 100°C approx. and preferably 0 to 50°C approx.

Compound (1) used in this invention obtained in this way can be provided for the next step by isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like or without isolating and purifying.

Compound of aforesaid each step may contain protecting group on each substituent. Aforesaid protecting group can be suitably eliminated in each step using well known method, method in accordance with that or method combined these and the conventional method. As for the embodiment of

elimination, suitable elimination reaction is possible depending on the kind of compound, reaction and other reaction conditions. However, it is considered the case in which each protecting group is eliminated individually and the case in which each protecting group is simultaneously eliminated and the like, and it can be suitably selected by a person skilled in the art. As aforesaid protecting group, for example protecting group of hydroxy group, protecting group of amino group, protecting group of carboxyl group, protecting group of aldehyde, protecting group of keto group and the like are nominated. Moreover, the order of elimination aforesaid protecting groups is not limited in particular.

As protecting group of hydroxy group, for example lower alkyl silyl group such as tert-butyldimethylsilyl group, tert-butyl diphenyl silyl group and the like, for example lower alkoxymethyl group such as methoxy methyl group, 2-methoxyethoxymethyl group and the like, for example aralkyl group such as benzyl group, p-methoxybenzyl group and the like, for example acyl group such as formyl group, acetyl group and the like are proposed, and among these, tert-butyldimethylsilyl group, acetyl group and the like are in particular preferred.

As protecting group of amino group, for example aralkyl group such as benzyl group, p-nitrobenzyl and the like, for example acyl group such as formyl group, acetyl group and the like, for example lower alkoxycarbonyl group such as ethoxycarbonyl group, tert-butoxycarbonyl group and the like, for example aralkyloxy carbonyl group such as benzyloxycarbonyl group, p-nitrobenzyl oxycarbonyl group and the like are proposed, and among these, nitrobenzyl group, tert-butoxy carbonyl group, benzyloxycarbonyl group and the like are particularly preferred.

As protecting group of carboxyl group, for example lower alkyl group such as methyl group, ethyl group, tert-butyl group and the like, for example aralkyl group such as benzyl group, p-methoxybenzyl group and the like are nominated, and among these, methyl group, ethyl group, tert-butyl group, benzyl group and the like are particularly preferred.

As protecting group of keto group, for example dimethyl ketal group, 1,3-dioxirane group, 1,3-dioxolane group, 1,3-dithiane group, 1,3-dithiorane group and the like are proposed, and among these, dimethyl ketal group, 1,3-dioxolane group and the like are more preferred.

As protecting group of aldehyde group, for example, dimethylacetal group, 1,3-dioxirane group, 1,3-dioxolane group, 1,3-dithiane group, 1,3-dithiorane group and the like are proposed, and among these, dimethylacetal group, 1,3-dioxolane group and the like are more preferred.

In the production of compound used in this invention, there is a case that the protecting group is introduced to functional group in order to proceed reaction with good efficiency. The introduction of these protecting groups can be suitably selected by a person skilled in the art, and elimination of aforesaid protecting groups can be carried out by a method described in aforesaid Protective Groups In Organic Synthesis and the like, a method in accordance with that or by combining that and conventional method. Moreover, the order of elimination of protecting groups can be suitably selected by a person skilled in the art.

Compound (1) obtained in this way can be subjected to the next step after isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, solvent extraction, re-precipitation, chromatography and the like or without isolating and purifying.

Moreover, the compound used in this invention (I) can be also produced by the following step.

Step 4 to Step 5 to Step 6
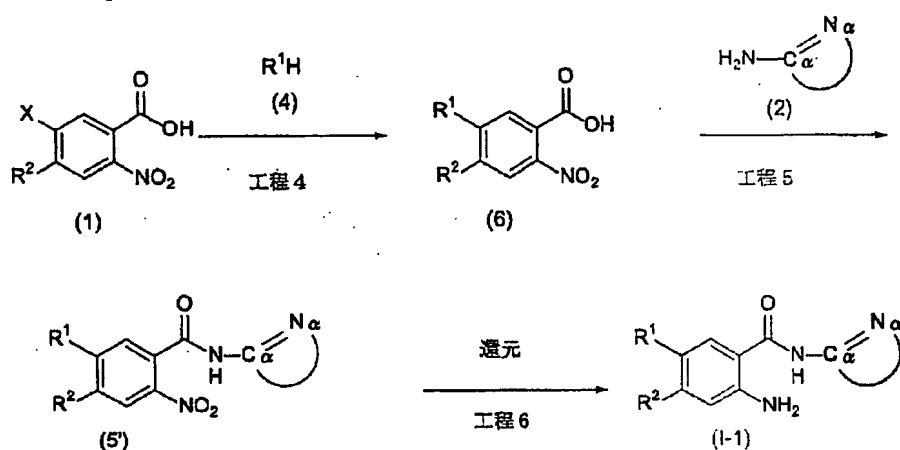


(wherein, each symbol has same aforesaid definition).

As far as the aforesaid Step 4, Step 5 and Step 6 are concerned, it can be carried out using the same amount of reagent, reaction solvent, reaction temperature and other reaction conditions as in aforesaid Step 1, Step 2 and Step 3.

When a protecting group is necessary for R2, it can be carried out by a person skilled in the art suitably selecting a process from a method described in aforesaid Protective Groups In Organic Synthesis and the like, a method in accordance with that or by combining that and conventional method.

Compounds (6) and (5') obtained in this way can be provided for the next step after isolating and purifying with well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, re-precipitation, solvent extraction and the like or without isolating and purifying.

Compound (1) used in this invention can be isolated and purified by well known separation and refinement means, for example concentration, vacuum concentration, crystallisation, re-precipitation, solvent extraction and the like.

In aforesaid step 1 to 6, the elimination of protecting groups differ depending on the kind of aforesaid protecting group and stability of compound, however, it can be carried out by aforesaid method described in Protective Groups in Organic Synthesis, written by T.W. Green, the second edition, John Wiley & Sons Co, 1991, or the like or a method in accordance with this or by combining these and conventional method. For example, it can be carried out by solvolysis using acid or base, chemical reduction using hydrogenated metallic complex and the like or catalytic reductions using palladium carbon catalyst, Raney nickel and the like.

The benzamide compound put forward by this invention can exist as pharmacologically acceptable salt. Aforesaid salt can be produced in accordance with conventional methods. In an embodiment, when aforesaid compound (1) contains basic group derived from for example amino group, pyridyl group within the molecule, it can be converted to corresponding pharmacologically acceptable salt by treating aforesaid compound with an acid.

As aforesaid acid addition salt, for example the acid addition salt of halide acid salt such as hydrochloride, hydrofluoric acid salt, hydrobromic acid salt, hydroiodic acid salt or the like, inorganic acid salt such as nitrate, perchlorate, sulfate, phosphate, carbonate or the like, lower alkyl sulfonate such as methanesulfonate, trifluoromethanesulfonate, ethanesulfonic acid salt or the like, aryl sulfonate such as benzensuplhonate, p-toluenesulfonate or the like, organic salt such as fumarate, succinate, citrate, tartrate, oxalate, maleate or the like and organic acid of amino acid or the like such as glutamic acid salt, aspartate or the like are nominated. Moreover, when the compound of this invention is containing acidic group in aforesaid group, for example when containing carboxyl groups, it can be converted to corresponding pharmacologically acceptable salt by treating aforesaid compound with a base. As aforesaid base addition salt, for example salt of alkali metal salt such as sodium, potassium and the like, alkaline earth metal salt such as calcium, magnesium and the like, organic base such as ammonium salt, guanidine, triethylamine, dicyclohexylamine and the like are nominated. Furthermore, the compound of this invention may exist as free compound or arbitrary hydrate or solventate of salts thereof.

In accordance with this invention, as explained in detail in the description of Examples, crystal of complex of GK protein containing amino acid sequence shown in Sequence Number 5 and compounds of aforesaid formula (IIIa)-formula (IIIc) are obtained. In GK protein shown in Sequence Number 5, it has been elucidated that compound binding site is constituted from the amino acid residue of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 by analysing these crystal three - dimensional structure coordinates.

Moreover, according to another embodiment of this invention, a process for the production of crystal containing a complex of protein and a compound that binds to the protein, wherein a protein production step to produce a protein containing amino acids sequence in which prescribed number of amino acid residues at N terminal side and/or C terminal side are deleted as described above from the protein containing amino acid sequence in accordance with Sequence Number 2 and a step to cause reaction of a compound which binds to the protein obtained in aforesaid protein production step with the protein obtained in said protein production step are included, is put forward.

As protein to be produced in the aforesaid protein production step, the number thereof is not restricted as long as it is within a range that steric hindrance between adjacent GK proteins in the crystal is eliminated. In an embodiment, for example, in the amino acids sequence shown in Sequence Number 2, the amino acids sequences in which amino acid residues at N terminal side are deleted in numbers of 1-50, preferably 3-30, more preferably 5-25, still more preferably 8-18, even more preferably 11-15 or the like are nominated. Moreover, the amino acid sequences in which amino acid residues at C terminal side of 1-8, preferably 1-7, more preferably 2-6 or the like are deleted, are nominated.

(The drug design process using three-dimensional structural coordinate).

Three-dimensional structure of GK protein of this invention obtained as above provides important information for drug creation system using CARDD (Computer Aided Rational Drug Design). It is an important step of the target drug creation and development to elucidate the active center and allosteric site of this GK protein and to search for a compound which is compatible to said site, interacts with the GK protein and thereby activates to inhibits the GK protein.

In other words, according to another embodiment of this invention, a drug design process of the kind to design structure of compound that binds to said protein based on stereostructure information of protein, characterised in that the stereostructure information of said protein comprises information to be obtained by analysing the crystal obtained as described above, is put forward. As such drug design process, there are techniques to make drug design using energy calculation, activity prediction value analogous to this or pharmacophore and a technique to visually design drug using computer graphics technique.

As process by technique using energy calculation, activity prediction value analogous to this or pharmacophore, (1) a drug design process including a binding site deduction step to deduce compound binding site of said protein based on stereostructural information obtained as above and a selection step to select a compound compatible to the compound binding site deduced in aforesaid binding site deduction step from the compound library, (2) a drug design process including a binding site deduction step to deduce compound binding site of said protein based on aforesaid stereostructural information and a compound structure assembly step to construct a structure of compound compatible to the compound binding site deduced in aforesaid binding site deduction step, or the like are exemplified.

As process to deduce compound binding site of aforesaid protein, for example, a process wherein the ligand bonded site in the co-crystal of compound is identified by confirming with visual observation on display of computer, and in addition to that, a process wherein the site to which ligand is likely to bind is identified with respect to the protein crystal structure solved under the condition that ligand is not bound, are nominated. In any processes, well-known method and commercial computer soft wear can be used. In former process, for example, it is possible to use software such as Insight II (Accelrys Inc.), SYBYL (Tripos Inc.), MOE (Chemical Computing Group) or the like. On the other hand, For example, in latter process, well known technique such as Cavity search: an algorithm for the isolation and display of cavity-like binding regions, (Journal of Computer-Aided Molecular Design. 4(4): 337-54, 1990) or the like can be used, and it can be carried out using software such as SiteID (Tripos Inc.) or the like.

Once the binding site of compound in protein was able to be deduced, a compound which can be compatible to the deduced binding site is selected. As process to select this candidate compound, structural information of the compound is acquired from existing compound library, and bindable candidate compound is selected by comparing the structural information of compound in the library and structural information of the binding site deduced as above.

In a further embodiment, 1 or more residues of amino acid residues of amino acid sequence shown in Sequence Number 5 (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or pharmacophore of hydrogen bonding or hydrophobic properties or the like formed from the functional group of ligand in the complex, and also the protein surface produced from the protein structure or a structure in which the orientation of a part of the side chain thereof is modified, are used as search condition, and the conformation and orientation of each compound is systematically searched from the compound library, and whether the conditions are satisfied or not is judged and it is selected.

As an alternative process, while systematically searching the conformation and orientation of each compound from the compound library, the candidate compound is virtually docked with respect to the structure of ligand binding site constructed from the amino acid residues (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or a structure in which the orientation

of a part of the side chain thereof is modified, the species that formed interaction of close proximity of 4 Å or less with 1 or more residues of amino acid residues of amino acid sequence (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) is selected, or selection is carried out using energy evaluation function.

On the other hand, the candidate compound can also be selected by designing a bindable compound based on the structural information of the binding site deduced as above. In a further embodiment, each atomic species and functional groups are connected so that interactions are possible with respect to the structure of ligand binding site constructed from the amino acid residues (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or a structure in which the orientation of a part of the side chain thereof is modified, and thereby a chemical structure is constructed. As this process, a process wherein chemical groups such as methyl, ethyl and the like are arranged in the active site and a compatible compound is searched, and a process wherein atoms are bonded at active site using a computer program.

Moreover, with the process by energy evaluation using computer, for example a process to determine the bond energy of a compound and GK protein using molecular force field calculation is nominated. The calculation thereof is applied to each compound in database, and candidate compounds which can form stable binding are selected from the library compound. With some computer programs, such as Ludi of Insight II, when three-dimensional structural coordinates of interacting amino acid residues in the protein molecule are input, candidate of bindable compounds are automatically selected and output, and it can be suitably used.

Moreover, as far as the drug design on the basis of three-dimensional structure of molecule is concerned, many literature are known including development of pharmaceutical Vol. 7 "molecular design" (Hirokawa Shoten). In an embodiment, first, using flexible ligand binding simulation software such as for example FlexiDock, FlexX or the like, a library of low molecular (molecular weight 1000 or less) compounds (for example about 150000 species) can be screened with computer. For chemical compounds in this library, three-dimensional structure is built using a program such as CONCORD or the

like, and compounds compatible to the active site can be selected.

On the other hand, as a process of visual drug design, a drug design process characterised in including a binding site deduction step to deduce compound binding site of said protein based on aforesaid stereostructural information and a design step wherein the structure of the compound is visually designed so that aforesaid compound binding site deduced in aforesaid binding site deduction step and a compound compatible to said compound binding site can interact, is nominated. For example, structure assembly or structure modification is carried out with respect to the structure of ligand binding site constructed from the amino acid residues (tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459) or a structure in which the orientation of a part of the side chain thereof is modified, so that it can interact with 1 or 2 or more residues among these residues.

In an embodiment, with visual process, first, crystal structure of the complex of GK protein and a compound bound to this is displayed on a computer screen according to the obtained structural coordinates. And, while considering the chemical interaction, the binding possibilities of the compounds in the library and GK protein are successively examined on computer. Wherein, the chemical interactions to be considered are electrostatic interaction, hydrophobic interaction, hydrogen bonding, van der Waals interaction or the like. In other words, the structure in three dimensional space of said compound is generally considered whether a structure favourable for the interaction is formed or not, so that among the functional groups thereof, the groups likely to be negatively charged such as carboxyl group, nitro group, halogen group or the like interact with amino acid residues having positive charge such as lysine, arginine, histidine of GK protein, the groups likely to be positively charged such as amino group, imino group, guanidyl group or the like interact with amino acid residues having negative positive charge such as glutamic acid, aspartic acid of GK protein, hydrophobic functional groups such as aliphatic group and aromatic group interact with hydrophobic amino acid residues such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine, the groups which participate in hydrogen bond such as hydroxy group, amide group or the like can for hydrogen bonding with the main chain or side chain part of the GK protein, furthermore steric hindrance is not caused by the binding of said compound and GK protein, moreover, furthermore, the void part is filled so that the void part is eliminated as much as possible so that the van der Waals interaction is increased, or the like. In this way,

the factors such as electrostatic interaction, hydrophobic interaction, van der Waals interaction, hydrogen bond or the like are comprehensively considered visually on the computer screen, and finally, whether the candidate compound can bind to the GK protein or not is determined.

As program for selecting compound candidate by visual observation in this way, simulation programs such as Insight II and MOE or the like are exemplified. In order to generate promising candidate compounds that interact with GK protein, the candidate compounds are contacted with GK protein, and activity of GK protein is measured. In practice, the promising candidate compound is mixed with GK protein, crystallised, and whether it is compatible or not is evaluated. Further, more desirable structure is formed by modifying the compatible complex using organic synthesis.

Moreover, the visual technique and the technique that considers energy may be suitably combined, and used. As such computer software, flexiDock (Tripos Inc.), FlexX (Tripos Inc.), SYBYL (Tripos Inc.), Insight II (Accelrys Inc.), MOE (Chemical Computing Group Inc.) or the like are nominated.

Moreover, in accordance with this invention, the compounds selected by aforesaid drug design process are synthesized, and these compound groups can be provided as compound array (compound library). Because a large quantity of candidate compounds can be assayed at one time using a technique such as high through-put screening or the like, the inhibitor or activator of glucokinase can be screened with good efficiency.

(Compounds obtained by process of this invention and therapeutic agent including these)
The compounds designed by aforesaid drug design process have has ability to bind to glucokinase, therefore they can be used as activators of glucokinase or glucokinase inhibitors. Moreover, the therapeutic agent or medicinal composition containing such compound can be effectively used as therapeutic agent of disease involving glucokinase activity (for example diabetes mellitus therapeutic agent).

Aforesaid medicinal composition contains a compound that binds to glucokinase of this invention as effective ingredient in pharmacologically effective dose thereof together with suitable pharmacologically permitted support or diluent. As the pharmacologically acceptable support which can be used in aforesaid

medicinal composition (drug formulation), diluent such as filler, extender, binding agent, humectant, disintegrating agent, surface active agent, lubricant or the like which are conventionally used corresponding to the form of the formulation or excipient or the like are exemplified. These carriers can be suitably selected and used corresponding to administration unit form of the obtained formulation.

As administration unit form of medicinal composition of this invention, various forms can be selected according to therapeutic purpose, and, as representative examples thereof, solid administrative form such as tablet, pill, powder, powder agent, granule, encapsulated formulation or the like and liquid agent administrative form such as solution, suspending agent, emulsion, syrup, elixir or the like are included. Further these are classified into orally administered agent, aoral drug, transnasal agent, vaginal agent, suppository, sublingual agent, ointment or the like according to administration route, and it can be formulated, molded and prepared each according to conventional process. For example, when it is formed to a tablet form, excipient such as lactose, lactose, refined sugar, sodium chloride, glucose, urea, starch, calcium carbonate, kaolin, crystalline cellulose, silicic acid, potassium phosphate or the like, binding agent such as water, ethanol, propanol, simple syrup, glucose syrup, starch solution, gelatin solution, carboxymethylcellulose, hydroxypropylcellulose, methylcellulose, polyvinylpyrrolidone or the like, disintegrating agent such as carboxymethylcellulose sodium, carboxymethylcellulose calcium, low degree of substitution hydroxypropylcellulose, dried starch, sodium alginate, agar powder, laminaran powder, sodium bicarbonate, calcium carbonate or the like, surface active agent such as polyoxyethylene sorbitan fatty acid ester species, lauryl sodium sulfate, stearic acid monoglyceride or the like, disintegration inhibitor such as refined sugar, stearin, cacao butter, hydrogenation oil or the like, absorption accelerating agent such as quaternary ammonium base, sodium lauryl sulfate or the like, humectant such as glycerol, starch or the like, adsorbent such as starch, lactose, kaolin, bentonite, colloidal silica or the like, lubricant or the like such as purified talc, stearate, boric acid powder, polyethyleneglycol or the like can be used. Further, the tablet can be formed into a tablet coated with ordinary agent coating in accordance with requirements, for example sugar coated tablet, gelatin encapsulation tablet, enteric coated tablet, film coatings tablet and moreover can be made into double layer tablet or multilayer tablet.

When a form of pill is formed, as formulation carrier, for example, excipient such as glucose, lactose, starch, cacao butter, hardened vegetable oil, kaolin, talc or the like, binding agent such as powdered gum

arabic, tragacanth powder, gelatin, ethanol or the like, disintegrating agent or the like such as laminaran, agar or the like can be used.

For encapsulated formulation, effective ingredient of this invention is mixed with the various formulation carrier exemplified as above according to normal method, and it is prepared by being packed into hard gelatin capsule, soft capsule or the like.

The liquid administration form for oral administration includes pharmacologically permitted solution, emulsion, suspension, syrup, elixir or the like containing generally used inert diluent, for example water, and furthermore, auxiliary such as wetting agent, emulsion, suspending agent or the like can be contained, and these are prepared according to normal method.

For the preparation of liquid administrative form for aoral administration, for example, sterile aqueous or non-aqueous solution, emulsion, suspension or the like, as diluent, for example water, ethanol, propylene glycol, polyethyleneglycol, ethoxylation isostearyl alcohol, polyoxyisosteary alcohol, polyoxyethylene sorbitan fatty acid ester and vegetable oil or the like such as olive oil or the like can be used, and moreover, injectable organic ester species, for example, ethyl oleate or the like can be formulated. Further, ordinary solubilser, buffer agent, wetting agent, emulsifier, suspending agent, preservative, dispersant or the like can be added to these. Sterilisation can be carried out for example by filtration operation through bacteria retaining filter, formulation of fungicide, irradiation treatment and heat treatment or the like. Moreover, these can be prepared as sterile solid composition which can be dissolved in sterile water or suitable sterilisable vehicle immediately before the use.

When forming into a form of suppository or vaginal administration, as formulation carrier, for example polyethyleneglycol, cacao butter, higher alcohol, higher alcohol ester, gelatin and semi-synthetic glyceride or the like can be used.

When forming into a form ointment such as paste, cream, gel or the like, as diluent, for example white petrolatum, paraffin, glycerol, cellulose derivative, propylene glycol, polyethyleneglycol, silicon, bentonite and vegetable oil or the like such as olive oil or the like can be used.

A composition for transnasal or sublingual administration can be prepared according to conventional method using standard excipient.

Moreover, in agent of this invention, colorant, preservative, flavor, flavor agent, sweetener or the like or other pharmaceutical or the like can be contained in accordance with requirements.

The amount of the effective ingredient to be contained in the aforesaid drug formulation and dose thereof are not restricted in particular, and it is suitably selected from a wide range corresponding to the desired therapy effect, administration method, therapy period, age, sex of patient, other conditions or the like. In general, the dose is about 0.01 mg - 1000 mg, preferably about 1 mg - 100 mg per 60 kg in weight per day usually, and it can be administered once or divided into several times per day.

Sequence number of sequence table of this specification shows following sequence.

(Sequence number: 1).
Base sequence of DNA encoding human derived liver type glucokinase is shown.

(Sequence number: 2).
Amino acid sequence of human derived liver type glucokinase is shown.

(Sequence number: 3).
Amino acid sequence of human derived beta cell glucokinase is shown.

(Sequence number: 4).
Base sequence of DNA encoding the protein in which 11 amino acid residues at N terminal side of human derived liver type glucokinase are deleted, is shown.

(Sequence number: 5).
Amino acid sequence of the protein in which 11 amino acid residues at N terminal side of human derived liver type glucokinase are deleted, is shown.

**39**

(Sequence number: 6).

Base sequence of primer-1 used in PCR reaction in the following Example 1 is shown.


(Sequence number: 7).

Base sequence of primer-2 used in PCR reaction in the following Example 1 is shown.


(Sequence number: 8).

Amino acid sequence of the protein in which 15 amino acid residues at N terminal side of human derived liver type glucokinase are deleted, is shown.


(Sequence number: 9).

Base sequence of the primer used in PCR reaction in the following Example 6 is shown.


(Sequence number: 10).

Base sequence of the primer used in PCR reaction in the following Example 6 is shown.


**Examples**

Hereinafter, this invention will be described in concrete terms using Examples.


A process for purification of mutant type enzyme

In human glucokinase, there are liver type and pancreas type depending on the difference of promoter, and 15 residues at N terminal are different. In order to carry out crystallisation for the purpose of three-dimensional structure analysis, a mutant type enzyme which lacked a part or a whole of this region was made by the following process.


PCR reaction was carried out using cDNA of human liver type glucokinase cloned on pCR2.1 (made by INTROGEN Co.) and two kinds of primer sets, comprising

a combination of      5'-gtcacaaggagccagaagcttatggccttgactctggtag-3' (sequence number 6) and

                    5'-gaagccccacgacattgttcccttctgc-3 (sequence number 7), and

a combination of      5'-ccaggcccagacagccaagcttatggtagagcagatcc-3' (sequence number 9) and

                    5'-gaagccccacgacattgttcccttctgc 3' (sequence number 10).


                                 

The Hind III, Cla I fragment of the obtained PCR product was substituted with Hind III-Cla I region of liver type GK cloned at Hind III, Eco RI site of pFLAG/CTC vector (Eastman Kodak), and thereby cDNAs encoding mutant type GK (Δ1-11) which lacked 1-11 residues of liver type GK and mutant type GK (Δ1-15) which lacked 1-15 residues were obtained. The sequence of the obtained DNA was confirmed, and thereafter, these vectors were made as expression vectors, and Escherichia coli DH alpha strain (made by Takara Shuzo company) was transformed.

Transformant was cultured in LB medium at 37°C till the absorption at 600 nm became 0.8, and thereafter, isopropyl-1-thio-beta-D-galactoside (made by Wako Pure Chemicals Co.) was added so as to become the final concentration of 0.4 mM, and the protein production was induced at 25°C for 16 hours.

Cultured Escherichia coli was collected using centrifuge, and it was suspended in a buffer containing the following components (50 mM potassium phosphate (Potassium Phosphate) pH 7.5, 50 mM NaCl, 2 mM DTT, 0.5 mM Pefabloc SC (made by Kanto Chemicals Company), a proteinase inhibitor mixture (made by Roche Co.)) .

Collected Escherichia coli was pulverised by ultrasonic pulverisation method, and soluble fraction was dialysed against aforesaid buffer, and thereafter, it was purified using HiTrapQ column (made by Amersham Corp.). The GK fraction eluted from HiTrapQ column by potassium chloride gradient was diluted to a salt concentration of 50 mM by dilution.

The diluted GK fraction was purified by Glucosamin Sepharose column produced by a process demonstrated in the paper (Preparative Biochemistry, 20(2), 163-178 (1990)). The GK fraction was adsorbed onto Glucosamin Sepharose column, and impurity was eliminated with 100 mM sodium chloride, and thereafter, it was eluted by glucose of 1 M.

The eluted GK fraction was refined by MonoQ10/10 column. The GK fraction eluted from the MonoQ10/10 column (made by Amersham Corp.) by sodium chloride gradient was purified by Superdex 200 column (made by Amersham Corp.) using 50 mM Tris-Cl pH 7.2, 50 mM NaCl buffer as mobile layer.

Crystallisation process

Crystal of mutant type GK [Δ1-11] / glucose / compound complex

The crystal of mutant type GK (Δ1-11) / glucose / compound complex was obtained using a technique of the following vapor diffusion. Moreover, mutant type GK (Δ1-11) denotes a glucokinase containing amino acid sequence represented by Sequence Number 5.

In other words, mutant type GK purified to a high purity was concentrated, and finally a solution of mutant type GK of about 10 mg/ml (25 mM Tris-Cl, 50 mM NaCl, 5 mM TCEP) was formed. Thereto were added glucose of final concentration 20 mM and following compound 1 (compound of formula IIIa) which activates GK of final concentration 0.3 mM, and this was used for crystallisation. To protein solution 1-5 μl was added as crystallisation solution, an equal quantity of 28-30 % PEG 1500 and 0.1 M Hepes-NaOH (pH 6.6), and this solution formed by admixing was placed in a closed container containing 0.5-1 ml of crystallisation solution as that both solutions did not form contact, and the container was left to stand at 20°C. After standing for about 3 days - 1 months, crystals with maximum size of about 0.4 mm x 0.4 mm x 0.7 mm was obtained in the sample solution (Example 1).

Furthermore, the crystals obtained by aforesaid method were immersed for about 3-7 days in 28-80 % PEG 1500, 0.1 M HePes-NaOH (pH 6.6) solution so that the following compound 2 (compound represented by formula IIIb) was contained in a concentration of 0.3 mM, and thereby a complex crystals of the following compound 2 and aforesaid mutant type GK were obtained.

Compound 1



(IIIa)

Compound 2

(IIIb)
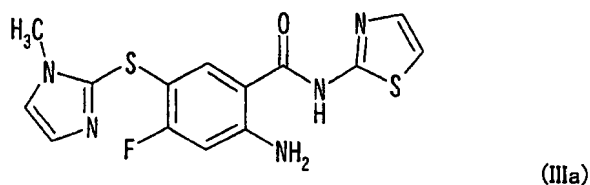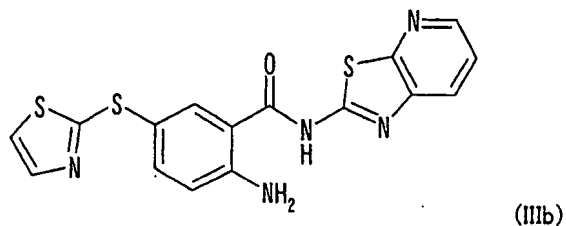
Moreover, crystallisation was carried out in the same way as in Example 1 except that compound 3 (compound represented by formula IIIc) was used in stead of aforesaid compound 1, and as a result, crystals were respectively obtained in the same way as in Example 1 (Example 3).

Compound 3



(IIIc)
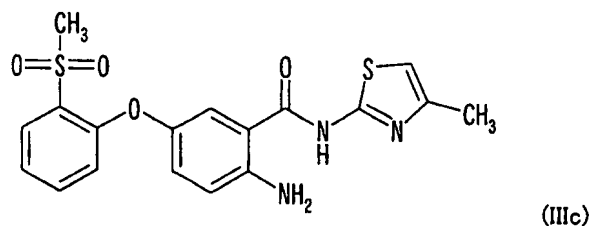
The obtained crystals were immersed into a crystallisation solution added with 10 % glycerol, thereafter it was rapidly frozen in liquid nitrogen. The X-ray diffraction data of the frozen crystal was collected in 100 K nitrogen gas stream by oscillation method at BL6B of synchrotron institution KEK-PF. From the obtained diffraction pattern, diffraction intensity was numerised using DENZO/SCALEPACK (made by HKL Co.), and crystal structure factor was determined. At this step, the crystal was found to be hexagonal system and had a space group of $P6_5 22$ or $P6_1 22$, and crystalline unit lattice was a = b = 79.9 angstrom, c = 322.2 angstrom, alpha = beta = 90°, gamma = 120°.

Using the obtained structure factor and three-dimensional structural coordinates of Human hexokinase type 1, the structure was analysed by molecular replacement method. Data with the resolution of 8 angstrom to 4 angstrom was used for the calculation, and it was performed by Amore program of CCP4 (Council for the Central laboratory of the Research Councils). The R factor of structure obtained by calculation was 53.7 %, and it was found that the space group of the crystal was $P6_5 22$ and a single molecule of mutant type GK was contained in asymmetrical unit. Electron density map was obtained

43

from this structure and structure factor, and the structure of mutant type glucokinase was determined using a program O (made by Dat-ONO Company).

Thereafter, refinement of the position of amino acid was carried out using CNX (Accelrys Inc.) and identification of amino acid residue was carried out using program O. This operation was repeated, and the structural coordinate of 448 amino acid residues from threonine 14 of the mutant type glucokinase to cysteine 461, 1 molecule of glucose molecule, 1 molecule of compound A, 1 sodium ion and 149 water molecules were identified, and the structural coordinates were determined. The R factor which is used as index of accuracy of finally determined structure was R = 23.2 % with respect to the data of resolution from 30 angstrom to 2.3 angstrom, and the R factor (Rfree) with respect to the data which was not used for the calculation in the refinement step of the structure was 27.4 %. There was no amino acid residue having the unacceptable structure by confirmation with Ramachandran plot.

The structure of the determined mutant type glucokinase was similar to the structure of the hexokinase which was isozyme, but the structure of the binding site of compound 1 (compound of formula IIIa) which activates glucokinase was different. This structural difference could not be expected with the ability of current computational chemistry and it became clear for the fist time by this structural analysis that this site was the binding site of activator and its detailed stereostructure. Figure 1a is ribbon diagram showing three-dimensional structure of the glucokinase elucidated here. As shown in Figure 1a, the newly found activator binding site was located between large domain and small domain, and it was about 20 angstrom away from the active center wherein glucokinase bonded with the substrate, glucose. The amino acid residue of glucokinase constituting the activator binding site was as follows. Tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459.

Moreover, the binding scheme of compound 1 (compound of formula IIIa) with respect to this binding site is shown in Figure 2 and the structure of binding site of glucokinase is shown in Figure 3. The thiazole ring formed van der Waals contact with each amino acid side chain molecule of valine 62, valine 452, valine 455, and moreover the nitrogen atom on thiazole ring was hydrogen bonded with nitrogen atom of main chain of arginine 63. The nitrogen atom of amide on compound 1 was hydrogen bonded with oxygen atom of main chain of arginine 63. Benzene ring part of compound 1 was formed van der

Waals contact with isoleucine 211, and the fluorine atom substituted to benzene ring formed van der Waals contacted with side chain of tyrosine 214. Aniline structure of compound 1 formed hydrogen bond with oxygen atom of side chain of tyrosine 215. Imidazole ring part bonded to the benzene ring via sulfur formed van der Waals contacted with amino acid side chain part of methionine 210, methionine 235, tyrosine 214. The serine 64-serine 69 part connecting the small domain and the large domain had a structure exposed to the solution, and compound 1 was bonded to the lower part of the arc-form structure formed by this part (Figure 3).

**Example 4**

Example of drug design

Using software UNITY (made by Tripos Company), pharmacophore of hydrogen bond acceptor and the hydrogen bond donor respectively generated from the main chain NH, CO of Arg 63, hydrophobic pharmacophore formed in the space corresponding to the phenyl group of aniline part of the ligand which formed the complex, and the protein surface formed on the basis of structure of the protein were used as search conditions, and Library compounds were screened, and the following compound 4 and compound 5 were obtained, and assay was carried out. As a result, activity of 780 % and 560 % was respectively observed. Wherein, the activity of 780 % denotes that the activity was enhanced upto 780 % by these compound when the activity of glucokinase of the control was 100 % (using glucose 2.5 M and ligand 10 µM).
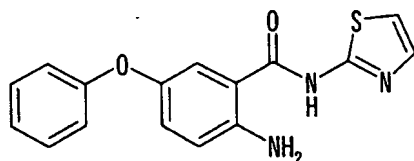
Compound 4



Activity: 780 %

Compound 5
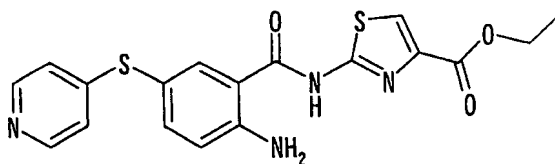


Activity: 560 %

**Example 5**

Crystal of mutant type GK (Δ1-15)

The crystal of simple substance of mutant type GK (Δ1-15) (glucokinase containing amino acid sequence represented by Sequence Number 8) was obtained using the following vapor diffusion technique.

In other words, mutant type GK purified to a high purity was concentrated, and finally a solution of mutant type GK of about 10 mg/ml (25 mM Tris-Cl pH 7.2, 50 mM NaCl, 5 mM TCEP) was formed. To protein solution 1-5 µl was added an equal quantity of crystallisation solution (1.5-1.6 M ammonium sulfate, 50 mM NaCl, 0.1 M Bicine NaOH (pH 8.7)), and this solution formed by admixing was placed in a closed container containing 0.5-1 ml of crystallisation solution as that both solutions did not form contact, and the container was left to stand at 20°C. After standing for about 3 days - 1 months, crystals with maximum size of about 0.07 mm x 0.07 mm x 0.5 mm was obtained in the sample solution.

The obtained crystals were immersed into the crystallisation solution added with 20 % glycerol, and continuing it was frozen rapidly in liquid nitrogen. The X-ray diffraction data of the frozen crystal were collected by oscillation method in 100K nitrogen gas stream at BL32B2 of synchrotron institution Spring-8. From the obtained diffraction image, the diffraction intensity was numerised using Mosflm, and crystal structure factor was determined. At this step, it became clear that the crystal was hexagonal system and had space group of $P6_522$ or $P6_122$, and crystal unit lattice was a = b = 103.2 angstrom, c = 281.0 angstrom, alpha = beta = 90°, gamma = 120°.

Next, molecular replacement method was carried out using the obtained structure factor and structure was analyzed. As model of stereostructure, three-dimensional structural coordinates of each domain of glucokinase determined from the mutant type GK (Δ1-11) / glucose / compound complex crystal was separately used. The calculation was performed by Amore program of CCP4 (Council for the Central laboratory of the Research Councils) using data of resolution of 8-4 angstrom. It was found that the space group of the crystal was $P6_522$, and a single molecule of mutant type GK (Δ1-15) was contained in the asymmetrical unit. Electron density map was obtained from this structure and structure factor, and the structure of mutant type GK (Δ1-15) simple substance was determined using program O (made by Dat-ONO Company).

Next, refinement of position of amino acid was carried out using CNX (made by Molecular Simulation Company) and identification of amino acid residue was carried out using program O. This operation was carried out repeatedly, and the structure coordinate of 424 amino acid residues from asparagine 180 to cysteine 461 and from methionine 15 to histidine 156 of mutant type glucokinase, and 2 molecules of sulfate ions, 1 sodium ion and 7 water molecules were identified, and the structural coordinates were determined. The R factor which is used as index of accuracy of finally determined structure was R = 23.8 % with respect to data of resolution of 50-3.4 angstrom, and the R factor (Rfree) with respect to the data which was not used for the calculation in the refinement step of structure was 30.6 %. There was no amino acid residue having the unacceptable structure by confirmation with Ramachandran plot.

The ribbon diagram showing the structure of glucokinase (Δ1-11) / glucose / compound 1 and the ribbon diagram showing the structure of glucokinase (Δ1-15) simple substance are respectively shown in Figure 1a and Figure 1b. Moreover, the figure on the right is a rotated figure of the figure on the left. In the structure of determined mutant type GK (Δ1-15) simple substance, the structures of main parts of the large domain and the small domain were similar to the respective structures of glucokinase determined by mutant type GK (Δ1-11) / glucose / compound complex crystal, but relative position of two domains was greatly different. In mutant type GK (Δ1-15) simple substance structure, the main part of the small domain was rotated by about 99 degrees from position of small domain in mutant type GK (Δ1-11) / glucose / compound complex structure. Moreover, alpha 13 helix located at C terminal region of glucokinase which constituted the small domain in the mutant type GK (Δ1-11) / glucose / compound complex structure no longer constituted the small domain in the mutant type GK (Δ1-15) simple substance structure, and it was located at between two domains. Moreover, because both the activator binding site and binding site of substrate, glucose were present between two domains in the mutant type GK (Δ1-11) / glucose / compound complex structure, the structures of their sites were greatly changed in the newly determined structure. The amino acid residues that play an important role in enzyme activity did not form active site in the mutant type GK (Δ1-15) simple substance structure, and the structure of mutant type GK (Δ1-15) simple substance analysed here was a structure of inactive state of glucokinase. Moreover, the activator binding site had completely disappeared in the structure of mutant type GK (Δ1-15) simple substance. The structural change of glucokinase (rotation of domains about 99°) observed by the mutant type GK (Δ1-11) / glucose / compound complex structure and the mutant type GK (Δ1-15)

simple substance structure was far greater compared with the previously known structural change of hexokinase (rotation of domains about 12°), and it could not be expected with the ability of current computational chemistry and it became clear from this structure analysis for the first time.

Moreover, in order to hinder the structural change to the inactive form mutant type GK (Δ1-15) simple substance structure, by designing a compound that binds to the compound binding site indicated by the mutant type GK (Δ1-11) / glucose / compound complex structure, it became clear that activator of glucokinase could be designed.

## Possible Applications in Industry

As described above, in accordance with this invention, crystal of the glucokinase protein which was difficult to crystallise in the prior art was obtained. The three-dimensional structural coordinates obtained by analysing this crystal structure can be suitably used in order to design compounds that bind to glucokinase. Moreover, because the compounds designed in this way bind to glucokinase, they can be used as therapeutic agent of disease involving the glucokinase activity (for example diabetes mellitus therapeutic agent) as glucokinase activator or inhibitor.

## Patent Claims

1. A glucokinase protein characterised in being used for crystallisation.

2. A protein in accordance with Claim 1 comprising amino acid sequence in accordance with Sequence Number 5.

3. A crystal of protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof.

4. A crystal in accordance with Claim 3, wherein the said protein is glucokinase protein.

5. A crystal in accordance with Claim 3 comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 5.

6. A crystal in accordance with Claim 3, wherein the lattice constant satisfies the following equations (1)-(4)

$$a = b = 79.9 +/- 4 \text{ Å} \qquad (1)$$

$$c = 322.2 +/- 15 \text{ Å} \qquad (2)$$

$$\text{alpha} = \text{beta} = 90° \qquad (3)$$

$$\text{gamma} = 120° \qquad (4)$$

7. A crystal in accordance with Claim 6, wherein the space group is $P6_522$.

8. A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 1.

9. A crystal wherein in three-dimensional structure coordinates data changed in at least one data of three-dimensional structure coordinates data in accordance with Table 1, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance with Table 1 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.
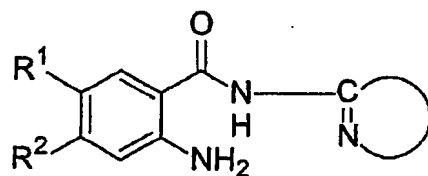
10. A crystal in accordance with any of Claims 3-9, wherein the compound binding site is constructed by at least one of amino acid residues of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.

11. A crystal including a complex of the protein comprising amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and a compound which can bind to the said protein.

12. A crystal in accordance with Claim 11, wherein aforesaid compound is represented by formula (1).
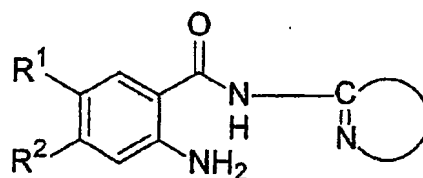
**(I)**

[wherein, R1 shows halogen atom, -S-(O)p-A, -S-(O)q-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and

**(II)**

denotes an optionally substituted monocyclic or bicyclic heteroaryl group having a nitrogen atom adjacent to the carbon atom bonded to amide group].

13. A crystal in accordance with Claim 12, wherein aforesaid compound is any of the compound represented by formula (IIIa)-(IIIc).
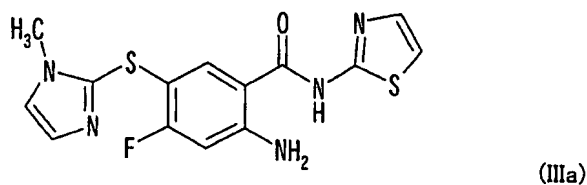
(IIIa)

(IIIb)

(IIIc)
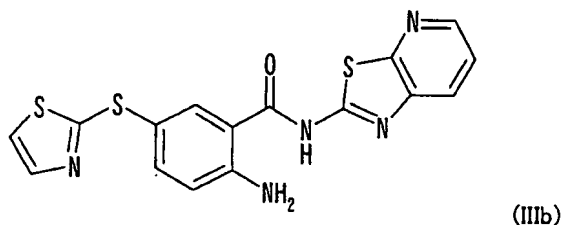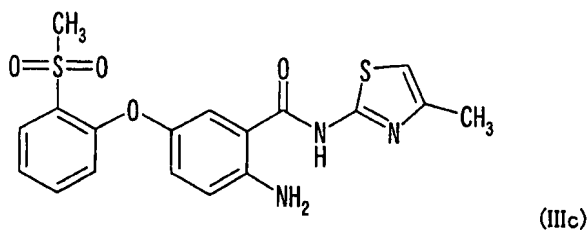
14. A protein in accordance with Claim 1 comprising amino acid sequence in accordance with Sequence Number 8.

15. A crystal of protein comprising amino acid sequence in accordance with Sequence Number 8 or amino acid sequence substantially the same amino acid sequence thereof.

16. A crystal in accordance with Claim 15, wherein the said protein is glucokinase protein.

17. A crystal in accordance with Claim 15 comprising crystals of protein containing amino acid sequence in accordance with Sequence Number 8.

18. A crystal in accordance with Claim 15, wherein the lattice constant satisfies the following equations

$a = b = 103.2 +/- 5 Å$      (5)

$c = 281.0 +/- 7 Å$      (6)

$alpha = beta = 90°$      (7)

$gamma = 120°$      (8)

19. A crystal in accordance with Claim 18, wherein the space group is $P6_522$.

20. A crystal of protein specified by three-dimensional structure coordinates data in accordance with Table 2.

21. A crystal wherein in three-dimensional structure coordinates data changed at least one data of three-dimensional structure coordinates data in accordance with Table 2, the mean square error between atoms of main chain of amino acid represented by three-dimensional structure coordinates data in accordance

with Table 2 (C alpha atom) and C alpha atoms represented by the said changed three-dimensional structure coordinates data corresponding to aforesaid C alpha atoms is 0.6 Å or less.

22. A process for the production of crystal containing a complex of protein and a compound that binds to the protein thereof, including

a protein production step wherein a protein containing the amino acid sequence having deletion of 1-50 amino acid residues from either or both of N terminal and C terminal of the protein containing amino acid sequence in accordance with Sequence Number 2 is produced, and

a protein reaction step wherein a compound that binds to the protein obtained in the said protein production step and the protein obtained in the said protein production step are reacted.

23. A process to produce crystal of the kind wherein a crystal of a protein is produced, characterised in that a protein including amino acid sequence in accordance with Sequence Number 5 or amino acid sequence substantially the same amino acid sequence thereof and having glucokinase activity and a compound which can bind to the said protein are used.

24. A process for the production of crystalline protein in accordance with Claim 23, wherein the compound which can bind to said protein is a compound represented by formula (1).



**(I)**

[wherein, R1 shows halogen atom, -S-(O)p-A, -S-(O)q-B or -O-B (wherein, p and q are the same or different and denote an integer of 0-2, A denotes C1-C6 alkyl group of optionally substituted straight chain, B denotes optionally substituted five-membered or six-membered ring aryl group or heteroaryl group, R2 denotes a hydrogen atom or halogen atom, and

(II)

denotes an optionally substituted monocyclic or bicyclic heteroaryl group containing nitrogen atom adjacent to the carbon atom bonded to amide group].

25. A process for the production of crystal in accordance with Claim 23 or 24 using co-crystallisation or soaking method

26. A drug design method of the kind wherein based on stereostructural information of a protein, the structure of compound that binds to said protein is designed, characterised in that the stereostructure information of said protein is the information obtained by analysing crystal in accordance with any of Claims 3-13 or 15-21.

27. A drug design method in accordance with Claim 26 characterised in that
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and
a selection step wherein a compound compatible to the compound binding site deduced in aforesaid binding site deduction step is selected from compound library,
are included.

28. A drug design method in accordance with Claim 26 characterised in that
a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and
a compound structure assembly step wherein the structure of compound compatible to compound binding site deduced in aforesaid binding site deduction step is constructed,
are included.

29. A drug design method in accordance with Claim 26 characterised in that

a binding site deduction step wherein the compound binding site of said protein is deduced based on aforesaid stereostructure information, and

a design step wherein the structure of compound is designed by visual observation so that the compound binding site deduced in aforesaid binding site deduction step and a compound compatible to said compound binding site interact,

are included.

30. A drug design method in accordance with any of Claims 26-29, wherein aforesaid compound binding site is constituted by at least one of amino acid residue of tyrosine 61 - serine 69, glutamic acid 96 - glutamine 98, isoleucine 159, methionine 210 - tyrosine 215, histidine 218 - glutamic acid 221, methionine 235, arginine 250, leucine 451 - lysine 459 in amino acid sequence shown in sequence Number 5.

31. A drug design method in accordance with any of Claims 26-30 further including a step to measure physiological activity of the candidate compound predicted to be compatible to aforesaid compound binding site.

32. A drug design method in accordance with any of Claims 26-30 further including a binding determination step wherein the candidate compound predicted to be compatible to aforesaid compound binding site and a protein including amino acid sequence in accordance with and Sequence Number 5 or amino acid sequence which is substantially the same amino acid sequence thereof are contacted, and whether the candidate compound binds to the said protein or not is assessed.

33. A process for the production of compound array including the compound group selected by drug design method in accordance with any of Claims 26-30 is combined as compound array.

WO03/97824

Rising Sun Communications Ltd. Terms and Conditions

Rising Sun Communications Ltd. shall not in any circumstances be liable or responsible for the accuracy or completeness of any translation unless such an undertaking has been given and authorised by Rising Sun Communications Ltd. in writing beforehand. More particularly, Rising Sun Communications Ltd. shall not in any circumstances be liable for any direct, indirect, consequential or financial loss or loss of profit resulting directly or indirectly from the use of any translation or consultation services by the customer.

Rising Sun Communications Ltd. retains the copyright to all of its' translation products unless expressly agreed in writing to the contrary. The original buyer is permitted to reproduce copies of a translation for their own corporate use at the site of purchase, however publication in written or electronic format for resale or other dissemination to a wider audience is strictly forbidden unless by prior written agreement.